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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

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/SIDS2/gcgdata/geneseq/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	BIG	ID	Description
ב	1670	100.0	į	22	AAB20106	Moraxella catarrha
N	1666	99.8	322	22	AAB20107	Moraxella catarrha
ω	209	12.5		21	AAB21225	Haemophilus somnus
4	203	12.2		21	AAY74313	Neisseria meningit
v	200	12.0		21	AAY74311	Neisseria gonorrhe
6	198	11.9		21	AAY74312	Neisseria meningit
7	158.5	9.5		23	ABB48721	Listeria monocytog
8	151.5	9.1		14	AAR45178	Listeria p60 prote
9	146.5	8.8		23	ABB53578	Lactococcus lactis
10	146.5	8.8		23	ABB48659	Listeria monocytog

ALIGNMENTS

DR XX	Pi	PA	PR A	g gg	18	Y P	E X	길 꾼	χç	3 ≵	3	Ž	DE XX	ဌ	×	ΑX	RESULT 1 AAB20106 ID AAB;
WET; 2001-112459/12. N-PSDB; AAF30046.	Thonnard J;	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.	25-JUN-1999; 99GB-0015031.	23-JUN-2000; 2000WO-EP05854.	04-JAN-2001.	WO200100838-A1.		Key Location/Qualifiers	MOIAXELIA CACAILHAILB.		antibacterial; antimicrobial; vaccine.	DECEMBER OF A STATE OF	Moraxella catarrhalis BASB110 protein.	23-APR-2001 (first entry)		AAB20106;	LT 1 0106 AAB20106 standard; Protein; 322 AA.

duct"

Claim 1; Page 82-83; 88pp; English.

X##X#XX88888888888888888888888888888

Matches

al Similarity 322; Conser

llarity 100.0%; Conservative 0

0;

Query Match Best Local (

Sequence

322 AA;

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The present sequence is that of BASBIIO protein from Moraxella CC catarrhalis strain Mc2931 (APCC 43617), a causative agent of otitis CC media in children and pneumonia in adults. The sequence is CC differs by 1 residue from the predicted polypeptide sequence (see AB20107) of a BASBIIO per product, having Ser rather than Gly at CC polymucleotides encoding them, as well as expression vectors, host CC cells and methods for producing BASBIIO polypeptides using CC recombinant methods. Also claimed is a vaccine composition and CC comprising a BASBIIO polypeptide, an immunogenic frament of a cid sequence identity to BASBIIO, or comprising at least 85% amino CC moraxella infection involves identifying a BASBIIO polypeptide or a cid sequence identity to BASBIIO, or comprising a polymetide composition comprising such a polypeptide. A claimed method of diagnosing a cc matibody. A claimed therapeutic composition useful in treating them the composition useful in catarrhalis infection comprises at least 1 antibody antibody antibody and sequence antibody. A claimed therapeutic composition useful in treating control of the composition useful in treating that useful in reating section useful in treating antibody antibody and section comprises at least 1 antibody antibodies also composition useful in treating that useful in treating section useful in treating section useful in treating that useful in treating section composition useful in treating composition useful in treating section composition and section antibody antibodies, and in screening for antibodies.
                                                                                                                                                                                                                      BASB110; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial; vaccine.
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Pred. No. 5.2e-134;
D; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of BASB110 protein from Moraxella CC Catarrhalds strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The sequence is a creative form of a BASB10 pCR product. The sequence is a constitute from the predicted polypeptide sequence (see AAB2016) of CC 104. The invention provides BASB10 pCR product because than Ser at posttion cells and methods for producting BASB10 polypeptides, and cclaimed them, as well as expression vectors, host CC polynucleotides encoding them, as well as expression vectors, host CC comprising a BASB110 polypeptide, an immunogenic fragment of a comprising a BASB110 polypeptide, an immunogenic fragment of a caid sequence identity to BASB10, or comprising a polynucleotide composition and infection involves identifying a BASB10 polypeptide or CC Moraxella infection involves identifying a BASB10 polypeptide or CC directed against a BASB110 polypeptide or CC directed against a BASB110 polypeptide. A claimed method of diagnosing a contibody. A claimed therapeutic composition useful in treating cCC directed against a BASB110 polypeptide. BASB110 polypeptide or CC directed against a BASB110 polypeptide. BASB110 polypeptide or CC directed against a BASB110 polypeptide. BASB110 polypeptide or CC directed against a BASB110 polypeptide. BASB110 polypeptide also composition antibody continued the composition and composition and composition and composition as a continued composition and composition composition composition and composition composition composition and composition composition and composition compo
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301 AALFEFRISRNGVYVDPLTVLK 322
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N-PSDB; AAF30047.
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSGYTIYTGQWLTLWSGDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWRBIGHINNLNSSYTIYTGQWLTLWSGDL 120
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                                                                              ASNAGTVÍQADHNHDGASÍVÍQHTNGFVSSYÍHÍKDÁQVKTGDTVRTGQRÍASHKNQÞSG 300
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21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.8%; Score 1666; DB 22; Length 322; 99.7%; Pred. No. 1.1e-133; tive 0; Mismatches 1; Indels 0
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RESULT 2
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23-APR-2001

AAB20107 standard; Protein; 322

Moraxella catarrhalis BASB110 protein.

(first entry)

Moraxella catarrhalis

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AALFEFRISRNGVYVDPLTVLK 322 AALFEFRISRNGVYVDPLTVLK 322

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                                                                                                                                                                                                                                                           The present sequence is the Haemophilus somnus lipoprotein LppB.

Recombinant vaccines containing H. somnus lipoproteins LppA, LppB
and LppC have been described. H. somnus transferrin-binding proteins Tbpl
and Tbp2 have also been found to be effective in vaccines against
cand Tbp2 have also been found to be effective in vaccines against
containing a genomic expression library of H. somnus strain HS25 in
containing a genomic expression library of H. somnus strain HS25 in
containing a genomic expression library of H. somnus strain HS25 in
containing a genomic expression library of H. somnus strain HS25 in
containing encount antiserum raised against affinity-purified Tbp1
and Tbp2 of H. somnus. The genes coding for Tbp1 and Tbp2 were obtained
by inverse PCR. The nucleotide sequence encoding Tbp1 and Tbp2 may be
used for the recombinant production of Tbp1 and Tbp2, which may then be
used to manufacture vaccine compositions for immunising against H. somnus
infections. The antibodies raised against the transferrin binding
proteins may also be used diagnostically to identify the presence of
the somnus infections. H. somnus is a pathological Gram-negative bacteria
that causes a number of diseases in cattle such as thromboembolic
meningencephalitis (ITEME), myocarditis, septicaemia, arthritis and
                                                                                                                                            Matches
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 11; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myocarditis and pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding Haemophilus somnus transferrin binding proteins useful for vaccinating against and diagnosing H. somnus infections e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-565601/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potter AA,
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24-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus somnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis; pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus somnus; lipoprotein B; lppB; transferrin-binding protein; tbp; antibacterial; vaccine; infection; tbromboembolic meningoencephalitis; ITEME; myocarditis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB21225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB21225 standard; Protein; 345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
180
                                                                                                     73
                                                                                                                                          63;
                                                                                                                                                           Similarity
                                                             YKVRKGDTMFLIAYISGMDIKELATLNNMSEPYHLSIGQVLKIANNIPDSNMIPTQTINE
SEVTQNTVNE-TWNANKPTNEQMKPVATPTHSTMPINK---TPPATSNIAWIWP-----
                               GVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAP
                                                                                                     YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSG----DLKVRERSISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                                                                                               345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rioux C,
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          somnus LppB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0267749
99US-0405728
                                                                                                                                                         12.5%; Score 209; DB 21; 24.8%; Pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schryvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in cattle
                                                                                                                                        49;
                                                                                                                                     Mismatches
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                                                                                                                                        106;
                                                                                                                                                                        Length 345;
                                                                                                                                      Indels
                                                                                                                                        36;
                                                                                                                                     Сарв
                                                                                                       129
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Fraser C, tersen J, F
                                                          represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be treated to the presence of Neisseria bacteria, or to raise antibodies.
be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invent may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                              Novel Neisserial polypeptides predicted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis ORF 025 protein sequence SEQ ID NO:112-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY74313 standard; Protein; 414
                                                                                                                                                                                                                                                                             AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                        Claim 2; Page 207; 1453pp;
                                                                                                                                                                                                                                                                                                                                                                           vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-1998;
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)B; AAZ53075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIRON CORP.
INST GENOMIC
                                                                                                                                                                                                                                                                                                                                                                         and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFR
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, Pizza M, Rappuoli
, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                         diagnostics
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98US-0099062.
98US-0103749.
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99US-0121528
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Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                           English.
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Ratti
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                                                                                                                                                                                                                                                                                                                                                                                                 be useful antigens
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meningitis;
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Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                        Fraser C, G
Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                               09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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                                               Novel Neisserial polypeptides predicted vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septiantibacterial; gene therapy.
Claim 2; Page 206- ; 1453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrheae ORF 025 protein sequence SEQ ID NO:118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY74311 standard; Protein; 337 AA
                                                                                                                     2000-062150/05.
DB; AAZ53073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                       CHIRON CORP.
INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAHTPSPVAVQSSRPPVQQHPAVQKPTPVVVVKKPTPTPVVQQPAPVAP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EASRTQLHFEVRQNGKPVNP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAAADGKVVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPOSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG-----NNKGVDIAGNAGQPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVTEAPFA----TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PKAAAVK-SRPAVP--AAVQTPV-----KPAAQPPVQSAPQPAAPAAENKAVPA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSGAALFEFRISRNGVYVDP
                                                                                                                                                                                        Galeotti C, Grandi G, Pizza M, Rappuoli R, Venter JC;
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                                                                                                                                                                                                                                                                                                                                                            98US-0093158.
98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
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; Pred. No. 5.8e-09;
42; Mismatches 97;
                                                                                                                                                                                                                    Hickey
Ratti
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                                                                     þe
                                                                     useful antigens
                                                                                                                                                                                                                 Masignani V, Mora M;
Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  septicaemia;
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Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gomorrheae polynucleotides and polypeptides. AAZ54573 to AAZ54576 and AAZ545616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic resegents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria (e.g. meningitis and septicaemia), to detect the be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
320
                                306
                                                                        260
                                                                                                             248
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                                                                                                                                                                                      189
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                                                                                                                                                                                                                                                              133
                                                                                                                                                                                                                                                                                                 105 HTIVRGDTVYNISKRYHISQDDFRAWNGMTDN-TLSIGQ-----IVKVKPAGYAAPKT 156
                                                                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                              SPSGTRSVGGIVWQRP--TQGKVVADFGGG-----NKGVDIAGNAGQPVLAAADGKV
                                                                                                                                                                                                                                                        TAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQ----PAPVAPPVTEA-
FEVRONGKPVNP 331
                                FRISRNGVYVDP 317
                                                                                                         IQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFE
                                                                                                                                                                                 -PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTV
                                                                                                                                                                                                                           AAVESRPAVPAAAQTPVK--PAAQPP-----VQSAPQPAAPAAENKAVPAPAPAPQSPAA 209
                                                                      VYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDASRTQLH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 AA;
                                                                                                                                                                                                                                                                                                                                                                          12.0%; Score 200; DB 21; ilarity 26.2%; Pred. No. 8e-09; Conservative 45; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                              109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 337;
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                                                                                                             305
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AAY74312 standard; Protein; 351 AA

AAY74312;

21-MAR-2000 (first entry)

Neisseria meningitidis ORF 025 protein sequence SEQ ID NO:110-1.

Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.

Neisseria meningitidis.

WO9957280-A2.

11-NOV-1999.

RESULT 6
AAY74312
ID AAY7
XX XX
AC AAX7
XX Neis
XX Nei 30-APR-1999; 99WO-US09346

01-MAY-1998; 31-JUL-1998; 02-SEP-1998; 02-SEP-1998; 09-OCT-1998; 09-OCT-1998; 09-OCT-1998; 09-OCT-1998; 25-FEB-1999; 98US-0083758. 98US-0094869. 98US-00998994. 98US-0099062. 98US-0103794. 98US-0103794. 98US-0103796.

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Best Local &
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                                                                      Antibacterial; gene therapy; vaccine; blosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
                                                                                                                  Listeria monocytogenes protein #1425
                                                                                                                                                 05-FEB-2002
                                                                                                                                                                                                             ABB48721 standard; Protein; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-062150/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petersen J, Pizza M,
Tettelin H, Venter JC;
                                          Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                        211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                   SMKNQPSGAALFEFRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                          DGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIA
                                                                                                                                                                                                                                                                                                                                                                                                         KAVPAPAPQSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG------NNKGVDIAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PVTEAPFA----TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKVKPAGYAAPKTAAVESRPAVP---AAVQTPV-----KPAAQPPVQSAPQPAAPAAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---VNTAHTPSP-VAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTIVRGDTVYNISKRY-----HISQDD-----FRAWNG---MTDNMLSIGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 206; 1453pp; English
                                                                                                                                                                                                                                                                                       LMGNTDASRTQLHFEVRQNGKPVNP 345
                                                                                                                                                                                                                                                                                                                                              AGQPVLAAADGKVVYAGSGLRGYGNLVI IQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%;
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Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 198; DB 21;
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hickey
Ratti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95;
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Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments it are useful for selecting probes and primers for detecting genes in monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maduenio E, De Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, an for biosynthesis and biodegradation, especially biosynthesis of Vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence for Listeria monocytogenes, useful e.g. and prevention of Listeria and related bacterial infectic related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchrieser C, Frangeul I, Couve E, Rusniok C, Feihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N; Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N; Madduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                          301
408
                                                                                                                                                                                                  196
                                                                                                                                                                                                                                          255
                                                                                                                                                                                                                                                                             136 TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSS 195
                                                                                                                                                                                                                                                                                                                                                           76 KQGDTYSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH 135
                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
66; Conserv
                                                                                                                   NAGTVIQADHNMDGAS-----IVIQHTNGFVSSYIHIKDAQVK--TGDTVRTGQRIAS
MGSTGQSTGQHL-HFEIHKNGIPVDP 432
                                                                                                                                                                                                  GVMQFRYPVGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 1426; 192pp;
                                   M--KNOPSGAALFEFRISRNGVYVDP 317
                                                                             ASGTVVFSGFGASGSGFGGYGYVVKIDHGNGFQTLYGHMRAGSLKVVTGQQVSQGQPIGI
                                                                                                                                                          GGGQFIKPASGILTSGFSERTNPVTGKYESHKGQDIAGGGTVT
                                                                                                                                                                                                                                      AKQEAAIKAAEEKRMQEAAAASSAKSAAVVK-----
                                                                                                                                                                                                                                                                                                                     EKNDLVMALANKKDLT------KSEQTLLASE-----QGALTDEEKRLASNIAGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000FR-0004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                     9.5%;
                                                                                                                                                                                              -----TNPVVRRF----GTATVAGSTVTSNGMWFSGRDGDLINAS 242
                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158.5; DB:
Pred. No: 3.8e-05
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial infections,
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                                                                                                                                                                                                                                          - QPSSSSNEATE --- TVSS
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                                                                                                                                                                                                                                                                                                                                                                                                     67;
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, Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F G
                                                                                                                                                            347
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RESULT 8 AAR45178

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of the Listeria p60 protein. Antibodies generated against the protein can be used in the detection of Listeria by immunoassay (partic. ELISA). The detection method allows determination of individual Listeria species, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 4; 19pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New primers for PCR detection of Listeria - including individual speciles, also new peptide(s) for raising antibodies for immunochemical detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-406956/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schubert P, Neumann S, Pawelzik M, Linxweiler W,
Hofmann G, Bubert A, Goebel W, Koehler B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1992;
25-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic polypeptide; antibodies; immunoassay; conjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria p60 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR45178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR45178 standard; Protein; 478
           431
                               289
                                                       374
                                                                                                                                                 150 QQHPAVQKPTPPVV-----APFATG
                                                                                                                                                                                           220
                                                                                                                                                                                                                  160 TTQQAAPVAETKTEVKQTTQATTPAPKVAETKETPVIDQNATTHAVKSGDTIWALSVKYG
                                                                                                                                                                                                                                                               102 írtsíkgá--tkvtvettesnöwhkityndöktgfvngkyltdkavstþvaþtgevkket
                                                                                                                                                                                                                                        66 --SQGVP-----PRYOYKQGDTVSKIAQRYG
                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                    25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITP-----------
                   QRIASMKNQPSGAALFEF--RISRNGVYV 315
                                                                                                                                                                                                                                                                                                                                83;
                                   LGKAYSWGGNGPTTFDCSGYTKYVFAKAGISLPRTSGAQYASTTRISESQAKPGDLV---
                                                                               nanktintnitnitnitnesknitninsnitnitnsnitnanogssinnisnssasai i aeaokh
                                                                                                    SSGVMQERYEVGATNEVVRREGTATVAGSTVTSNGMWESGRDGDLINASNAGTVIQADHN 253
                                                                                                                          - EAPÄAEKQAAPVVKENTNTNTATTEKKETATQ----QQTÄPKÄP--TEAAKPAPÄPSTNT 313
                                                                                                                                                                       VSVQD MSWNVLSSS-SIYVGQKLAI-------KQTANTATEKAEVKT----
                                                                                                                                                                                            LNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVNTAHTESPVAVQSSRPPV 149
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                        478 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92DE-4219111.
92DE-4239567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93DE-4318450.
---FFDYGSGİSHVĞIYV 445
                                                                                                                                                                                                                                                                                                                    9.1%; Scu
21.3%; Pre
1ve 46;
                                                        ------GASIVIQHTNGF-VSSYIHIKDAQVKTGDTVRTG 288
                                                                                                                                                                                                                                                                                                          Score 151.5; DB 14; Length 478;
Pred. No. 0.0017;
6; Mismatches 117; Indels 143; Gaps
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                                                                                                                                                                                                                                                             Query Match :
Best Local Si
Matches 69;
                                                                                                                                                                                                                                                                                                             The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB5621). The nucleic acid sequence is useful in the detection and/or amplification of related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The production helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID No 280; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequence useful in the identification lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolotine A, Sorokine A, Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR~2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis protein acmA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB53578 standard; Protein; 439
                   383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB53578;
                      249 QADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTV-----RTGQRIASMK 295
                                                                  337
                                                                                                                                       133
                                                                                                                                            243 YTVKSGDTLWGISQKYGISVAQIQSANNLKST-VIYIGQKLVLTTSSSSSSNTNSSTSSGN
                                                                                                                                                                                                                184
                                                                                                                                                                                        73
                                                                                                                                                                                                                   26 TTCILAGCASKPTYNST------SGSGSHRTSGSGGLAIGSQVITDSQGVPNR 72
                                                                                                                                                                                                                                                            l Similarity
69; Conserv
       SSTSNSSAAS-----NTSIH---
                                                   KYKTTIAQLKSWNHLNSDTIFIGQNLIVSQSÅGSSSSSTG
                                                                     PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI 248
                                                                                                                   TAHŢPSPVAVQSSRÞPVQQHPAVQKPTPPVVVVKKPŢPTPPVVQQPAPVAPPVŢ----EA 188
                                                                                                             SAGTTTPTT----
                                                                                                                                                                YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                            TAALTGKYÁTDÁNÝGASLNRI ISQYNLTRFDGÁSSAGTSNSGG-STATNTNNNSNTSSTT
                                                                                                                                                                                                                                                                                                           439 AA;
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                8.8%; Score 146.5; DB 23; 23.6%; Pred. No. 0.00041; tive 39; Mismatches 107;
                                                                                             -----SVTPAKPASQTTIKVKSGDTLWGLSV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
-KVVKGDTLWGLSQKSGSPIASIK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrlich SD;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                        Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or Lactococcus
                                                                                                                                                                                                                                               77;
                                                                                                                                                                                                                                               Gaps
                                               382
                                                                                                                                             301
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ARBSULT 10
ABB48
XX ABB48
XX ABB48
XX D5-FE
XX D7 05-FE
XX Antib
KW Vitam
XX W0200
XX Liste
XX W0200
XX Iste
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                                                                                                                                                                                                                                                                                                                                                                                                                                  monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. comproytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.
                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides -
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                    specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID No 1364; 192pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perez-Diaz J, I
Maduenio B, De
Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-0004629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dominguez-Bernal G,
                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-010914/01
                                                             100
                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form fication, but was obtained in electronic format
                                                                                                                    25
      66
                                                                                                                                                                               81;
                                                          IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET
                                                                                                                 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITD------
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                                                                                                                                                                                                                                                                                                 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
O, Chetcouani F, Nedjari H, Glaser P, Cossart P;
Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
y T, Domann E, Hain T, Berche P, Charbit A, Durant L;
J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                               Conservative
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    gene therapy; vaccine; biosynthesis; biodegradation,
bacterial infection; disease.

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20.6%;
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                                                                                                                                                                            Score 146.5; DB 2
Pred. No. 0.00046;
6; Mismatches 121
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                                                                                                                                                                         121;
                                                                                                                                                                                                                                      23;
   -NRYQVKQGDTVSKIAQRYG
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                   Length 482;
                                                                                                                                                                                                                                                                                                                                                                                    part of the printed directly from WIPO
                                                                                                                                                                            145;
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           peptides
NB: Ident
                                      AAR73913 is the Listeria monocytogenes protein P60 precursor. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73891-R73894 and AAR73903-R73906, which are recognised by a monoclonal antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis treatments. The
                                                                                                                                                                                                                      New peptide(s) and corresp. antibodies meningitis - the peptide(s) corresp. t sites on bacterial and viral agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes; protein P60 precursor; vaccine; meningitis related homologous antigenic sequence; MRHAS; RV immunoassay; diagnosis; treatment; prophylactic; bacterial;
                                                                                                                                                                       Claim 47; Fig 7/10; 98pp; English.
                                                                                                                                                                                                                                                                                      WPI; 1995-147431/19.
                                                                                                                                                                                                                                                                                                                    Sharma LR,
                                                                                                                                                                                                                                                                                                                                                  (SHAR/)
(VALS/)
                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1994;
           ides may also be used as vaccines against meningitis. Identified by matching corresponding MRHAS peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 VSVQDIMSWNNLSSS-SIYVGQKLAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 TTQQAAPAAETKTEVKQTTQATTPAPKVAETKETPVVDQNATTHAVKSGDTIWALSVKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                  SHARMA L R.
VAN ALSTYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monocytogenes protein P60 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRTGQRIASMKNQPSGAALFEF--RISRNGVYV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKHLGKAYSWGGNGPTTFDCSGYTKYVFAKAGISLPRTSGAQYASTTRISESQAKPGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKTNTNTNTNTNTNTNTTTPSKNTNTNSNTNTNSNTNANQGSSNNNSNSSASAI I AE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQHPAVQKPTPPVV------VVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - EAPAAEKQAAPVVKENTNTNTATTEKKETATQ - - -
                                                                                                                                                                                                     and preventing meningitis
                                                                                                                                                                                                                                                                                                                    Van Alstyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    93US-0127499
                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-CA00516.
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                                                                                                                                                                                                                      ies for the treatment of p. to homologous antigenic and on chemokine(s), used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GASIVIQHTNGF-VSSYIHIKDAQVKTGDT
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ÖS

Sequence

484

A

Matches Query Match Best Local

81;

Conservative

Similarity

20.6%;

Score 146.5; DB 16; Length 484; Pred. No. 0.00046; 6; Mismatches 121; Indels 145;

Gaps

14;

65

S

160 ttoqaabaaetktevkottoattpapkvaetketpvvdonatthavksgdtimalsvkyg

-----NRYQVKQGDTVSKIAQRYG

IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTFVAFTQEVKKET 159 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITP-------

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RESULT 12
AAO17658
ID AAO17
New isolated non-typeable Haemophilus influenzae BASB201 polypeptides,
                          WPI; 2002-426267/45.
N-PSDB; AAL46626.
                                                    Thonnard J;
                                                                                13-OCT-2000; 2000GB-0025169.
                                                                                                05-OCT-2001; 2001WO-EP11561
                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                     WO200230967-A2
                                                                                                                                                               Domain
                                                                                                                                                                                                            BASB201; otitis media; pneumonia; sinusitis; nos auditive nerve damage; delayed speech learning; antibacterial; auditory; antiinflammatory.
                                                                                                                                                                                                  Haemophilus influenzae.
                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                    H influenzae BASB201 #3.
                                                                                                                                                                                                                                                                   05-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                 AAO17658 standard; Protein; 410 AA
                                                                                                                                     301..400
/label= peptidase_M37-like_domain
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                           32..300

'label= KEQ_rich_domain

301..400
                                                                                                                                                                                                                              nosocomial
                                                                                                                                                                                                                             infection;
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. Children, pneumonia in elders, simusitis, nosocomial infections, or chronic otitis media in infants and invasive diseases, chronic otitis media with hearing loss, fluid eccumulation in the middle ear, auditive merve damage, delayed speech the middle ear. The present sequence is a version of the BASB201 protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 88; 90pp; English.
     394
                                                                 335
                                                                                                        279 STSGLGAAKKQYSLÞVSGS--ILHTÞG--SIQAGEVRWKGMVIGASAGTÞVKAIAAGRVI
                                                                                                                                   193 GSSGV----MOFRYPYGATNEVVRRFGTATVAGSTYTSNGMWFSGRDGDLINASNAGTYI 248
                                                                                                                                                                    237 AEQAAREQEKREREALAGROKAEEKRT-------SKPYQPTVQERQLLN 278
                                                                                                                                                                                                   134 AHTESEVAVQSSREEV-QQHEAVQKETEEVVVVKKETETEEVVQQQAAFVAFEYTEAEFAT
                                                                                                                                                                                                                                                                 74 QVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSI8SGVNT 133
                                                                                                                                                                                                                                                                                                        ch 8.0%; Score 134, DB 23; 1 Similarity 24.6%; Pred. No. 0.0043; 62; Conservative 37; Mismatches 111;
FGISRKGTPVNP
                           FRISRNGVYVDP 317
                                        LAGYLNGYGYMVIVKHGETDLSLYGFNQAVSVKVGQLVSAGQVIAQVGNTGEISRSALY- 393
                                                                     QADH-NMDGASIVIQHTNGEVSSYIHIKDAQVKTGDTVRTGQRIASMKN---QPSGAALFE 305
                                                                                                                                                                                                                                  ÓKKÓQQALQKAQQEHQFS-----LNEĽNKNLALDQDK-----LNAĽKANÉQALRQEIQR 236
                                                                                                                                                                                                                                                                                                                                                                                     410 AA;
                                                                                                                                                                                                                                                                                                                                       Length 410;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                     192
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В Ś В Ś B Ś 밁 Ş

376 AQKHLGKAYSWGGNGPTTFDCSGYTKYVFAKAGISLPRTSGAQYASTTRISESQAKPGDL

----GASIVIQHTNGF-VSSYIHIKDAQVKTGDT 284

316 NKTNTNTNTNTNTNTNTNTPSKNTNTNSNTNTNTNSNTNANOGSSNNNSNSSASAIIAB

200 FRYPVGA-----TŅPVVRRFGŢATVAGSTVTŞNGWWFSGRDGDLIŅAŞNAGTVIQ

249

259

219 89

- EAPÄAEKQAAÞVVKENTNTNTATTEKKETATQ----QQTAÞKÁÞTEAAKPAPAFSTNTNA QQHPAVQKPTPPVV------VVKKPTPTPVVQQPAPVAPPTTAPFATGSSGVMQ 199 LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149

260 150 220

250 ADHNMD----

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RESULT 13
AAO17656
13-OCT-2000; 2000GB-0025169
                05-OCT-2001; 2001WO-EP11561
                                       18-APR-2002.
                                                       WO200230967-A2
                                                                                                                                BASB201; otitis media; pneumonia; sinusitis; nosocomial infection; auditive nerve damage; delayed speech learning; vaccine; antibacterial; auditory; antiinflammatory.
                                                                                                   Domain
                                                                                                                         Haemophilus influenzae.
                                                                                                                                                                           H influenzae BASB201 #1.
                                                                                                                                                                                                05-AUG-2002
                                                                                                                                                                                                                 AA017656;
                                                                                                                                                                                                                            AAO17656 standard; Protein; 410 AA.
                                                                                                                                                                                            (first entry)
                                                             /label= KEQ_rich_domain
301..400
/label= peptidase_M37-like_domain
                                                                                                Location/Qualifiers 32..300
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RESULT 14
AAR85285
ID AAR85285
AC AAR85
XX AAR85
XX O1-AP
DT O1-AP
XX Lysin
XX Lysin
XX Lysin
XX Chees
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. influenzae infection, which can cause otitis media in infants and children, pneumonia in elders, sinusitis, nosocomial infections, or invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech learning, infections of the upper respiratory tract and inflammation of learning.
                       23-NOV-1995.
                                            WO9531561-A1
                                                                  Lactococcus
                                                                                                  Lysin; autolysis;
                                                                                                                        Lysin.
                                                                                                                                               01-APR-1996
                                                                                                                                                                     AAR85285;
                                                                                                                                                                                          AAR85285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the middle ear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
 12-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                                                                                                                                                                                    237
                                                                                                                                                                                                                                                  394
                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                                                                                                                            193 GSSGV----MOFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI
                                                                                                                                                                                                                                                                                                                                                                                                         134
                                                                                                                                                                                                                                                                                                                                                                                                                                 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le ear. The present sequence is a version of the invention.
                                                                                                                                                                                          standard; Protein;
                                                                                                                                                                                                                                                                     FRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                            LAGYLNGYGYMVIVKHGETDLSLYGPNQAVSVKVGQLVSAGQVIAQVGNTGEISRSALY-
                                                                                                                                                                                                                                                                                                                 QADH-NMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAALFE
                                                                                                                                                                                                                                                                                                                                        STSGLGAAKKQYSLPVSGS--ILHTFG--SIQAGEVRWKGMVIGASAGTPVKAIAAGRVI
                                                                                                                                                                                                                                                                                                                                                                                    AEQAAREQEKREREALAQRQKAEEKRT
                                                                                                                                                                                                                                                                                                                                                                                                         AHTPSPVAVQSSRPPV-QQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFAT
                                                                                                                                                                                                                                                                                                                                                                                                                               QKKQQQALQKAQQEHQ-----STLNELNKNLALDQDK-----LNALKANEQALRQEIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 87; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 AA;
                                                                  lactis
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                                                                                                                                               (first
 95WO-NL00170.
                                                                                                  culture; lactic
                                                                  (Strain MG1363)
                                                                                       induction
                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.00
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 131;
Pred. No. (
                                                                                                                                                                                          B
                                                                                                   acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                  bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 410;
                                                                                                  fermentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the BASB201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                    ---SKPYQPTVQERQLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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le ear
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ABBOGE

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XX IBOGE

XX Micro

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In situ production of a homologous autolysin or a heterologous autolysin from a food grade Gram positive bacteria, can be used a process for the lysis of a culture of lactic acid bacteria. The process can be used in the manufacture of products containing cultures of lactic acid bacteria e.g. cheese, where the culture lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and lysin does not need to be isolated or encapsulated. The time of
                                                           WO200155180-A2
                                                                                                                                                          Micromonospora carbonacea; antibiotic; everninomicin;
                                                                                                                                                                                                 Micromonospora carbonacea everninomicin locus protein
                                                                                                                                                                                                                                        18-JUN-2002
                                                                                                                                                                                                                                                                                                                    ABB06928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 55-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lysis of a culture of lactic acid bacteria in, e.g. cheese production - by in situ prodn. of an auto:lysin, regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT06135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-010946/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inducible promoter.
                                                                                                                                       cluster;
                                                                                                                                                                                                                                                                                                                                                                                                                      399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WNHLSSDTIYIGQNLIVSQSAAASNP----STGSGSTATNNSNSTSSNSNASIHKVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGSNNS-----ASTTPTTSVTPA--KPTSQTTVKVKSGDTLWALSVKYKTSIAQLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSTTYTVKSGDTLWGISQRYGISVAQIQSANNLKST-IIYIGQKLVLTGS----ASSTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---RYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                  standard; Protein; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAPFATGSSGVMQ---FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVNTAHTESEVAVQSSREEVQQHEAVQKETEEVVVVKKETET--EEVVQQEAEVAEEVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCILAGCASKPTYNST------SGSGSHRTSGSGGLAIGSQVITDSQGVPN-
                                                                                                                                                                                                                                                                                                                                                                                                                  KGDTLWGLSQKSGSPI-----ASIKAWNHL----SSDTILIGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAALTGRYATDPSYGASLNRIISQYNLTRFDGASSAGNTNSGG---STTTITNNNSGTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be precisely controlled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kok J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437 AA;
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24.1%;
                                                                                                                                       manipulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103pp;
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                                                                                                                                                          biosynthesis;
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02-AUG-2001

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RESULT 16
ABB54367
XX ABB54
XX ABB54
XX ABB54
XX Lacto
XX Biosy
XX Biosy
XX Lacto
XX FR280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR2807446-A1.
                              Lactococcus lactis IL1403
                                                               Biosynthesis;
                                                                                Lactococcus lactis protein pi244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local !
                                                                                                                     16-MAY-2002
                                                                                                                                                  ABB54367;
                                                                                                                                                               ABB54367 standard; Protein; 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL50555 to ABL50562 represent contigs 1 to 8 from the Micromonospora carbonacea everninomicin biosynthetic locus gene cluster. The contigs encode the protein sequences designated ORF (open reading frame) 1 to 49, given in ABB06881 to ABB06930. The gene cluster is useful for the construction of the everninomicin antibiotic in overproducing strains, and to allow chemical modifications of everninomicin to enhance certains, gene cluster can be used to produce genetic systems and genetic manipulation or combinational biosynthesis. The gene cluster can be used to produce genetic systems and genes encoding novel enzyme activities, and avoid the problems of low yield and quality of everninomicins produced by chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Fig 1; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated gene cluster encoding polypeptides involved in everninomicin biosynthesis useful for construction of everninomicin strains, and to allow chemical modifications of everninomicin to enhance certain properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staffa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-476185/51.
N-PSDB; ABL50562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2000; 2000US-0177711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2001; 2001WO-CA00128.
                                                                                                                                                                                                                                                   223
                                                                                                                                                                                                                                                                 233 GR-PGDLINASNAGTV 247
                                                                                                                                                                                                                                                                         169 T--PPPTTPPPTGAAPALKVSG----NRLVTASGATYRLLGVNRASGEPACVQGKGMNDS
                                                                                                                                                                                                                                                                                                                                 175
                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                          64 -----TDSQGVPNRYQV----KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LIFQVITTCILAGCASKPTYNSTSGSG-----SHRTSG-SGGLAI---GSQVI---- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LAVGTTATLVAAGLAGLTFPASAAATGCSVAYTVQSQWTGGFSGNVALTNLGSALTGWTL 67
                                                                                                                                                                                                                                      GPVDQASVNAMKAWNI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                               VQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAG--STVTSNGMWFS 232
                                                                                                                                                                                                                                                                                                                               WŚŚSNPVPKSFALNGTTCTGSVTŚPTPEPTTTPP-----PTTPPPTTPPPTTPPPT
                                                                                                                                                                                                                                                                                                                                                     WSGDLKVRERSISSGVN-TAHTESPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPV 174
                                                                                                                                                                                                                                                                                                                                                                                 TFDFFTSGQQVTQGWSATWSQSGTSV8AAS----LSWN--GSLGTGGSTTIGFNGS---- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 27.0
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECOPIA BIOSCIENCES INC
                                                    biodegradation; lactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zazopoulos E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%;
27.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 130.5; DB 22; Length Pred. No. 0.012; Length Pred. No. 10.012; Indels
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                                                                                                                                                                   A
                                          bacterium; yogurt;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 518;
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유 성 밁 Ş Ъ Ś В Ş 밁 Ş

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RESULT 17
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Best Local S
Matches 69
           Key
                                     BASB201; otitis media; pneumonia; sinusitis; nos auditive nerve damage; delayed speech learning; antibacterial; auditory; antiinflammatory.
                        Haemophilus influenzae.
                                                                                             H influenzae BASB201 #2.
                                                                                                                            05-AUG-2002
                                                                                                                                                                  AAO17657 standard; Protein;
                                                                                                                                                    AA017657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is related to a Lactococcus lactis nucleotide nucleic acid sequence (ABA90521) and related proteins (ABB53300-ABB55521). The nucleic acid sequence is useful in the detection and/or amplification of related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The production helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bolotine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INRG ) INRA INST NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000;
                                                                                                                                                                                                               807 QVVQÁGSNYYDWYĞNYTVİKHADĞLYTGYAHQSRIDVSVĞQNVKKĞQQİGLM 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2001.
                                                                                                                                                                                                                                     246 TYIQADHY---MDGASIVIQHTNGFVSSYIHIKDAQYKTGDTVRTGQRIASM 294
                                                                                                                                                                                                                                                                                   194 SSGVMOFRYFVGATNFVVRRFGTATVAGSTVTSNGMVFSGRDGDLIN-----ASNAG
                                                                                                                                                                                                                                                                                 771 EMG-----
                                                                                                                                                                                                                                                                                                                                    718
                                                                                                                                                                                                                                                                                                                                                     676 PĎŤIT--ÁQFKLÍMŴ----ĤAQŃ-----ĠÓWIAKSŚYPYSWTQFMTLTNINTÁ--- 717
                                                                                                                                                                                                                                                                                                                               138 SPVAVOSSRPPVOOHPA----VOKETPPVVVVKKPTPTPVVOOPAPVAPPVTEAPFATG 193
                                                                                                                                                                                                                                                                                                                                                                                                     620 LĹGNAQGESDAŃPŤADEĠ----GĠRPĠPGYĠVWQWŤĎŚSĠASSGRVÝMINLMTRAGVTDN 675
                                                                                                                                                                                                                                                                                                                                                                              78 GDŢVSKIĄQRYGĻNŅREIGHINŅLNSSYTIYTGQŅLTLMŞGDLKVRERSISSGVŅTAHTP 137
                                                                                                                                                                                                                                                                                                                                                                                                                           29 ILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNR---YQVK------Q 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; SEQ ID No 1069; 2504pp; French.
                                                                                                                                                                                                                                                                                                         TQAFVANFERÞLNGHÞERSTWAQEWYNKFVNLKIÞSGGGGYI---ÀÞISSÞIÍ----VÍS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 7.8%; Score 130.5; DB 23; Similarity 23.6%; Pred. No. 0.023; 69; Conservative 32; Mismatches 112;
                                                                                                                      (first entry)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renault P, Ehrlich SD;
                                                                                                                                                                  ΑA
                                                        nosocomial infection;
                                                   vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 894;
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RESULT 18
AAY31384
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AC AAY31
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. influenzae infection, which can cause other sed in infections, or children, pneumonia in elders, simusitis, nosocomial infections, or invasive diseases, chronic other sedia with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech learning, infections of the upper respiratory tract and inflammation of the middle ear. The present sequence is a version of the BASB201 prote
              12-OCT-1999
                                          AAY31384;
                                                                AAY31384 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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)B; AAL46625.
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                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                         AHTPSPVAVQSSRPP---VQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         le ear. The present sequence of the invention.
                                                                                                                                    Y-FGISRKGTPVNP
                                                                                                                                                             FEFRISRNGVYVDP
                                                                                                                                                                                        VILAGYLNGYGYMVIVKHGETDLSLYGFNQAVSVKVGQLVSAGQVIAQVGNTGEISRSAL
                                                                                                                                                                                                                VIQADH-WMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAAL
                                                                                                                                                                                                                                            LNSTSGLGAAKKOYSLPVSGS--ILHTFG--SIQAGEVRWKGMVIGASAGTPVKAIAAGR
                                                                                                                                                                                                                                                                     ATGSSGV----MOFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGT
                                                                                                                                                                                                                                                                                                  AE - - QAVREQEKREREALAQRQKAEEKRT
                                                                                                                                                                                                                                                                                                                                                    QKKQQQALQKAQQEHQ-----STLNELNKNLALDQDK-----LNALKANEQALRQEIQR
                                                                                                                                                                                                                                                                                                                                                                               QVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               410
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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               (first
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301..400
/label= p
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                                                                  Protein;
              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%;
                                                                                                                                    405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEQ_rich_domain
                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                   1708
                                                                                                                                                                                                                                                                                                                                                                                                       Score 130; DB 23;
Pred. No. 0.0094;
3; Mismatches 111;
                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is a version of the BASB201 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                ----SKPYQPTVQERQL
                                                                                                                                                                                                                                                                                                                                                                                                           46;
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The invention provides a method for detecting a US (sub)type hepatitis E virus (US-HEV), or its naturally occurring variants in a sample by treatment with a binding partner specific for a marker of the virus, and then detecting any complex formed. The method is used to diagnose infection with US-HEV. Polypeptides from US-HEV, antibodies specific for open reading frames (ORF) in US-HEV and host cells expressing these ORFs are useful in vaccines or for passive immunisation. The polypeptides are also used to raise specific antibodies (useful as immunoassay respents). Fragments of nucleic acid from US-HEV are useful as immunoassay respents) usual hybridisation and amplification assays for detecting infection. The present sequence represents a HEV-US2 ORF1 protein.
Sequence
                                                                                                                                                Claim 6; Page
                                                                                                                                                                    Detection
                                                                                                                                                                                         N-PSDB; AAZ00267
                                                                                                                                                                                                   WPI; 1999-288017/24
                                                                                                                                                                                                                       Dawson GJ,
                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                               15-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEV-US2 ORF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            passive immunisation
                                                                                                                                                                   of United States isolates of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E virus.
 1708 AA
                                                                                                                                                                                                                       Desai SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                               216-221; 260pp; English.
                                                                                                                                                                                                                                                                97US-0061199.
                                                                                                                                                                                                                                                                                     98WO-US21941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   811
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                                                                                                                                                                                                                                                                                                                                                                                /label= unknown
/note= "encoded
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                                                                                                                                                                    E virus
                                                                                                                                                                                                                       Schlauder
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Query Match

7.6%;

Score 127;

DB 20;

Length 1708;

186

292

288 236 228

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RESULT 19
ARAZIATIO AARZA
XX AARZA
AC AARZA
XX 15-NO
DE Beta-
XX Gram-
XX Gram-
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XX JP041
XX JP041
XX LPSD
XX (WAKP
PR WPI;
DR WPI;
DR WPI;
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                                                                                                                                                                                                     The protein sequence of the beta lytic peptidase from Achromobacter lyticus was deduced from the DNA sequence obtd. by PCR using primers based on the sequence of the L. enzymogenes beta-protease. The beta-lytic protease is expected to be an enzyme which can decompose not only Gram-positive bacteria but also some Gram-negative bacteria.
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-lytic protease gene and DNA encoding it - Gram-positive and some Gram-negative bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-lytic protease.
                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 1; 13pp; Japanese.
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DB; AAQ25083.
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  117 SGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 VIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQP-SGAALFEFRISRN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 XGGAPSAAPGEVXAFCSALYRYNRFTQRHSLTGGLWLHPEGLLGIFPPFSPGHIWESANP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 TCILAGC---ASKPTYNSTSGSGSHRTSGSGGLAI-----GSQVITDSQGVPNRYQVK
                                                     50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EESHVDAASVPSVPEPAGLTSPIVLT--PPPPPPPPVRKPATSPPPRTRR-----LL
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                                                                                                                                                         374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 22.7%; P: Conservative 37;
                                                     7.6%; ilarity 25.9%; Conservative 29
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                                                     29;
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07; Mismatches 120;
                                                                            Score 126.5; DB 13;
Pred. No. 0.017;
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                decomposing
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                                                     49;
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                                                                                                                                                                                                                                                       The present sequence is a Achromobacter lyticus beta-lytic protease which has anti-staphylococcal activity. The beta-lytic protease gene is used in the production of altered genes which allow expression and preferably secretion of active protein in mammalian cells/tissues. The altered gene is produced by operably linking the beta-lytic protease coding sequence with mammalian promoter, signal peptide and translation initiation sequences. The modified sequence is used in gene therapy to treat staphylococcal mastitis infections truninants, e.g. goats, sheep, and cows. It is also used to produce transgenic animals which are resistant to staphylococcal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-lytic protease; antibiotic; anti-staphylococcal; gene therapy; mastitis; staphylococcal infection; rum transgenic animal; altered beta-lytic protease gene.
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of Staphylococcal infections, such as animals, especially cows -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bramley JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1998;
21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Achromobacter lyticus beta-lytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 14B; 61pp; English.
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N-PSDB; AAZ49721.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Achromobacter lyticus.
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  154 AGGRAARRRVPAGL
                                                                                                                                 Similarity
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                                                     SGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQ 176
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Pred. No. 0.017;
9; Mismatches
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  Query Match
Best Local S
Matches 52
                                                                                                                                                                                 mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. are useful for identifying the mutation point of a gene derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-376931/40
N-PSDB; AAH67706.
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Tateishi N,
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     1 Similarity
52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           orm bacterium; amino acid synthesis; vitamin; saccharide; acid synthesis.
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                                                                                                                                                                Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO: 6241; 246pp + Sequence Listing; English
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7.5%;
nilarity 33.8%;
Conservative 1
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Senoh A,
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2000JP-0280988.
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Pred. No. 0.0093;
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            CC The invention relates to RP-factors which are substances that can CC resuscitate dormant, moribund or latent cells, possibly also having CC growth-stimulating activity. Host cells containing a vector comprising CC the RP-factor or its receptor encoding nucleic acid can be used for the CC recombinant production of the RP-factor. RP-factors, their receptors or CC convertases, antibodies (against the RP-factors and RP-factor receptors or CC convertases), antegonists and agonists. Are useful in vaccines and for CC excipients, generally as antimicrobials and especially for infections CC excipients, generally as antimicrobials and especially for infections CC associated with latency. They can be used as potentiators of antibiotics such as isoniazid, streptomycin etc., in treatment of tuberculosis. CC RP-factor can also be used: to determine the microbiological quality of foods, pharmaceuticals, medical products; as culture additive for bacteria; to stimulate growth and/or to resuscitate microvganisms and to produce libraries of biomolecules and microorganisms (which may then be corporated for useful products). Probes complementary to the RP-factor culcia acid are used identify and clone other RP-factor genes. The corporations may also be used to prevent bacterial resuscitation. Breaking CC dormancy with RP-factor facilitates detection, culture and enumeration of the corporation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RP-factor; resuscitate; latent cell; growth-stimulation; receptor; Y convertase; vaccine; immunotherapy; prophylaxis; excipient; antibiot antimicrobial; tuberculosis; food; pharmaceutical; culture additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bacterial resuscitation factors - useful for stimulating bacteria and growth, particularly for use as antimicrobials, vaccines comprising bacteria with mutations in resuscitation
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04-JUN-1997;
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In situ production of a homologous autolysin or a heterologous autolysin from a food grade Gram positive bacteria, can be used in process for the lysis of a culture of lactic acid bacteria. The cultures of lactic acid bacteria and the manufacture of products containing lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and the lysin does not need to be isolated or encapsulated. The time of
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                                                                                                                                                                                                                                 Disclosure; Page 69-72; 103pp; English.
                                                                                                                                                                                                                                                                                   Lysis of a culture of lactic production - by in situ prodinducible promoter.
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The present invention describes primer sets for synthesising 5602 (C full-length cDNAs defined in the specification. Where a primer set (C comprises (a) an oligo-dr primer and an oligonucleotide complementary for the following strand of a polymucleotide which comprises one of complementary strand of a polymucleotide which comprises one of configuration of a polymucleotide which comprises one of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination composition of a polymucleotide which comprises a 5'-end complementary strand of a polymucleotide which comprises a 5'-end complementary to a complementary to a complementary to a complementary to a complementary to a complementary to a complementary to a complementary to a complementary to a complementary to a complementary to a complementary comprises at least 15 nucleotides and the combination of the specification. The primers sets can be used in antisense therapy and comparises at least 15 nucleotides and the combination of the specification. The primers are useful for synthesising polymucleotides and the comprises at least 15 nucleotides and the combination of the specification. The primers are useful for synthesising polymucleotides and the complementary that comparise complementary that the complementary that comparise comparises and the complementary and comparise comparises at least 15 nucleotides and the complementary that comparise comparises comparises comparise comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises comparises c
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Ishii S,
                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 14222; 2537pp +
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
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; 2000JP-0183767.
; 2000JP-0241899.
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99JP-0300253
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Pred. No. 0.063;
1; Mismatches
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A, Nagai K,
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BVH-P1
                                                Claim 21; Fig 16;
                                                                                                    New Streptococcus pyogenes antigen useful for diagnosing, treating streptococcal infection, e.g. pharyngitis, erysiningetigo, scarlet fever, and invasive diseases
                                                                                                                                                                                                                                                                                   Martin D,
                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-2000; 2000US-216465P
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immune response; anti-inflammatory; immunisation; antibacterial
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scarlet fever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes strain B514 BVH-P1 mature protein
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                                                                                                                                                                                                                                                                                 Hamel J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 120.5; DI
Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSHSPTPGKVSSPLSPLS--PGIKSPTIPRAERGNPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharyngitis; erysipelas; impetigo;
ng fascitis; toxic shock; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
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                                                                                                                            erysipelas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639;
                                                                                                                            preventing
pelas and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                    S
R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543
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invention

relates to antigens,

more particularly an antigen

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WPI; 2002-171701/22

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RESULT 26
AAE18360
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial pathogen. The polypeptides and polynucleotides encoding them are useful for diagnosing, preventing or treating streptococcal infection, such as pharyngitis, erysipelas, impetigo, scarlet fever, invasive diseases (bacteraemia, necrotising fascitis, toxic shock), and for eliciting an immune response. The polypeptides may also be used as immunogens for producing antibodies for the diagnosis and treatment of Streptococcus infection, or for passive immunisation. DNAs encoding polypeptides may also be used to design DNA probes for detecting the presence of Streptococcus in biological samples suspected of containing the bacteria. The vaccine composition is useful as a prophylactic or the bacteria. The vaccine composition is useful as a prophylactic or
                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                   BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo; scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine; immune response; anti-inflammatory; immunisation; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                             Martin D,
                                                                                               06-JUL-2000; 2000US-216465P
                                                                                                                                06-JUL-2001; 2001WO-CA01001.
                                                                                                                                                                                                 WO200204495-A2.
                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE18360 standard; Protein; 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutic treatment of Streptococcal infection in an individual susceptible to or infected with streptococcal infection. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes (also called group A Streptococcus (GAS))
                                                               (SHIR-) SHIRE BIOCHEM INC
                                                                                                                                                                 17-JAN-2002.
                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRERSISSGVNTAHTPS----PVAVQSSRPPVQQHP----AVQKPTPPVVVVKKPTPT- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYA--PNHAYNPMNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATVAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YQVKQGDTVSKIAQRYGLNWR---EIGHINNLNSSY--TIYT-----GQWLTLWSGDLK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDVSTESSSESQKQPEVPQEAVPTPKAAETTEVEPKTDIS----EDPTSANRPVPNESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVQAPASSPASVSHVPSSEPLPQASATSQPTVPMAPSATPLASAKPDSSVTASSELTSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVKYGDTLSTIAEAMGIDVHVLGDINHIANIDLIFPDTILTANYNQHGQATTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is Streptococcus pyogenes strain B514 BVH-P1 mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------PPVVQQ--PAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFG 215
                            Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                  pyogenes B514.
                                                                                                                                                                                                                                                                                                                                                                                                                                      pyogenes strain B514 BVH-P1
                                                                                                                                                                                                                                                  /label= Signal_peptide 26..382
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                 note= "Mature_BVH_P1_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%;
                               Brodeur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 120; DB 2
Pred. No. 0.056;
                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antigens, more particularly an antigen of Streptcoccus pyogenes (also called group A Streptcoccus (GAS))

C bacterial pathogen. The polypeptides and polynucleotides encoding them are useful for diagnosing, preventing or treating streptcocccal infection, such as pharyngitis, erysipelas, impetigo, scarlet fever, invasive diseases (bacteraemia, necrotising fascitis, toxic shock), and for eliciting an immune response. The polypeptides may also be used as immunogens for producing antibodies for the diagnosis and treatment of streptcocccus infection, or for passive immunisation. DNAs encoding polypeptides may also be used to design DNA probes for detecting the presence of Streptcoccus in biological samples suspected of containing the rapputic treatment of Streptcocccal infection in an individual susceptible to or infected with streptcocccal infection. The present sequence is Streptcocccus pyogenes strain B514 BVH-P1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                      Cellulase; proteinase; truncated; Cel B5; Cel B4/5; Cel E1/2; Cel I/2/3, Cel 67 Cel E3/85; laundry detergent; stain-removing; cotton-containing fabric; stonewashing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Streptococcus pyogenes antigen useful for diagnosing, preventing treating streptococcal infection, e.g. pharyngitis, erysipelas and impetigo, scarlet fever, and invasive diseases
                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Fig 8; 74pp; English.
                                                    19-SEP-1997;
                                                                                   15-SEP-1998;
                                                                                                                                                                                                                                                                                            Truncated cellulases Cel B4/5 and
                                                                                                                                                                                                                                                                                                                             30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                               AAY13492 standard; Protein; 1426
                 (CLRN ) CLARIANT FINANCE BVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 VRERSISSGVNTAHTPS----PVAVQSSRPPVQQHP----AVQKPTPPVVVVKKPTPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYA--PNHAYNPMNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDVSTESSSESQKQPEVPQEAVPTPKAAETTEVEPKTDIS-----EDPTSANRPVPNESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVQAPASSPASVSHVPSSEPLPQASATSQPTVPMAPSATPLASAKPDSSVTASSELTSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATVAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQVKQGDTVSKIAQRYGLNWR----EIGHINNLNSSY--TIYT------GQWLTLWSGDLK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTVKYGDTLSTIAEAMGIDVHVLGDINHIANIDLIFPDTILTANYNQHGQATTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%; Score 120; DB 23; Length 382; larity 25.8%; Pred. No. 0.061; Conservative 21; Mismatches 78; Indels 79
                                                                                                                                                                                                                                                                                                                             (first entry
                                                    97US-0932571.
                                                                                     98EP-0810919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PPVVQQ--PAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFG
                 LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----STVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                                                                                            Ce1
                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217
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                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant cellulase active protein free of CC proteinases of native thermophilic and alkalinophilic origin, comprising the truncated sequences Cel B5, Cel B4/5, Cel E1/2/3, Cel 1/2/3, Cel 6 or Cel E3/B5, or a stability region from one of the defined full-clength sequences, or functional equivalents. Cel B5 extends from amino acid K635 to N1426 or N1426, and Cel B4/5 extends from amino acid Y39 to D481, Cel E8/2 extends from amino acid Y39 to D481, Cel E8/2 extends from T39 to G812, Cel E8/2 extends from T39 to G812, Cel E8/2/3 extends from T39 to G812, Cel E8/2/3 extends from T39 to G812, Cel E8/2/3 extends from T39 to G812, Cel E8/2/3 extends from T39 to G812, Cel E8/2/3 extends from T39 to G812, Cel E8/2/3 extends from T39 to G812, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G812, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 extends from T39 to G835, Cel E8/2/3 exte
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson P, Bergquist PL, Day
Gibbs MD, Morgan H, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 34-37; 65pp; English
1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-315403/27.
DB; AAX55661.
                                               193
                                                                                                     962
                                                                                                                                                     159
                                                                                                                                                                                                           920
                                                                                                                                                                                                                                                              102 NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSPVAVQSSRP-PVQQHPAVQKP
                                                                                                                                                                                                                                                                                                                 868
                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                            GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                                                                                                                 SGAGVLAAGOSTKEIRLSIOKGSGSYNOSNDYSIRS----ANSYIENEKVTGYIDG-
                                                                                                                                                                                                                                                                                                                                                                    SGSGGLAIGS-----QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNL 101
                                                                                                                                                     TPPVVVVKKPTPTPPVVQQPAPVAPP-----VTEAP------FAT 192
                                                                                                                                                                                                        -----AIVWG-----REPSRGTKPAGVVTPTPAPTPTSTPTPTPTPTPTP
GNKIVDKDGKPVWLTG--VNWFGFNT---GTNVFDGVWSCNLKSALAEIANRG 1069
                                                                                                     TPTVTVTPTSTPTPVSSSTPTPTATPTPTPSITITPAPTATPTPTPSVTDDTNDDWLFAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 119.5;
; Pred. No. 0.3;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                               .37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in detergents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farrington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    욨
                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                              961
                                                                                                                                                                                                                                                                                                                       919
                                                                                                                                                                                                                                                                 158
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AAE16323 standard; Protein; 1426,AA.
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26-MAR-2002

(first entry)

RESULT 28
AAB16323
ID AAB16
AXX AAB16
AXX AAE16
XX 26-MA
XX ACTIV
XX ACTIV
XX ACTIV
XX CELBS
XX Unide
XX Unide
XX Tegio
FT Regio Active cellulase protein; alkalinophilic; textile processing; detergent additive; stonewashed appearance; cotton-containing CelB5; thermophilic; commercial detergent; celB gene. Domain Region Unidentified Active cellulase Location/Qualifiers 635..1426 /note= "B4/5 protein" 999..1000 protein, CelB.

bacteria; fermentation;

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RESULT 29
AAR85287
ID AAR85
XX
AC AAR85
XX
AC AAR85
XX
XX
DT 02-AE
XX
DE Ly8ir
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a cellulase active protein, which is substantially free of proteinases of native thermophilic and alkalinophilic oxigin, where the cellulase active protein consists of the CelB5 amino acid sequence. The cellulase active protein is useful for treating cellulosic materials including cotton-containing fabrics, as detergent additives. The cellulase active protein is also useful for improving the feel and/or appearance of cotton-containing fabrics, for removing surface fibers from cotton-containing knits or for imparting stonewashed appearance to cotton-containing denims. The present proteins are stable under condition of alkaline pH and elevated temperatures, thus suitable for textile processing and in commercial detergents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cellulase active protein, useful in textile processing commercial detergents, e.g. for improving the feel or appear cotton-containing fabrics, is stable under conditions of all
                   Lysin carboxy terminal repeat region.
                                                      02-APR-1996
                                                                                        AAR85287
                                                                                                                      AAR85287 standard; Protein; 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 55-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farrington GK, Ande
Morgan H, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6294366-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CLRN ) CLARIANT FINANCE BVI LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                           1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elevated temperatures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-081780/11.
                                                                                                                                                                                                                                                                             962
                                                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                                                             159
                                                                                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                                                                                                                                                                                                                                                                  868
                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                           TPPVVVVKKPTPTPPVVQQPAPVAPP----VTEAP----
                                                                                                                                                                                                          GNKIVDKDGKPVWLTG---VNWFGFNT---GTNVFDGVWSCNLKSALAEIANRG
                                                                                                                                                                                                                                          GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG
                                                                                                                                                                                                                                                                           TPTVTVTPTSTPTPVSSSTPTPTATPTPTPSITITPAPTATPTPTPSVTDDTNDDWLFAQ
                                                                                                                                                                                                                                                                                                                                                                             NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSPVAVQSSRP-PVQQHPAVQKP
                                                                                                                                                                                                                                                                                                                                                                                                                SGAGVLAAGQSTKEIRLSIQKGSGSYNQSNDYSIRS-----ANSYIENEKVTGYIDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSGGLAIGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1426 AA;
                                                                                                                                                                                                                                                                                                                                             -----AIVWG-----REPSRGTKPAGVVTPTPAPTPTSTPTPTPTPTPTPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0932571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0136574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Linker domain"
1001..1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is CelB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "B/5 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                -QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 119.5; 1
Pred. No. 0.37
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergquist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the feel or appearance of conditions of alkaline p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibbs
                                                                                                                                                                                                                                                                                                           ----FAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
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                                                                                                                                                                                                                                           245
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 RESULT 30
AAY95030
ID AAY95
XX
AC AAY95
XX
DT 19-JU
XX
DE Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autolysin from a food grade Gram positive bacteria, can be used a process for the lysis of a culture of lactic acid bacteria. The process can be used in the manufacture of products containing cultures of lactic acid bacteria e.g. cheese, where the culture lysed following the completion of fermentation. The enhanced
Human clone vb22_1 ORF2, SEQ ID NO:130.
                                   19-JUN-2000
                                                                     AAY95030;
                                                                                                     AAY95030 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lysis of a culture of lactic acid bacteria in, e.g. cheese production - by in situ prodn. of an auto:lysin, regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 57-58; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buist G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lysin; autolysis; culture; lactic acid cheese; foodstuffs; induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In situ production of a homologous autolysin or a heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inducible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lysin does not need to be isolated or encapsulated. Lysis can be precisely controlled. See AAR85285 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNIL ) QUEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                           147
                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                           206
                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                             91 NWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 AGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Conser
                                                                                                                                                                                        ASIKAWNHL-----SSDTILIGQ 211
                                                                                                                                                                                                                                                                                                                                                             QHPAVQKPTPPVVVVKKPTPT--PPVVQQPAPVAPPVTEAPFATGSSGVMQ---FRYPVG 205
                                                                                                                                                                                                                                                                                                                                                                                             SVAQIQSANNLKST-IIYIGQKLVLTGS----ASSTNSGGSNNS------ASTTPTTS
                                                                                                                                                                                                                        GFVSSYIHIKDAQVKTGDTVRTGQ
                                                                                                                                                                                                                                                                                           ATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTN 265
                                                                                                                                                                                                                                                                                                                               VTPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGSTTTITNNNSGTNSSSTT------YTVKSGDTLWGISQRYGI 41
                                                                                                                                                                                                                                                           ASNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kok J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                 (first entry)
                                                                                                                                                                                                                                                                                                                           -KPTSQTTVKVKSGDTLWALSVKYKTSIAQLKSWNHLSSDTIYIGQNLIVSQSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INT BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94EP-0201353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-NL00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in situ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ledeboer
                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Strain MG1363).
                                                                                                                                                                                                                                                           -STGSGSTATNNSNSTSSNSNASIHKVVKGDTLWGLSQKSGSPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 118; DB 1
Pred. No. 0.043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venema
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DB 17; 106;

Length Indels

216; 60;

Gaps

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The invention relates to 40 human secreted proteins (AAY94981-Y95020), CC and cDNA sequences encoding them (AAA2423-A23462). The secreted components of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the convention may exhibit one or more activities selected from the following: CC cytokine activity, cell proliferation; differentiation; immune cc activities activity; and tumour matchinish activity; anti-inflammatory activity; and tumour cativities selected from the following: CC and thrombolytic activity, anti-inflammatory activity; and tumour conditions, and the nucleotides may be administered to patients as concleotides of the invention include autoimmune diseases; genetic cd disorders; haemophilia; cardiovascular diseases; cancer; bacterial, cf fungal and viral infections, especially HIV, multiple sclerosis; casthma and anaemia. They may also be used for treating wounds, burns, cludes, osteoarthritis, periodontal diseases, harheimer's disease, parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activin/Inhibin activity may cadditionally be useful as contraceptives. Nucleic acid sequences of the invention may be used in chromosome mapping, and as a source of che convention may be used in chromosome mapping, and as a source of the cDNA clones of the invention.
                                                                                                     Matches
                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-AUG-1998;
24-AUG-1998;
09-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1998;
25-NOV-1998;
23-DEC-1998;
23-DEC-1998;
23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflammati infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive; open reading frame;
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 350-351; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valenzuela D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ALPH-) ALPHAGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200011015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              m, useful
                                              132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185
                                                                                                  l Similarity
36; Conser
STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPA---PAPAAPPS
                                                                                                                                                                                                       284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or transmembrane proteins and for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0097638.
98US-0097659.
98US-0099618.
98US-0102092.
98US-010978.
98US-0113646.
98US-0113646.
99US-0379246.
                                                                                                                                                                                                       ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuan O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US19351
                                                                                                                      7.1%;
39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoffman
                                                                                            ; Score 118; DB; Pred. No. 0.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hall
                                                                                                                         DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e disorders, autoimmune
                                                                                         33;
                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rapiejko
                                                                                                                                                   Length 284;
                                                                                                  Indels 14;
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QPAVPLPQNTQAPSQATNVPVAPPPPPASLGQSQIPQSAPSAPIPPTLPSTTSAAPPPPP

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447

DLKV-----RERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTP

PPPRASRPTPNVTMQQNPQQYNNSNRPFGYQTNSNMSSPPPPPVTTFNTLTPQ-MTAATG

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RESULT 31
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                                                                                                   Query Match
Best Local S
Matches 65
                                                                                                                                                                                                The present invention relates to a method for identifying modulators of actin polymerisation. The method involves using proteins that contain least one binding motif for proteins of the Ena/NASP (Vasodilator-stimulated phosphoprotein) family in the preparation of reagents for identification/screening of modulates that modulate formation of the actin cytoskeleton. The proteins used in the method (i.e. the proteins with binding motif(s) for Ena/VASP proteins) do not bind to the Arp2/3 protein complex. The modulators identified by the method are potentially useful for treating disorders of actin polymerisation, e.g. metastatic cancer or parasitic infection; and as cytotoxic agents. The present sequence one such protein with binding motif(s) for Ena/VASP proteins, which was used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying modulators of actin polymerization, potentially useful for treating tumor metastasis and parasitic infection, using proteins that contain Ena/VASp binding sites -
                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Pages 105-107; 109pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actin polymerisation; Ena/VASP; vasodilator-stimulated phosphoprotein; metastatic cancer; parasitic infection; cytotoxic; Las17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Las17 protein
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                                                                                                                                                           Sequence
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                                                                                                                Similarity
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                                         PMRTTTEGSGVRLPAPPPPPRRGPAPPPPPHRHVTSNTLNSAGGNSLLPQATGRRGPAPP
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 -VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSS-----YTIYTGQWLTLWSG
                                                                     PTYNSTSGSG------SHRTSGSGGLAIGSQVITDSQG-----
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                                                                                                 7.1%; Score 118; DB 23.0%; Pred. No. 0.17; ative 34; Mismatches
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RESULT 32
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                                                                                                         Best Loc
Matches
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                          the WASP (Wiskott-Aldrich Syndrome protein) family of proteins.

Peptide fragments of WASP-family proteins of eukaryotic cells are used to prepare reagents for detecting compounds that inhibit or stimulate formation of the actin cytoskeleton, and thus inhibit or stimulate cell motility. The peptides are used to detect and identify compounds which are potentially useful for treating diseases associated with dysfunction of actin polymerisation, particularly metastatic cancer and parasite infection; as cytotoxic agents for inhibiting/stimulating formation of the actin cytoskeleton and for detecting side-effects, on actin polymerisation, of pharmaceuticals. By modulating actin polyment, the immune
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Fig 7; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticancer and antiparasitic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fragments of WASP family proteins, useful for detecting identifying modulators of actin cytoskeleton formation, pote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-536241/59.
N-PSDB; AAH77917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wiskott-Aldrich syndrome protein; WASP; actin cytoskeleton; Lasl cell motility; actin polymerisation; cancer; parasite infection; embryonic development; immune response; wound repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG67365;
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                                                                                                                                                                                                                                                                            response
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                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents a Las17 protein. Las17 is a member of
     329
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                                                                                                                                      Similarity
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                                                         PTYNSTSGSG-----
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                                                                                                                                                                                                                         633
                                                                                                            Conservative
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                                                                                                                                   7.1%;
23.0%;
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                                                                                                      Score 118; DB 22;
Pred. No. 0.17;
4; Mismatches 104;
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132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185

Matches Best Local Query Match

36;

Conservative

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Similarity

7.1%;

Score 118; DB Pred. No. 0.39; Mismatches

21; 33,

Length 1192; Indels

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                            The invention relates to human MAGI protein, which is similar to neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, stroke and inflammatory disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence represents the human MAGI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGI protein; neuroendocrine-specific protein; neuropathy; human; spinal injury; neuronal degeneration; neuromuscular disorder; can psychiatric disorder; developmental disorder; inflammatory disord stroke; cytostatic; cerebroprotective; neuroprotective.
                                                                                                                                                                                                                                  Novel polypeptides related to neuroendocrine-specific proteins and polynucleotides useful for diagnosis of various diseases and for treatment of cancer and neurological disorders -
Sequence
                                                                                                                                                                                                     Claim 2; Page 20-21; 35pp; English.
                                                                                                                                                                                                                                                                                                                          WPI; 2000-182693/16.
                                                                                                                                                                                                                                                                                                                                                          Michalovich D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MAGI polypeptide.
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1192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0016024.
99GB-0016898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-GB02360.
                                                                                                                                                                                                                                                                                                                                                          Prinjha
                                                                                                                                                                                                                                                                                                                                                          RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder;
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RESULT 34 AAU04591

밁 Ś 뭕

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Novel Nogo receptor protein useful for identifying modulator of Nogo protein or Nogo receptor protein, which is useful for treating central
                                                                    WPI; 2001-442138/47
N-PSDB; AAS09453.
                                                                                                                     Strittmatter SM;
                                                                                                                                                                               12-JAN-2000; 2000US-0175707.
26-MAY-2000; 2000US-0207366.
29-SEP-2000; 2000US-0236378.
                                                                                                                                                    (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                              12-JAN-2001; 2001WO-US01041
                                                                                                                                                                                                                                                                                                                    W0200151520-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein; cranial trauma; cerebral trauma; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasis demyelination; encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy; Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Pep5
/note= "Receptor binding inhibitory peptide.
sequence is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                   /label= Pep4
/note= "Receptor binding
sequence is specifically
1095..1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Receptor binding inhibitory peptide. sequence is specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= pep1
/note= "Receptor binding
sequence is specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Receptor binding sequence is specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Lumenal_extracellular_domain
note= "This sequence is specifically claimed"
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                                                                                                                                                                                                                                                                                                                                                                                                         inhibitory peptide. claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitory claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitory peptide. This claimed"
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RESULT 35
AAB82349
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Best Local S
Matches 36
                       New polypeptide designated NOGO-C is a splice variant of the gene and may be useful in the treatment of neural disorders i Alzheimer's and Parkinson's diseases
     Disclosure; Page 26-27;
                                                                                                                                                      Michalovich D,
                                                                                                                                                                                                                 15-NOV-1999; 99GB-0026995.
24-JAN-2000; 2000GB-0001550.
                                                                                                                                                                                                                                                                14~NOV-2000; 2000WO-GB04345
                                                                                                                                                                                                                                                                                                                                                                                                 NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; parkinson's disease; neuromacular disorder; psychiatric disorder; developmental disorder; neuroprotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis;
                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                         25-MAY-2001
                                                                                                                                                                                                                                                                                                                                    WO200136631-A1
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NOGO-A protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system disorders
                                                                                                     2001-343822/36.
DB; AAF90324.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 T-EAPFATGSSGVMQ---FRYPVGATNPVVR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 STVPAPŠĖLSAAAVSPĖKLPEDDEPPARPPPPPPPPASVSPQAEPVWTĖPA---PAPAAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 NTAHTESPV---AVQSSREPVQQHPAVQKFTPPVVVVK---KFTETEPVVQQPAPVAEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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Similarity 39.6%;
36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                    Prinjha
 25pp; English
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Pred. No. 0.39;
8; Mismatches 33;
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Peptide

Peptide

Peptide Domain

Peptide

e human NOGO including

Peptide

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RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia
                   The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent
                                                                                                                                                                                                                    Claim 20;
                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy \mbox{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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     in treatment of a
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                                                                                                                                                                                                                                                                                                                                                                                                          Liu
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2001US-0770160.
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                                                                                                                                                                                                                 737; 765pp; English
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39.6%;
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Pred. No. 0.39;
8; Mismatches
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on or
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         This invention describes a swine hepatitis E virus (HEV) and its natural mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used tincrease stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AMU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                 New isolated swine hepatitis E virus - used to develop products the diagnosis, prevention and treatment of hepatitis E virus infection in mammals, particularly humans
                                                                                                                                                                                                                                 Example 1; Fig 6D-J; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9904029-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis E virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Swine hepatitis E virus; HEV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Swine HEV ORF 1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPPASVSPQAEPVWTPPA---PAPAAPPS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
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                                                                                                                                                                                                                                                                                                                                                                              SU,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPAAPKRRGSSGSVDETLFALP-AASEPVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunise;
                                                                                                                                                                                                                                                                                                                                                                                                              DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1246 AA;
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                                                                                                                                                                                                                                                                                                                                                                          Meng X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection;
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39.6%;
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                                                                                                                                                                                                                                                                                                                                                                                쟢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-reaction; antibody; human; therapy;
detection; diagnosis; prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local S
Matches 79
New Streptococcus pyogenes antigen useful for diagnosing, preventing treating streptococcal infection, e.g. pharyngitis, erysipelas and impetigo, scarlet fever, and invasive diseases -
                                                                                                                                                                                           Martin
                                                                                                                  N-PSDB; AAD29298.
                                                                                                                                                                                                                               (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                                                                                                                         06-JUL-2001; 2001WO-CA01001
                                                                                                                                                                                                                                                                               06-JUL-2000; 2000US-216465P
                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                WO200204495-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pyogenes SPY57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BWH-P1 gene; streptococcal infection; pharyngitis; erysipelas; iscarlet fever; bacteraemia, necrotising fascitis; toxic shock, vimmune response; anti-inflammatory; immunisation; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes strain SPY57 BVH-P1 mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE18363 standard; Protein; 364 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE18363;
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                                                                                                                                           2002-171701/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 849 FIMREGLAAYTLTPRPIIHAVAPDYRVEQN 878
                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 DTVRTGQRIASMKNQP-SGAALFEFRISRN 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 HTPSPVAVQSSRPPVQQHPAVQKPTPPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               668 LWLHPEGLLGIFPPFSPGHIWEPANPFCGEGTLYTRTWST------SGESSD 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              608 LTYELTPAGLÓVRISSNGLDCTATFPPGGAPSAAPGEVAAFCSALYRYNRFTORHSLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        548 LTATVELTASPDRLECRTVLGNKTFRTTVVDGAHLEANGPEQYVLSFDASROSMGAGSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTVTIAINSQNQKPIKRLGLIFGVITTCILAGC---ASKPTYNSTSGSGSHRTSGSGGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFESDCNW------LVNASNPG-----HRPGGG---LCH----AFYQRFPEAFYPTE 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSPP----EAAAPVLAAAPGLPHPTPPVSDIWVLPPPSKESQVDAASVPPAPEPAGLPSS 769
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7.1%; Score 118; DB:
Similarity 20.3%; Pred. No. 0.63;
79; Conservative 44; Mismatches :
                                                                                                                                                                                     Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVLTLPPPLPPVRKPPTP--PP-----SRTRRLLYTYPDGA-----KVYAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V,VKKPTPTPTPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -WR-----EIGHI----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I-----GSQVITDSQGVPNRYQVKQGDTVS------KIAQRYGLN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1708 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       impetigo;
vaccine;
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or
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RESULT 39
ABP25889
ID ABP25
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                                                                                                                                                                                                                                                                                                                                                               D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antigens, more particularly an antigen of CC Streptococcus gyogenes (also called group A Streptococcus (GAS))

CC are useful for diagnosing, preventing or treating streptococcal for infection, such as pharyngitis, erysipelas, impetigo, scarlet fever, CC for eliciting an immune response. The polypeptides may also be used as CC Streptococcus infection, or for passive inmunisation. DNAs encoding the CC infection for producing antibodies for the diagnosis and treatment of CC Streptococcus infection, or for passive inmunisation. DNAs encoding the CC polypeptides may also be used to design DNA probes for detecting the CC polypeptides of Streptococcus in biological sampless suspected of containing the CC the bacteria. The vaccine composition is useful as a prophylactic or CC therapeutic treatment of Streptococcal infection in an individual CC sequence is Streptococcus pyogenes strain SPY57 BVH-P1 mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
ABP25889;
                        ABP25889 standard; Protein; 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Fig 14; 74pp; English.
                                                                                                          198 SASEEVSSAAPAQAPAEKEETSAPAAQKAVADTTŠVATŠNGLSYA--PNHAYNPMNAG
                                                                                                                                                                                   143 STNDVSTELSSESQKQPEVPQEAVPTPKÅAETTEVEPKTDIS-----EAPTSÅNRPVPNE 197
                                                                                                                                          214 FGTATVAG------ STVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                       167 ------KPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRR 213
                                                                                                                                                                                                                                                                                               127 ISSGVNTAHTPS----PVAVQSSRPPVQQHPAV---QKPTPPVVVVK------- 166
                                                                                                                                                                                                                                                             83 AŚŚPASVSHVPŚSEPLPQASATSQPTVPMAPPATPSDVPTTPFASAKPDSSVTASSELTS 142
                                                                                                                                                                                                                                                                                                                                    24 YTVKYGDTLSTIAEANGIDVHVLGDINHIANIDLIFFDTILTANYNQHGQATNLTV-QAP 82
                                                                                                                                                                                                                                                                                                                                                                 73 YOVKQGDTVSKIAQRYGLNWRBIGHINNLNSSYTIYTGQWLTL-----WSGDLKVRERS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 23.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 117.5; DB
23.5%; Pred. No. 0.094;
ative 22; Mismatches
                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                     87;
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02-JUL-2002 (first entry)

Streptococcus polypeptide SEQ ID NO 954.

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.

WO200234771-A2. Streptococcus pyogenes.

27-OCT-2000; 2000GB-0026333 24-NOV-2000; 2000GB-0028727 07-MAR-2001; 2001GB-0005640 29-OCT-2001; 2001WO-GB04789

02-MAY-2002.

(CHIR-) CHIRON SPA. INST GENOMIC RES.

Telford J, P Masignani V, Margarit Ros YI, Grandi ģ Fraser C

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RESULT 40
AAE18359
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                BVH-P1 gene; streptococcal infection; pharyngitis; erysipelas; impetigo; scarlet fever; bacteraemia; necrotising fascitis; toxic shock; vaccine; immune response; anti-inflammatory; immunisation; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for
                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                                                          07-MAY-2002
                                                                                                                                                                                                                                                                                                                                           AAE18359 standard; Protein; 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3249; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-352536/38.
N-PSDB; ABN66520.
WO200204495-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection of disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting a compound that binds to the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   223
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SASEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYA--PNHAYNPMNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGTATVAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STNDVSTELSSESQKQPEVPQEAVPTPKAAETTEVEPKTDIS-----EAPTSANRPVPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSPASVSHVPSSEPLPQASATSQPTVPMAPPATPSDVPTTPFASAKPDSSVTASSELTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------KPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRR
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                                                                                                                                                                                                                                    pyogenes strain SPY57 BVH-P1
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                                                                                                                                   pyogenes SPY57
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A
                                                             /label= Signal_peptide
                                                                                               Location/Qualifiers
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23.5%; Pred. No. 0.1;
                            "Mature_BVH_P1_protein"
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                                                                                                                                                                                                                                                                                                                                                                                                              infection, such as pharyngitis, erysipelas, impetigo, scarlet fever, invasive diseases (Dacteraemia, necrotising fascitis, toxic shock), and for eliciting an immune response. The polypeptides may also be used as immunogens for producing antibodies for the diagnosis and treatment of Streptococcus infection, or for passive immunisation. DNAs encoding polypeptides may also be used to design DNA probes for detecting the presence of Streptococcus in biological samples suspected of containing the bacteria. The vaccine composition is useful as a prophylactic or therapeutic treatment of Streptococcal infection in an individual suspected to or infected with streptococcal infection. The present
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antigens, more particularly an antigen Streptococcus youghnes (also called group A Streptococcus (GAS)) bacterial pathogen. The polypeptides and polynucleotides encodin are useful for diagnosing, preventing or treating streptococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Fig 6; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus pyogenes antigen useful for diagnosing, preventitreating streptococcal infection, e.g. pharyngitis, erysipelas and impetigo, scarlet fever, and invasive diseases
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SASEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYA--PNHAYNPMNAG
                                                                                                                                             ASSPASVSHVPSSEPLPQASATSQPTVPMAPPATPSDVPTTPFASAKPDSSVTASSELTS 167
                                                                       STNDVSTELSSESQKQPEVPQEAVPTPKAAETTEVEPKTDIS-----EAPTSANRPVPNE 222
                                                                                                                                                                                                                  YTVKYGDTLSTTAEAMGIDVHVLGDINHIANIDLIFPDTILTANYNQHGQATNLTV-QAP 107
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                                                                                                                                                                                                                                                                                                                                                                                                   is Streptococcus pyogenes strain SPY57 BVH-P1 protein.
                                                                                                                                                                                                                                                                                                                                                                 389 AA;
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23.5%;
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1.
2: /cgn2_6/ptodata/1.
3: /cgn2_6/ptodata/1.
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1670
1 MTVTIAINSQNQK
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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US-08-456-670B-40
US-08-127-499A-26
US-08-137-716-2
US-08-737-716-2
US-08-737-716-3
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US-09-136-574A-44
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US-09-136-59A-1
US-09-328-59A-1
US-09-328-59A-1
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Sequence 5, Appli
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Sequence 11, Appl
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US-08-821-355A-6	US-09-136-605-5	US-09-003-687A-5	US-08-821-355A-5	US-09-579-181-1	US-09-579-181-2	US-09-553-427-7	US-09-128-275A-7	US-08-478-507-7	PCT-US95-10661A-5	US-08-296-791-5	US-09-165-239A-4	US-08-431-387-4	US-09-442-100-4	US-09-298-568-2	US-08-728-323A-2	US-08-276-213-3	US-09-120-927-2
Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	•	Sequence 2, Appli

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Rioux, Clement

APPLICANT: Rioux, Clement

APPLICANT: Schryvers, Anthony B.

TITLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS SOMNUS

TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS

FILE REFERENCE: 9000-0049.20

CURRENT APPLICATION NUMBER: US/09/405,728

CURRENT FILING DATE: 1999-09-24

EARLIER APPLICATION NUMBER: US 09/267,749

EARLIER APPLICATION NUMBER: US 09/267,749

EARLIER APPLICATION STORY OF SEQ ID NOS: 5

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 5

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US-09-405-728-5
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                                                                                                                                                                                                                                                                                                                                                                                l Similarity
63; Conserv
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                                                                                                                                                                                                                                                                                              IRYKGQSVDPMRYL 342
                                                                                                                                                                                     FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ 249
                                 ISRNGVYVDPLTVL 321
                                                                       AGDALRGYGNLIIIKHNDSYLSAYAHNESILVKDQQEVKAGQQIAKMGSSGTNTIKLHFE
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Pred. No. 1.
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RESULT 2 US-08-456-670B-40

40, Application US/08456670B o. 5932415

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; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
US-08-456-670B-40
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Best Local Similarity 21.3
Matches 83; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 64191
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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TITLE OF INVENTION:
NUMBER OF SEQUENCES: 43
NUMBER OF SEQUENCES:
MILLEN, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TELEPHONE: // TE
160 TTQQAAPVAETKTEVKQTTQATTPAPKVAETKETPVIDQNATTHAVKSGDTIWALSVKYG 219
                                                                                                                                                                     102 IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET 159
                                                                                                         66 --SQGVP--
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E: 2200 CLARENDON BLVD., SUITE 1400
ARLINGTON
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PAWELZIK, MARTINA
LINXWEILER, WINFRIED
BUDGER CURICER
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WERNER
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                                                                                                                                                                                                                                                                                                                                               9.1%; Score 151.5; DB 2;
21.3%; Pred. No. 5.7e-06;
tive 46; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOTTFRIED
                                                                                     ----NRYQVKQGDTVSKIAQRYG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 478;
                                                                                                                                                                                                                                                                                                                                               Indels 143; Gaps
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39	6SQGVP	Οу 66	
159	ITTCLIAGCASKFTYNNTSGSGSHRTSGSGTAIGSQVITD	Db 102	
14;	8.8%; Score 146.5; DB 1; Length 484; Similarity 20.6%; Pred. No. 1.7e-05; 1; Conservative 46; Mismatches 121; Indels 145; Gaps	Query Matc Best Local Matches	
		; INFORMATION FO ; SEQUENCE CHA ; LENGTH: 4 ; TYPE: ami ; STRANDEDNE ; TOPOLOGY: US-08-127-499A-26	
	ATION CE/DOC CE/DOC NICATI NE: (20: (20: 90413	; REGISTRA ; REFERENC ; TELECOMMUN ; TELEPHON ; TELEFAX: ; TELEX:	
	ATION NUMBER DATE: 28-S /AGENT INFOR BENT, Steph	; APPLIC; FILING; ATTORNEY; NAME:	
	TER: IBM TING SYST ARE: Pat APPLICAT	; COMPUTER: ; OPERATING ; SOFTWARE: ; CURRENT APPI	
•	Y: 1 2000' REAI TYPI	; COUNTRY: ; ZIP: 20 ; COMPUTER R ; MEDIUM T	
	NDENCE ADDRESS SEE: Foley & : 3000 K Stre Washington D.C.	; CORRESPON ; ADDRESS ; STREET: ; CITY: ; STATE:	
	ANT: VAN ALSTYNE, Diane ANT: SHARMA, Lawrence Rajendra OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES OF SEQUENCES: 40	APPI APPI TITI TITI	
	7-499A-26 162 26, Application US/08127499A No. 5510264 AL INFORMATION:	RESULT 3 US-08-127-4 ; Sequence ; ; Patent No ; GENERAL	
	31FPDYGSGISHVGIVV 445	Db 4	
	289 QRIASMKNQPSGAALFEFRISRNGVYV 315	0у 2	
430		Db . 3	
288	N I	Qy 2	<u> </u>
253 373	194 SSGVMQFRYFVGATNFVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVTQADHN 25: 191	Qy 1 Db 3	
313		Db 2	·
259	S-SIYVGOKLAI		
149	TIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV	40	

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RESULT 4
US-08-482-847-26
      Query Match
Best Local Similarity 20.6
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       SOFTMARE: Patentin Release #1.0, Version #
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-UN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 484 amino acid
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & I
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                                                                                                                                                                                                                          TELEPAX: 1-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                            amino acid
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                                                                                                                                                                               484 amino acids
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VENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
VENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGE
VENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES
                                                                                                                                                                                                                                                           (202) 672-5399
                                                                                                                       unknown
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                  8.8%; Score 146.5; DB 1; 20.6%; Pred. No. 1.7e-05; tive 46; Mismatches 121;
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                                                         DB 1;
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                                                         Length 484;
                      Indels 145;
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SES THEREOF
                  Gaps
                    14;
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US-08-737-716-2
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  Query Match
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZII: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                      FILING DATE: 12-MAY-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 9
FILING DATE: 12-MAY-1994
INFORMATION FOR SEQ ID NO: 2
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APPLICANT: Adrianus
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1
FILING DATE: 12-MAY-1995
                                                         MOLECULE TYPE:
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                                                                          TYPE: ami
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                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKTNTNTNTNTNTNTNTTNTPSKNTNTNSNTNTNSNTNANQGSSNNNSNSSASAIIAE 375
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ص
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADHIMD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQHPAVQKPTPPVV------VVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SQGVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQKHLGKAYSWGGNGPTTFDCSGYTKYVFAKAGISLPRTSGAQYASTTRISESQAKPGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EAPAAEKQAAPVVKENTNTNTATTEKKETATQ---QQTAPKAPTEAAKPAPAPSTNTNA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Pillsbury Madison & Sutro, L.L.P
1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adrianus Marinus LEDEBOER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerard VENEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Girbe BUIST
                                                         protein
                                                                                                                                                                                                                                                                                                                   22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Process for the lysis of a acid bacteria by means of a
7.8%;
                                                                                                                                                                                                 EP 94201353.3
                                                                                                                                                                                                                                                         PCT/NL95/00170
                                                                                                                                                                                                                                                                                                                                       US/08/737,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFDYGSGISHVGIYV 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GASIVIOHTNGF-VSSYIHIKDAQVKTGDT
Score 130.5;
В
2
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a lysin, and uses
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Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the
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resulting

435 284 259

219

159 65

Best Local Similarity 24.1%; P. Matches 69; Conservative 39;

26 TTCILAGCASKPTYNST------SGSGSHRTSGSGGLAIGSQVITDSQGVPN- 71

Pred. No. 0.00046; 9; Mismatches 119;

Indels

59; Gaps

12;

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Matches

36; Conservative

21; Mismatches

40;

Indels

17;

Gaps

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4 Ş

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APPIICATE: 12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MAI-12-MA
                                                                                                                           US-08-737-716-14
                             Query Match
Best Local Similarity
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US-08-737-716-14
                                                                                    ORIGINAL EULC.
ORGANISM: EULC.
IMMEDIATE SOURCE:
CLONE: Fig.5a (E. hirae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: DIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,716
FILING DATE: 22-APR-1997
                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VOL. ACTIONS MATINUS LEDEBOER
TITLE OF INVENTION: Process for the lysis of a culture of lactic
TITLE OF INVENTION: acid bacteria by means of a lysin, and uses of the resulting
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 KGDTLWGLSQKSGSPİ-----ASIKANNHL-----SSDTILIGQ 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 AGTVIQADHNMDGASIVIQHTNGEVSSYIHIKDAQVKTGDTVRTGQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 WNHLSSDTIYIGONLIVSQSAAASNP-----STGSGSTATNNSNSTSSNSNASIHKVV 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 EAPFATGSSGVMQ----FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 GGSNNS-----ASTTPTTSVTPA--KPTSQTTVKVKSGDTLWALSVKYKTSIAQLKS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 SGVNTAHTESEVAVQSSRPEVQQHPAVQKPTEPVVVVKKPTET--PEVVQQDAPVAEPVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SSTTÝTÝKSGÓTLWGÍSÓRÝGISVAQÍOSANNLKST-IÍYIGÓKLVLTGS----ASSTNS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 TAALIGRYATDÞSYGASLNRIISQYNLTRFDGASSAGNTNSGG---STTTÍTNNNSGTNS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XY: U.S.A.
20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 ---RYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington D.C.
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                                                                                                                                                                                         Enterococcus hirae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BUIST
                Score 123.5; DB 2;
Pred. No. 0.0038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22201

COMPUTER READABLE FORM:

MEDLIM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/08/456,670B

FILING DATE: 01-UNN-1995

CTASSIFICATION: 435
                                                                                                                                        TELEX: 64191
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-456-670B-39
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/075,248
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE 4219111.4
FILING DATE: 11-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIAMA
BEGITETRATION TATANA
BEGITETRATION TATANA
BEGITETRATION TATANA
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                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 93,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEPAX: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION NUMBER: US 08/075,248
PRITANG PARTICATION NUMBER: US 08/075,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                          TELEPHONE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 HGISMNQLIEWNNIKNNF-VYPGQQLVVSKGSSSA--SGSTSNTSTGNTSSNTÄ 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 YGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOPMANN, GOTTERIED
BUBERT, ANDREAS
GOEBEL, WERNER
KOHLER, STIEFAN
NVENTION: PROCESSES AND AGENTS FOR DETECTING
NVENTION: LISTERIAS
Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08456670B
                                                          peptide
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EUMANN, SIEGFRIED
AWELZIK, MARTINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESS
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                                                                                                                                                                                             39:
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RESULT 8
US-09-136-574A-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/09136574A Patent No. 6294366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                            INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fabrics Using
Cellulase Enzyme Compositions
                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6294366e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                            REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19477
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Farrington, Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 QQHPAVQKPTPPVV------VVKKPTPTPPVVQQPAPVAP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA--IGSQVITD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EAPAAEKQAAPVVKENTNTNTATTEKKETATQ---QQTAPKAP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSVQDIMSWNNLSSS-SIYVGQKLAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTQQAAPVAETKTEVKQTTQATTPAPKVAETKETPVIDQNATTHAVKSGDTIWALSVKYG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SQGVP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IITSIKGG--TKVTVETTESNGWHKITYNDGKTGFVNGKYLTDKAVSTPVAPTQEVKKET 90
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                         LENGTH: 1426 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Spring House Corporate Center; P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Howson and Howson
                                                                                                                                                TELEX:
                                                                                                                                                               TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bergquist, Pete:
Daniels, Roy
Morgan, Hugh W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibbs, Moreland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inderson,
                                                                                                                                              <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 121.5; DB Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NRYQVKQGDTVSKIAQRYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KQTANTATPKAEVKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190
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// MOLECULE TYPE: protein
US-08-737-716-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                         Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08737716 Patent No. 5955258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Girbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 94201353.3
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/:
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatib
OPERATING SYSTEM: PC-DOS/
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3918
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adrianus Marinus LEDEBOER
TITLE OF INVENTION: Process for the lysis of a culture of lactic
TITLE OF INVENTION: acid bacteria by means of a lysin, and uses of the resulting
TITLE OF INVENTION: lysed culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/737,716 FILING DATE: 22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New CITY: Washington
                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 TPPVVVVKKPTPTPPVVQQPAPVAPP-----VTEAP------FAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSPVAVQSSRP-PVQQHPAVQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    868 SGAGVLAAGQSTKEIRLSIQKGSGSYNQSNDYSIRS-----ANSYIENEKVTGYIDG-
                               31 AGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 SGSGGLAIGS------QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNL
                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
   3 SGGSTTTITNNNSGTNSSSTT-----
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                                                                                                                                                                                            : 216 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNKIVDKDGKPVWLTG--VNWFGFNT---GTNVFDGVWSCNLKSALAEIANRG 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jan KOK
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                                                                                                                                                                                                                                                                       12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%;
25.3%;
                                                                   7.1%; Score 118; DB 2; 1
23.9%; Pred. No. 0.0024;
ative 35; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                            PCT/NL95/00170
                                                                                                                                                                                                                                                        4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                       Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1426;
                                                                     Indels
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   YTVKSGDTLWGISQRYGI
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                                                                       60;
                                                                     Gaps
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 41
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APPLICANT: MENG, XIANG-JIN-
APPLICANT: EMECSON, SUZANNE U.
APPLICANT: EMECSON, SUZANNE U.
APPLICANT: PURCELI, ROBERT H.
ITILE OF INVENTION: A SWINE HEPATITIS E VIRUS ANI
FILE REFERENCE: 20264267US1
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 60/053069
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: PCT/US98/14665
PRIOR APPLICATION NUMBER: PCT/US98/14665
PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 65
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-462-606-2
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Hepatitis E virus
-09-462-606-2
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             849 FIMREGLAAYTLTPRPIIHAVAPDYRVEQN 878
                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             668 LWLHPEGLLGIFPPFSPGHIWEPANPFCGEGTLYTRTWST------SGFSSD 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 LTYELTPAĞLQVRISSNĞLDCTATFPPĞGAPSAAPGEVAAFCSALYRYNRFTQRHSLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548 LTATVELTASPDRLECKTVLGNKTFRTTVVDGAHLEANGPEQYVLSFDASRQSMGAGSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 I-----GSQVITDSQGVPNRYQVKQGDTVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 VTPA--KPTSQTTVKVKSGDTLMALSVKYKTSIAQLKSWNHLSSDTIYIGQNLIVSQSAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTVTIAINSQNQKPIKRLGLIFGVITTCILAGC---ASKPTYNSTSGSGSHRTSGSGGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 7.1%;
Similarity 20.3%;
79; Conservative 4.
                                                                                                                                                                    TVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTG 282
                                                                                                                                                                                                                                                                                              VVVKKETETEPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGS
                                                                                                                                                                                                                                                                                                                                                                                                             HTPSPVAVQSSRPPVQQHPAVQKPTPPV----------
                                                                                                                                                                                                                                                                                                                                                          FSPP----EAAAPVLAAAPGLPHPTPPVSDIWVLPPPSKESQVDAASVPPAPEPAGLPSS
                                                                                                                                                                                                                                           IVLTLPPPLPPVRKPPTP--PP----SRTRRLLYTYPDGA-----KVYAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATNPVVRREGTATVAGSTVTSNGMWESGRDGDLINASNAGTVIQADHNMDGASIVIQHTN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVAQİQSANNLKST-IİYIĞQKLVLTGS----ASSTNSGĞSNNS------ASTTPTTS 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -WR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EIGHI-----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTA 134
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                                                                                                                         LVNASNPG-----HRPGGG---LCH----AFYQRFPEAFYPTE 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 118; DB 4; Length 1708;
; Pred. No. 0.048;
44; Mismatches 129; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
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Patent NO. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

ITILE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAP

ITILE OF INVENTION: EPIDENKIDIS FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,796

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4002

LENGTH: 330

TYPE: PRI

CRANTUM: PRIOR PRI

CRANTUM: PRIOR PRI SECOND NOS: 5674
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US-09-136-574A-44
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US-09-134-001C-4002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/09136574A Patent No. 6294366 GENERAL INFORMATION:
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Best Local
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNUBER: US/09/136,574A
FILING DATE: 19-AUG_1998
PRIOR APPLICATION UNUBER: US 08/932,571
APPLICATION UNUBER: US 08/932,571
APPLICATION UNUBER: US 08/932,571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fabrics Using Truncated
Cellulase Enzyme Compositions
                                                                                                                                                                                                                                                                                                                  ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center,
CITY: Spring House
STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 IKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 TAKEKSENGETSNEIFPNQVEK-----VSGSSSRATSTNSGTV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
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                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%; Score 111; DB 4; Length 330; Pred. No. 0.02; Conservative 17; Mismatches 41; Indels
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Anderson, Paige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibbs, Moreland
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US-09-136-574A-44
                                Best Loc
Matches
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                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09189035 Patent No. 6020165
                                                                                                                                                                                                                                                                                                                                                                    GENERAL
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Best Local Similarity
                                                                Query Match
                                                                                               OTHER INFORMATION: g2245671 -09-189-035-5
                                                                                                                                                                                                                              APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
CURRENT APPLICATION NUMBER: US/09/189,035
CURRENT FILING DATE: 1998-11-10
                                                                                                                           LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1751 amino acids
                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1176
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                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 GATNPVVRREGTATVAGSTVTSNGMWFSGRDGDLINASNAGT------VIQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ADHNMDGASIVIQH-----TNGFVSSYIHIKDAQVKTGD-TVRTGQ-----RIASMKNQP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 NSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH--TPSPVAVQSSRPPVQQHPAVQKPT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 SGSGGLAIGS-----
                                53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
9 SQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQG 68
                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGALSLOPDVNDNYVYMD 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDKNVPAAVVSKFHEQSIKQNAYSAITLQMVGYVAKDGNGTVSESETAPSPRWAEVKFKK 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPVVVVKKPTPTPPVVQQPAPVAPPVTE-----APFATGSSGVMQFRYPV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AIVWG-----REPSRGTKPAGGVTPTPAPTPTSTP-----TPT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGAGVLAAGQSTKEIRLSIQKGSGSYNQSNDYSVRS-----ATGYIENEKVTGYIDG- 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGAALFEFRISRNGVYVD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVVHP-ARRLG-----GNRLTGYN-WEN-----NMSNAGSDWYHSSDDYMCYIMGITG 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTTT----PTPTPTVTVTPTP-TPAVTPDVKISIDTSRGRTKISPYIYGANQDIQ----- 1258
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-540-5818
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REFERENCE/DOCKET NUMBER: 19:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: SEQ ID NO:
                             6.6%; Score 109.5; DB 3; 22.8%; Pred. No. 0.048; tive 19; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 110.5;
23.3%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99;
                                                             Length 480;
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                               Indels
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                               81;
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                                                                                                                                                           RESULT 15
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US-09-136-574A-47
; Sequence 47, Application
; Patent No. 6294366
; GENERAL INFORMATION:
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US-09-382-086-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09382086
Patent No. 6201106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/382,086
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/189,035
EARLIER FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 480
                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                                                     302
                                                                                                                                                                                                                                                                                                                                                                                                                          129 SGVNTAHTPSPVAVQSSRPPVQQHP-----AVQKPTPPVV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 VVKKPTPTPP-----VVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
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                                                                                                                                                                                                                                                                                                                                     164 VVKKPTPTPP-----VVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 - PPTIGPAPG---SAPGSQYGTMTRQISRHNSTTS-----STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 SLNORPRTHSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 IADSPTPPPPPPDDIPMFDDSPPPPPPPPVDYEDEEAAVVQYNDPYADGDP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 SLNQRPRTHSG------SSGGSGSRENSGSSSIGIPIAVPTPS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 SQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQG 68
                                                                                                                                                                                                                                                                                           IADSPTPPPPPPPDDIPMFDDSPPPPPPPPPVDYEDEEAAVVQYNDPYADGDP
                                                                                                                                                                                                                                                                                                                                                                                SG-GYRRTPSVTAQFSAQPHVNGGPLYSQNSISIAPPPPPPPPPPQLTPQIPLTGFVARVQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVNTAHTPSPVAVQSSRPPVQQHP-----AVQKPTPPVV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PPTIGPAPG---SAPGSQYGTMTRQISRHNSTTS-----STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG-GYRRTPSVTAQFSAQPHVNGGPLYSQNSISIAPPPPPPMPQLTPQIPLTGFVARVQEN 360
                                                                                                                                                                                 Application US/09136574A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
Bergquist, Peter
Daniels, Roy
Morgan, Hugh W.
                                                                     Anderson, Paige
Gibbs, Moreland
                                                                                                            Farrington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.6%; Score 109.5; DB 22.8%; Pred. No. 0.048; vative 19; Mismatches
                                              Peter
                                                                                                                Graham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSGGSGSRENSGSSSIGIPIAVPTPS--
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                                                                                                                                                                                                                                                                                           412
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NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for Treating Cellulose Containing Fabrics Using Cellulase Enzyme Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                           132 NTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAP-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 ASKPTYN----STSGSGSHR-----TSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSK
                                                                                                                                                                                                                                                                                             TDDTNDDWLFAQGNKIVDKDGKPVWLTG---VNWFGFNT----GTNVFDGVWSCNLKSALAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASNVTFNFVKLSSGVSGADYYLEVGFSSGAG------QLQPGKDTGD
                                                                                                                                                                                                                                                                                                                                            -----FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAQRYGLN------WREIGHINNL--NSSYTIYTGQWLTLWSGDLKVRERSISSGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQVRFNKNDWSNYNQADDWSWLQSMTNYGENAKVTLYV-DGVLVWG-----QEPGGAV 157
                                                                                                                                                                                                                                                                                                                                                                                          -PTPTAT----PTPTPSITITPAPTATP-TPTPSV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 83;
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US-09-328-599A-1
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 15-JAN-1997
CLASSIFICATION NUMBER: US/08/783,77;
FILING DATE: 15-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7662-0
TELECOMMUNICATION: INFORMATION:
TELEPAN: 212-69-8864
TELEPAN: 212-69-8864
TELEPAN: 212-69-8864
TELEZ: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
                                                                                                                                                           Sequence 1, Application US/09328599A Patent No. 6432679
ARERIT NO. BEACHTON:
GENERAL INFORMATION:
APPLICANT: MOND, James J. and Lees, Andrew
TITLE OF INVENTION: Enhancement of B Cell Activation by
TITLE OF INVENTION: Co-Ligation of Receptors for Antigen
TITLE OF INVENTION: Using EBV gp350/220 or EBV gp350/220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches (
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Best Local &
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TITLE OF INVENTION: GP3
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                                              581 SAVTTPTPNATSPTLGK-TSPTSAVTTPTPNATGPTVGETSPQANATN------HTLG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 MQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFS-GRDGDLINASNAGTVIQADHNMD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATG-----SSGV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 -- TADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 TSPTLNTTGFADPNTTTG------LPSSTHVPTNLTAPASTGPTVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 REIGHINNLNSSYTIYTGQWLT----LWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 6.5%; Score 109; DB 3; Length 907; l Similarity 23.2%; Pred. No. 0.13; Indels 66; Conservative 34; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                          GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                               -PTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPS 670
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19
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                                  and Complement C3d
Peptide Adjuvants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             580
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-136-574A-47

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:

TYPE: amino acid STRANDEDNESS: single

COMPUTER: IBM COMPACTIBLE
COMPUTER: IBM COMPACTIBLE
COPERATING SYSTEM: DOS
CURRENT APPLICATION DATA;

APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: COMPACTION: COMPACTION:
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 08/932,571
APPLICATION NUMBER: US 08/932,571
APPLICATION NUMBER: US 08/932,571
APPLICATION NUMBER: 19, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION UMBER: 31,215
REGISTRATION UMBER: 1997US001/CIP
TELEPHONE: 215-540-5818
TELEPHONE: 215-540-5818
TELEPAX: 215-540-5818

ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

USA

Query Match Best Local Matches

ch 6.6%; Score 109.5; I Similarity 23.7%; Pred. No. 0.00 58; Conservative 24; Mismatches

.068; DB 4; , 08

84 65

RESULT 16 US-08-783-774-2 Patent No. GENERAL INFORMATION: APPLICANT: Spacte , Application US/08783774 Winthrop

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                                                                                                                                                                                                                                                                                                    RESULT 18
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                                                                                                                                                                                                                                             Sequence 19, Application PC/TUS9504611A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                       STREET: 5...
STREET: 5...
STREET: Palo Alto
CITY: Palo Alto
CITY: Palo Alto
CITATE: California
CITATE: USA
                                                                                                                                                                                                  MTATTER OF INVENTION: Non Splicing Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                      DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                              581 SAVTTPTPNATSPTLGK-TSPTSAVTTPTPNATGPTVGETSPQANATN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 MQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFS-GRDGDLINASNAGTVIQADHNMD 255
                                                                                                                                                                                                                                                                                                                                                                                           256 GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATG-----SSGV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 --TADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW 92
                                                           94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSPTLNTTGFADPNTTTG------LPSSTHVPTNLTAPASTGPTVS------
                                                                                                                                                                                                                                                                                                                                                        GTS----PTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPT 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DC
                                                                                                                                 E: Cooley Godward Castro Huddleson & Tatum
5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               907 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                      Non Splicing Variants
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                                                                                                    CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2285
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09308375 Patent No. 6300117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                 LENGTH: 2285
TYPE: PRT
ORGANISM: Bacillius subtilis
                                                                                                                                                                                                                                                        FILE REFERENCE: GC394-PCT
                                                                                                                                                                                                                                                                   APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Proteases From Gram-Positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Luann Cserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATG-----SSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 MQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFS-GRDGDLINASNAGTVIQADHNMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 TSPTLNTTGFADPNTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 REIGHINNLNSSYTIYTGQWLT----LWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                                                                                   GTS----PTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- TADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT---
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In Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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6.5%;

Score 108.5; D Pred. No. 0.56;

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63; Conservative

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NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEPAS: (415) 327-3231
INFORMATION FOR SEQ ID NO. 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THEISEN, MICHAEL HARLAND, RICHARD J. RIOUX, CLEMENT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VACCINES FOR HAEMOPHILUS SOMNUS
                                                                                                                                                                                                                                                                                                                                                 US 08/038,719
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                                                                                                                                                                                                                                                9000-0019.20
  Score 108;
  DB 3;
Length 265;
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US-08-619-812-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER US 08/038
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches 39; Conservative 35;
                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 327-32
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION UNMBER: US/08/619,812
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                        130 GVNTAHTESPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTBTPPVVQQPAPVAPPVTEAP 189
                                                                              180 SEVTONTVNE-TWNANKPTNEOMKPVATPTHSTMPINK---TPPATSNIAWIWP-----
                                                                                                                    73 YQVKQGDTVSKIAQRYGLIWREIGHINNLNSSYTIYTGQWLTLWSG---DLKVRERSISS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 SEVTQNTVNE-TWNANKPTNEQMKFVATFTHSTMFINK---TFPATSNIAWIWP----- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GVNTAHTESEVAVQSSRPPVQQHEAVQKETPEVVVVKKETETPEVVQQEAEVAEEVTEAE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 YKVRKGDIMFLIAYISGMDIKELATLNNWSEPYHLSIGQVLKIANNIPDSNMIPTQTINE 165
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                                                                                                                                                                        Conservative
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THEISEN, MICHAEL
HARLAND, RICHARD J.
RIOUX, CLEMENT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                              327-3231
                                                                                                                                                                 6.5%; Score 108; DB 3; Length 279; 22.0%; Pred. No. 0.03; tive 35; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VACCINES FOR HAEMOPHILUS SOMNUS
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5; Mismatches
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RESULT 20 US-08-619-812-9

INFORMATION:

1665 İEQNGKTIDP 1674

308 ISRNGVYVDP 317

CORRESPONDENCE ADDRESS

CALIFORNIA

INVENTION

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1515

; MOLECULE TYPE: US-08-619-812-9

TYPE: an

LENGTH:

APPLICATION NUMBER: US 0 FILING DATE: 29-MAR-1993 ATTORNEY AGENT INFORMATION:

APPLICATION NUMBER: FILING DATE: 15-MAI CLASSIFICATION: 435

15-MAR-1996

Query Match

6.5%;

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US-08-737-716-13
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Matches
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: Fig.5a (S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL95/00170
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 12-MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 22-APR CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W.
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 226
                                     473
                                                                      166
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                                                                                                                                         106 TIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVV
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SNG---MWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGD 283
                                                                    KKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVT 225
                                                                                                                                                                               DTLNKIAAQYGVSVANLRSWNGISGDLIFVGQKLIVKKGASGNTGGSGNGGSNNNQSGTN 428
                                                                                                                                                                                                              DTVSKIAQRYGL----NWREI-----
                                                                                                                                                                                                                                                  ATDPSYNAKLNNVITAYNLTOYDTPSSGGN--TGGGTVNPGTGGSNNQSGTNTYYTVKSG
                                                                                                        TYY----TVKSGD-TLNKIAAQYGVTVANLRSWNGISGDLIFVGQK----
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VENTION: Process for the lysis of a culture of lactic
VENTION: acid bacteria by means of a lysin, and uses or
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                                                                                                                                                                                                                                                                                                                                         6.4%; Score 107.5; DI 20.8%; Pred. No. 0.12;
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US-09-109-841-2
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                                 US-09-556-706B-2
                                                    RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bjornvad, Mads E.
APPLICANT: Hatakeyama, Mariko
APPLICANT: Schulain, Martin
APPLICANT: Nielsen, Jack B.
TITLE OF INVENTION: Bado-Beta-1,
TITLE OF INVENTION: Saccharothrix
FILE REFERENCE: 5195.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
Sequence 2, Application US/09556706B Patent No. 6458364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/053,506
EARLIER FILING DATE: 1997-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 0812/97
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 0846/97
EARLIER FILING DATE: 1997-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/109,841
CURRENT FILING DATE: 1998-07-02
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492 QSGTNTYYTIKSGDTLNK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VTVTNLGDPLSSWELSWTFPDGQGVQQLWNGVHSTSGSNVTVKEMSWNGSVGTNASVQVG
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                                                                                                                                                                             TSAAAAAGRTAVLVVYAIPGRDCGQHSSGGVSTSEYAQWIDTVAQGIVGNPWVVLDPDAL
                                                                                                                                                                                                                                                    NQSYRAWQAA----
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                                                                                                        PMLGDCDGQGDRVGFLK 343
                                                                                                                                                                                                                  -----GASIVI-----
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RESULT 25
US-08-155-171B-15
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PRIOR FILING DATE: 1994-04-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.0
IEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jackman, Winthrop
TITLE OF INVENTION: NON SPLICING VARIANTS OF GP350/220
FILE REFERENCE: 7662-050-999
CURRENT APPLICATION NUMBER: US/09/556,706B
CURRENT FILING DATE: 2000-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Spaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/783,774
PRIOR FILING DATE: 1997-01-15
                                                                                                                                 MEDIUM TYPE': Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Virus
                                                                                                                                                                                                                                                                                                          ORRESPONDENCE ADDRESS:
                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
RERENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 19-NOV-1993
                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 22.1 les 63; Conservative
                                                                                                                                                                                                                                                                                                                                                 LICANT: Anderson, Carl W.
LICANT: Mangel, Walter F.
LICANT: Mangel, Walter F.
LE OF INVENTION: Co-Factor Activated Recombinant
LE OF INVENTION: Adenovirus Proteinases (As Ameno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 VQQHPAVQKPTP----PVVVVKKPTP--TPPVVQQPAPVAPPVTEAPFATGSSGVMQFRY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 SPQANATNHTLGGTSPTPVVTSQPKNATSAVTTGQH-----NRPS 659
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>. 5543264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 TSPTLNTTGFADPNTTTG------LPSSTHVPTNLTAPASTGPTVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 REIGHINNLNSSYTIYTGQWLT----LWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPS 299
                                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                            E: Hamilton, Brook, Smith & Reynolds, P.C Two Militia Drive
                                                                                                                                                                                                  USA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 106.5; D
22.1%; Pred. No. 0.22;
tive 29; Mismatches
                  US/08/155,171B
                                                              Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ATSPTLGKTSPTSAVTTPTPNATGPTVGET 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                    (As Amended)
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RESULT 26
US-08-435-998-15
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                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/08/435,998

FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 15:
                             FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/545,585
                                                                                                                                                                                                                                                                                                                                               STREET: 1 STREET Lexington
CITY: Lexington
STATE: Massachusetts
THEY: USA
                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,171
FILING DATE: 19-NOV-1993
APPLICATION NUMBER: US 07/851,217
FILING DATE: 13-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, Pat
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 6.2%; Score 103.5; DB Local Similarity 24.0%; Pred. No. 0.067; es 42; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TVSPEGRGEKRPRPDREETLVTQIDEPPSYEEALKQGLPTTRPI--APMATGVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 KPTPPVVVVKKPTP-----TPP----VVQQPAPVAPPVTEAPFATGSSG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 SKIAQRYGL----NWREIGHINNLNSSYTIYTGQWLTLWSGDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STGOMLRDKLKÉQNFQQKVVDGLASGISGVVDLANQÁVQNKINSKLDPRPPVEEPPPÁVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08435998
                                                                                                                                                                                                                                                                                                                                                                                                                          E: Hamilton, Brook, Smith & Reynolds, P.C. Two Militia Drive
TE: 29-JUN-1990
ENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson, Carl W. Mangel, Walter F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                              Release #1.0, Version
                                                                                                                                                                                                            US/08/435,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/545,585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 250;
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Best Local Similarity 24.0
42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                               SEQUENCE CHARACTERISTICS LENGTH: 214 amino acid
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 250 amino acid
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
MOLECULE TYPE:
                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          NAME: Seay, Nicholas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
               TOPOLOGY:
                                                                                                           TELEPHONE:
                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 KPTPPVVVVKKPTP-----
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5. 5474925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 STGQMLRDKLKEQNFQQKVVDGLASGISGVVDLANQAVQNKINSKLDPRPPVEEPPPAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 SKIAQRYGL-----NWREIGHINNLNSSYTIYTGQWLTLWSGDL-------
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                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Madison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.O.
                                             214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617)
                                                                                               608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                John, Maliyakal E
Barton, Kenneth A
/ENTION: Immobilized Proteins in Cotton Fiber
                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                             608-251-5000
                                                                                                                                                                        Nicholas J
                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Box 2113
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                                                                                                                                                         27,386
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                                                                                                                                             1122990831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TPP----VVQQPAPVAPPVTEAPFATGSSG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 250;
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US-09-120-927-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2,
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                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 447 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kim, Jihyun E
APPLICANT: Beer, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING TO PERAFE #1.0
                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                 ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AME: Goldman, Michael
147 SDQFGQPGTGNNSASSGTSSSGGSPFNDLSGGKAPSGNSPSGNYSPVSTFSPP--
                            109 TGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 FAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 NTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPT-PPVVQQPAPVA-PPVTEAP 189
                                                             90 GTAGTTPQSDSQ---NMLSEMGNNGLDQAITPDGQGGGQIGDNPLLKAMLKLIARMMDGQ 146
                                                                                           57 -AIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTI-----Y 108
                                                                                                                             30 ANSALGQQPIDRQTIEQMAQLLAELLKSLLSPQSGNAATGAGGNDQTTGVGNAGGLNGRK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 STPATPTPPA--STPPPTTQAPPTPTATPPPVSTPPPTSSPPPVTASPPPVSTPPPSSPP
                                                                                                                                                           6 AINSQNQKPIKRLGL-IFGVITTCILAGCASKPTYNSTSGSGSH-RTSG---SGGL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rochester
New York
RY: U.S.A.
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                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                      447 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                    (716) 263-1600
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim, Jihyun Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                    (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-197
                                                                                                                                                                                                        6.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hargrave, Devans & Doyle LLP
1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 60/055,108
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                                                                                                                                                                                                        Score 102; DB 4; Length 447; Pred. No. 0.21;
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Pred. No. 0.06;
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ITS USE
                                                                                                                                                                                          147;
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US-08-276-213-3
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                                                                                                                                                                                     Best Local
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Best Local :
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: prot. HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-ter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 80401-3393
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,213
FILING DATE:
COUNTRY: US/08/276,213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: O'Connor, Edna
REGISTRATION NUMBER: 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 151.
STREET: Golden
CITY: Golden
COTTE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                             373 SPSPSPSASRTPTPTPTPTASPTPTLTPTATPTPTASPTPSPTAASGARCTASYQVNS
                                                                                                                        315
                                                                                                                                             111 QWLTLWS-----GDLKVRERSISSGVNTAHTP-----SPVAVQSSRPPVQQHPAV 155
                                                                            156 Q-KPTPPVVVVKKPTPTPPVVQQPAPV-----APPVTBAPFATGSSGVM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 -ADGIHLYGDAKIDNLHVTNVGEDAITVKPNSAG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 VSSYIHI-KDAQVKTGDTVRTGQRIASMKNQPSG 300
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5. 5536655
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                                                                                                                                                                                     l Similarity
53; Conser
----QFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNM 254
                                                                                                               QW-TFWSWNPDSGDTGGTLKDDWQTVDTVKDGYLAPIKSSIFDPVGASAS-PSSQPSPSV
                                                                                                                                                                                                                                                                                                                                                            : 521 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -TVAGSTVT-SNGMWFSGRDGDLINASNAGTVIQADHNM-----DGASI--VIQHTNGF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPTSPTSPLDFPSSPTKAAGGSTPVTDHPDPVGSAG-----IGAGNSVA--FTSAGAN 251
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    National Renewable Energy Laboratory
1617 Cole Boulevard

                                                                                                                                                                                6.1%; Score 101.5; Ilarity 25.2%; Pred. No. 0.3; Conservative 20; Mismatches
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Himmel,
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                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                Length 521;
                                                                                                                                                                                  Indels
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                                               432
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US-08-728-323A-2
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Best Local S
Matches 40
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                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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APPLICANT:
APPLICANT:
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STREET: 1185 Av
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                     180
     239
                             185 VTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVA-GSTVTSNGMW 230
                                                                                                                                  120 VSPGTTDTHSPSPALPPTQSPESSORPPLSSPTGRPDSSTPMRPPPSQQTTPPHSPTTPP
                                                                                                                                                                  127 ISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPT-----PPVVVVKKP----TPT 171
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                                                                                                                                                                                                  ch 6.1%; Score 101.5; D) Similarity 24.0%; Pred. No. 0.95; 40; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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ATESPIYVGSSS-----DGDTPP--RQPPTSPISIGSSSPSEGSW 276
                                                                 PEPPSKSSPDSLAPSTLRSLRKRRLSSPQGPSTLNPICQSP-PVSPPRCDFANRSVYPPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chany, ... J.
Bohenzky, ... James J.
Russo, James J.
T: Edelman, Isidore S.
Tore, Patrick S.
Immediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Encoding Same And
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/728,323A
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                                                                                                   0575/52268/JPW/MSC/SKS
                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                     Length 1162;
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                                                                                                                                                                                                  Gaps
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RESULT 31 US-09-298-568-2 ; Sequence 2, Application US/09298568 ; Patent No. 6322792

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09442100 Patent No. 6359193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 3
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APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yu, Wan
IITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
IITLE OF INVENTION: GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65
                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 ISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPT-----PPVVVVKKP----TPT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 VSPGTTDTHSPSPALPPTQSPESSQRPPLSSPTGRPDSSTPMRPPPSQQTTPPHSPTTPP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
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                                                                                                                                                                                                                                                                                                                                                New York
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, Sheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Weiyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu, Tian
                                                                                                                                                                                                                                                                   Floppy disk
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                                                                                             08/411,111
                                                                                                                                                                        US/09/442,100
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Pred. No. 0.95;
.2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PVVQQPAPVAPP-----
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6.0%; Score 10.1.;
Rest Local Similarity 24.3%; Pred. No. 1.1;
Rest Local Similarity 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Mainze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/950,856A
FILING DATE: September 24, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1130 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSES: Genencor International, Inc
STREET: 180 Kimball Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC
                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                     STREET: 180 Kimball way
CITY: South San Francisco
                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 FMIHQNVVPAGTVNRQPPPPYPLTAANGQSPSALQTGGSAAPSSYTNGSIPQSMMVPNRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 QVKQGDTVSKIAQRYGL-----NWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 FGVITTCILAGCASK---PTYNSTSGSG-SHRTSGSGGLAIGSQV----ITDSQGVPNRY 73
                                                                                                                                                                                                                                                                                          94080
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5677163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lad, Pushkaraj J. Schmidt, Brian
                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleaning Compositions Containing No. 5677163el Alkaline Proteases
                                                                                                                                                               US/08/431,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100.5; I
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAHTPSPV--AVQSSR---PPVQQHPAVQKPT--PPVV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; · Length 1130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
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TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 4:

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS: LENGTH: 268 amino acid

Patent No. 6245337

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RESULT 35
US-08-296-791-5
; Sequence 5, Application US/08296791
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-431-387-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/068,065
PRIOR PILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 750
                                                                                                                                                                                                                                                                                                                                  Query Match 5.9%; Score 98.5; DB 4; Length 750; Best Local Similarity 31.5%; Pred. No. 0.96; Matches 46; Conservative 12; Mismatches 65; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09165239A Patent No. 6344554 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.,
71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 220022000700
CURRENT APPLICATION NUMBER: US/09/165,239A
CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JOHNSON, ALEXANDER
APPLICANT: BRAIN, BURKHARD R
TITLE OF INVENTION: POLYMUCLEOTIDE SEQUENCES FROM CANDIDA
TITLE OF INVENTION: ALBICANS ENCODING POLYPEPTIDES ASSOCIATED WITH FILAMENTOUS
TITLE OF INVENTION: GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-165-239A-4
                                                                                                                                                  246
                                                                                                                                                                                         660
                                                                                                                                                                                                               186 TEAPFAIGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAG 245
                                                                                                                                                                                                                                                                   603
                                                                                                                                                                                                                                                                                            128 SSGVNTAHTESEVAVQSSREPVQQHPAVQKETEPVVVVKKETETEPVVQQEAPVAE--PV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 AGVAALVKSRYPSYTNNQIRQRINQTATYLGSPSLYGNGLVHAGR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 TGSSGVMQFRYPVGATNPVVRRFG-TATVAGS-TVTSNGMWFSGR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 GVMAVAAVDONGOPPSFSTYGPEIEISAPGVNVNSTYTGNRYVSLSGTSMA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 SPVAV----QSSRPP--VQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 INNNMHIINMSLGSTSG-----SSTLELAVNRANNAGILLVGAAGNTGRQGVNYPARYS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 EIGHINNLNSSYTIYTGQWLTLWSGDLKVR-ERSISSGV------NT-----AHTP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HGTH---VAGTIA----ALNNSIGVLGVAPSADLYAVKVLDRNGSGSLASVAQ--GIEWA 111
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                                                                                                                                                                           SSAP-AVEŚŚPVA----PGVETTPV-----APVAPŚTTAKTSALVŚTTEGTIPTTLESV 708
                                                                                                          PAIQPSANS-----SYTIASVSSF 727
                                                                                                                                              TVIQADHIMDGASIVIQHTNGFVSSY 271
                                                                                                                                                                                                                                                          SSPVAPGTESSPVAPESSAPATESAPATE -- SSPVAPGTETTPATPGAES-TPVAPVAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTIA, INSQNOKPIKRLGLIFG-----VITTCI-----LAGCA----SKPTYNSTSG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVVWGISFINTQQAHNRG-IFGNGARVAVLDTGIATHPDLRIAGGASFISSEPSYHDNNG
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;; Pred. No. 0.22;
46; Mismatches 95;
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RESULT 36
PCT-US95-10661A-5
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/296,791

FILING DATE: 25-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Trecartin, Richard F.

REGISTRATION UNMBER: A-59941/RFT/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 789-3249

TELEFAX: 415) 398-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1702 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-296-791-5
                                                                                                                                                                    Sequence 5, Application PC/TUS9510661A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                        APPLICANT: Washington University, et al.
TITLE OF INVENTION: Haemophilus Adherence and
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: St. Geme 1
APPLICANT: Falkow, St
TITLE OF INVENTION: H
TITLE OF INVENTION: F
NUMBER OF SEQUENCES;
  ADDRESSEE: Flehr, Hohbach, Les
STREET: 4 Embarcadero Center,
CITY: San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
ADDRESSEE: Flehr, Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRIE: Californ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal
                                                                                                                                                                                                                                                                       1047 ENS 1049
                                                                                                                                                                                                                                                                                                             192
                                                                                                                                                                                                                                                                                                                                             999
                                                                                                                                                                                                                                                                                                                                                                      132 NTAHTDSPVAVQSSRPBVQQHPAVQKPTPFVVVVKKPTPTPPVVQQPAPVAPPVTEAPFA 191
                                                                                                                                                                                                                                                                                                                                                                                                          953 N--ATRNNLNVSLVGNTVDLGAWKYKLRNVNGRYDLYNPE------VEKR--NQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          896 TVNSLSGNGSFYYLTDLSNKQGDKVVVTKSATGNFTL---QVADKTGEPTKNELTLFDAS 952
                                                                                                                                                                                                                                                                                                                                                                                                                                        82 SKIAQRYGLNWREIGH------INNLNSSYTIYTGQWLTLWSGDLKVRERSISSGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 TYNSTSGSGSH-------RTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 5.9%; Score 98.5; Di Similarity 23.0%; Pred. No. 3.1; 42; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acids
                                                                                                                                                                                                                                                                                                           TGS 194
                                                                                                                                                                                                                                                                                                                                             DTTNITTPNNIQADVPSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geme III, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joseph
                                                              Test, Albritton & Herbert
er, Suite 3400
                                                                                                                                                                                                                                                                                                                                     ---PSNNEEIARVETPVPP----PAPATPSETTETVA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
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                                                                                                                              Penetration Protein
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                                                                                                                                                                                                                                                                                                                                          Sequence 7, Applic Patent No. 6120988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                  ITTLE OF INVENTION: DNA TITLE OF INVENTION: NO. TITLE OF INVENTION: NO. TITLE OF ARCHIENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: FP-59941/RFT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-AUG-
                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                     STREET: 350
CTTY: Palo Alto
                                                                                                                                                                                                                                                           PPLICANT:
                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      COUNTRY: U
ZIP: 94306
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                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1047 ENS 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 TGS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 NTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             953 N--ATRNNLNVSLVGNTVDLGAWKYKLRNVNGRYDLYNPE-----VEKR--NQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            896 TVNSLSGNGSFYYLTDLSNKQGDKVVVVTKSATGNFTL---QVADKTGEPTKNELTLFDAS
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                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 SKIAQRYGLNWREIGH-----INNLNSSYTIYTGQWLTLWSGDLKVRERSISSGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 TYNSTSGSGSH-------RTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1702 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                          Application US/08478507
                                                                                                                 3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 781-1989
(415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                     Tam, Albert
Fry, Kirk E
                                                                                                                                                                                                                                                                    Yarbough, Patrice O
Bradley, Daniel W
                                                                                                                                                                                                                                                      Krawczynski,
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                                                                                                                                                                                    DNA Sequences of Enterically Transmitted No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
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                                                                                                                                                                                                                                                        Krzysztof Z
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Pred. No. 3
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                                                                                                                                                                         Sequence 7,
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER: US 07/420,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-ARR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
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PRIOR APPLICATION NUMBER: US 07/505,888
               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                              TITLE OF INVENTION:
                                                                APPLICANT:
                                                                            APPLICANT:
                                                                                               APPLICANT:
                                                                                                                              APPLICANT:
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PRIOR APPLICATION NUMBER: US 07/367,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/279,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rela
CORRESPONDENCE ADDRESS:
                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                              685 GHVWESANPFCGESTLYTRTW------
                                                                                                                                                                                                                                                                               786 ---
                                                                                                                                                                                                                                                                                                           204 VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDG 256
                                                                                                                                                                                                                                                                                                                                                                          151 QH---PAVQKPTPPVVVVKKPTPTPPVVQQPA----PVAPPVTEAPFATGSSGVMQFRYP
                                                                                                                                                                                          ,7
                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           96 GHI----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPS-PVAVQSSRPPVQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                           SRAATPTLAAPLPPPAPDPSPPPSAPALAEPASGATAGAPAITH---QTARHRRLLFTYP
                                                                                                                                                                                            Application US/09128275A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1693 amino acids
                                                             Tam, Albert
Fry, Kirk E
                                                                                                         Yarbough, Patrice O
Bradley, Daniel W
                                                                                              Krawczynski, Krzysztof Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                            keyes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                              -- DGSKVFAGSLFESTCTW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324-0960
                                                                                                                                            Gregory R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 98; DB 3; Length 1693; 24.9%; Pred. No. 3.4;
           DNA Sequences of Enterically Transmitted
No. 6229005-A/No. 6229005-B Hepatitis Vi
20
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                             6229005-B Hepatitis Viral Agent
                                                                                                                                                                                                                                                                               LVNASN--
                                                                                                                                                                                                                                                                                                                                                                                                            --SEVDAVSSPARPDLGFMSEPSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Indels
                                                                                                                                                                                                                                                                              --VDHRPGG 815
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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-128-275A-7
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REFISERENCE/DOCKET NUMBER: 4600-0183.24
FTELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
FTELEPAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1693 amino acids
TYPE: amino acids
                                                                            RESULT 39
US-09-553-427-7
                                                                                                                                                                                                                                                                                                                       Ś
                                         Sequence
Patent No
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 43
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/326 CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
APPLICATION NUMBER: 25-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
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FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 07/681,078

PILING DATE: 05-APR-1991

PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
Cice 7, Application US/09553427
No. 6379891
AL INFORMATION:
LICANT: Reyes, Gregory R
                                                                                                                                                                         204 VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDG 256
                                                                                                                                                                                                                                               151 QH----PAVQKPTPPVVVVKKPTPTPPVVQQPA----PVAPPVTBAPFATGSSGVMQFRYP
                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                          SRAATPTLAAPLPPPAPDPSPPPSAPALAEPASGATAGAPAITH---QTARHRRLLFTYP
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ION NUMBER: US 07/420,921
ATE: 13-OCT-1989
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                                                                                                                                            -DGSKVFAGSLFESTCTW--
                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 98; DB 4; Length 1693; 24.9%; Pred. No. 3.4; ative 14; Mismatches 62; Indels !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
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                                                                                                                                                                                                                           ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-553-427-7
                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/420,921
APPLICATION NUMBER: US 07/420,921
PRIOR APPLICATION DATA:
APPLICATION MATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UN-1989
PRIOR APPLICATION NUMBER: US 07/336,672
                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 324-096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-ARR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/553,42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
ADDRESSEE: 350 Cambridge Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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TITLE OF INVENTION: DNA Sequences of
TITLE OF INVENTION: NO. 6379891-A/No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sholtz, Charle REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 11-AP
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                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                         685 GHVWESANPFCGESTLYTRTW----
729 SRAATPTLAAPLPPPAPDPSPPPSAPALAEPASGATAGAPAITH---QTARHRRLLFTYP
                                151 QH----PAVQKFTFFVVVVKKFTFTFPVVQQPA----PVAFFVTEAFFATGSSGVMQFRYF 203
                                                                                                      96 GHI----NNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPS-PVAVQSSRPPVQ 150
                                                                                                                                                   43;
                                                                                                                                                                    Similarity
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Bradley, Daniel W
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. 6379891-B Hepatitis Viral Agent
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                                                                       SEVDAVSSPARPDLGFMSEPSIP 728
                                                                                                                                                                                    Length 1693;
                                                                                                                                                 Indels
                                                                                                                                                 54;
                                                                                                                                               Gaps
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
IENGTH: 2972
IENGTH: 2972
TORGANISM: Human
US-09-579-181-2
Search completed: July 8, 2003, 11:08:55 Job time: 30 secs
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US-09-579-181-2
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Patent No. 6365372
GENERAL INFORMATION:
APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEC IN NOC. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.8%; Score 97; DB 4; Length 2972; Best Local Similarity 25.7%; Pred. No. 9.6; Matches 52; Conservative 20; Mismatches 52; Indels
                                                                                                  1010 LTFQTQGNKLTLTGAQVRQLAV 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                            137 PSPVAVQS--SRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGS 194
                                                                                                                                                      304 FEFRISRN-----GVYVDPLTV 320
                                                                                                                                                                                                     974 LSPD----
                                                                                                                                                                                                                                                 248 IQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQP----SGAAL 303
                                                                                                                                                                                                                                                                                                       928 SSLLKPLTVPPGYTFPPAAATTTSTTTATATTT------AVPAPTPAPQRLI 973
                                                                                                                                                                                                                                                                                                                                                                                                       890 PSPLGVLSGTSRP-------PTPTLSL--KPTPPAPVRLSPAP--PP------GS 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDG 256
                                                                                                                                                                                                                                                                                                                                                      195 SGVMQ-FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGT-----V 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DGSKVFAGSLFESTCTW-----LVNASN------VDHRPGG 815
                                                                                                                                                                                                       -----MOARLPSGEVVSIGO-LASLAORPVANAGGSKP 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Indels 78;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
July 8, 2003, 11:07:43; Search time 53 Seconds (without alignments) 707.305 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
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1670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	89	7	σ	S	4	ω	N	1	Result No.
108.5	110	110	110.5	112	112	112	117	118	118	118	118	118	125.5	127	127.5	142	182.5	209	Score
6.5	6.6	6.6	6.6	6.7	6.7	6.7	7.0	7.1	7.1	7.1	7.1	7.1	7.5	7.6	7.6	8.5	10.9	12.5	Query Match I
474	360	258	312	1228	1228	957	237	1192	1192	1192	1192	1192	205	1708	397	203	301	345	Query Match Length DB
9	10	9	9	9	9	9	9	10	10	10	10	9	ø	9	9	9	9	9	: B
US-09-738-626-3548	US-09-925-301-1116	US-10-156-761-9957	US-10-101-464A-930	US-09-917-383-1	US-09-917-384-1	US-10-155-400-1	US-09-738-626-4458	US-09-972-599A-6	US-09-893-348-23	US-09-758-140-6	US-09-789-386-2	US-10-060-036-71	US-09-738-626-6241	US-09-468-147-166	US-10-156-761-14779	US-10-156-761-12234	US-10-156-761-9179	US-10-098-808-5	ID
Sequence 3548, Ap	Sequence 1116, Ap	Sequence 9957, Ap	Sequence 930, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 4458, Ap	Sequence 6, Appli	Sequence 23, Appl	Sequence 6, Appli	Sequence 2, Appli	Sequence 71, Appl	Sequence 6241, Ap	Sequence 166, App	Sequence 14779, A	Sequence 12234, A	Sequence 9179, Ap	Sequence 5, Appli	Description

108 6.5 877 9 US-10-245-103-90 108 6.5 877 9 US-10-245-107-90 108 6.5 877 9 US-10-245-107-90 108 6.5 877 9 US-10-245-851-90 108 6.5 877 9 US-10-245-83-90 108 6.5 877 9 US-10-238-33-90 108 6.5 877 9 US-10-238-33-90 108 6.5 877 9 US-10-238-370-90 108 6.5 877 9 US-10-238-370-90 108 6.5 877 9 US-10-238-370-90 108 6.5 877 9 US-10-245-055-90 108 6.5 877 9 US-10-245-739-90 108 6.5 877 9 US-10-245-739-90 108 6.5 877 9 US-10-245-739-90 108 6.5 877 9 US-10-245-739-90 108 6.5 877 9 US-10-245-30-90 108 6.5 877 9 US-10-245-033-90 108 6.5 877 9 US-10-245-880-90 108 6.5 877 9 US-10-245-880-90 108 6.5 877 9 US-10-245-880-90 108 6.5 877 9 US-10-245-880-90 108 6.5 877 9 US-10-245-880-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90 108 6.5 877 9 US-10-245-821-90	6.5 877 9 US- 6.5 87	4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 5 877 9 US-1 6 877 9 US-1 6 877 9 US-1 6 877 9 US-1 7 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1 8 877 9 US-1	5 877 9 US-10-245-103-90 Sequence 5 877 9 US-10-245-107-90 Sequence 5 877 9 US-10-245-113-90 Sequence 5 877 9 US-10-245-851-90 Sequence 5 877 9 US-10-238-133-90 Sequence 5 877 9 US-10-238-283-90 Sequence 5 877 9 US-10-238-370-90 Sequence 5 877 9 US-10-245-147-90 Sequence 5 877 9 US-10-245-730-90 Sequence 5 877 9 US-10-245-730-90 Sequence 5 877 9 US-10-245-730-90 Sequence 5 877 9 US-10-245-030-90 <t< td=""><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td><td>108</td></t<>	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108
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	10-245-103-90 Sequence -10-245-17-90 Sequence -10-245-17-90 Sequence -10-245-831-90 Sequence -10-245-831-90 Sequence -10-245-831-90 Sequence -10-237-535-90 Sequence -10-238-391-90 Sequence -10-238-390 Sequence -10-245-055-90 Sequence -10-245-730-90 Sequence -10-245-730-90 Sequence -10-245-730-90 Sequence -10-245-739-90 Sequence -10-245-147-90 Sequence -10-245-033-90 Sequence -10-243-024-90 Sequence -10-245-621-90 Sequence -10-245-621-90 Sequence -10-245-621-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence -10-245-821-90 Sequence	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877	877
	10-245-103-90 Sequence -10-245-17-90 Sequence -10-245-171-90 Sequence -10-245-831-90 Sequence -10-245-831-90 Sequence -10-245-831-90 Sequence -10-238-335-90 Sequence -10-238-339-90 Sequence -10-238-370-90 Sequence -10-245-055-90 Sequence -10-245-147-90 Sequence -10-245-130-90 Sequence -10-245-130-90 Sequence -10-245-130-90 Sequence -10-245-130-90 Sequence -10-245-033-90 Sequence -10-243-0249-90 Sequence -10-245-033-90 Sequence -10-245-033-90 Sequence -10-245-033-90 Sequence -10-245-033-90 Sequence -10-245-033-90 Sequence -10-245-033-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence -10-245-031-90 Sequence	9	φ	ø	9	9	φ.	9	9	9	9	φ	9	ø	ø	9	9	9	9	φ	9	9	ø	y	9	ø
		-10-245-473	-10-245-427	-10-245-185	-10-243-095	-10-245-880	-10-245-621	-10-245-033	-10-243-409	-10-243-024	-10-239-196	-10-246	-10-245-739	-10-245-730	-10-245-147	-10-245-055	JS-10-238-370-90	JS-10-238-283-90	10-238-183	10-237-535-	10-245-883	-10-245-851-	-10-245-771-	10-245-143	-10-245-107	

ALIGNMENTS

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GVNTAH : SEVTQN FATGSS ADHNML	Query Match 12.5 Best Local Similarity 24.8 Matches 63; Conservative 73 YQVKQGDTVSKIAQRY : : : 120 YKVRKGDTMFLIAYIS	SULT 1 1-10-098-080-5
TVNE-1	ity Iservat DTVSKJ	aation US/220300079 N: N: N: Clement Vers, Ant N: CLONIN N: TRANS ON NUMBER: I CONT I UMBER: I CHARLIER I NUMBER: E EARLIER I NUMBER: E EARLIER I NUMBER: I EARLIER I EARLIER I NUMBER: I EARLIER I EARLIER I NUMBER: I EARLIER I
YVQSSRPI ::: WNANKPI YPVGATI YPVGATI YPVGATI	12.5%; 24.8%; 2ive 4 [AQRYGLN [AYISGMD	pplication US/1009880 o. US20030007981A1 MATION: votter, Andrew A. Rioux, Clement Schryvers, Anthony B. ENTION: TRANSFERRIN- CCE: 9000-0049.20 ICATION NUMBER: US/10 NG DATE: EARLIER FILING ATION NUMBER: EARLIER DATE: EARLIER FILING ATION NUMBER: EARLIER LOTE: EARLIER FILING ATION NUMBER: EARLIER LOTE: EARLIER FILING ATION UMBER: EARLIER LOTE: EARLIER FILING ATION UMBER: EARLIER LOTE: EARLIER FILING ATION UMBER: EARLIER LOTE: EARLIER FILING O ID NOS: 5 tentIn Ver. 2.0
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PAVQKPJ	Score 209; DB 9; Le Pred. No. 9.6e-09; 49; Mismatches 106; NWREIGHINNLNSSYTIYTGQWI : : : : : : : : COLUMNSEPYHLSIGQVI DIKELATLNNMSEPYHLSIGQVI	(PRESSION OF HAEMOPH: SINDING PROTEINS (198,808 APPLICATION NUMBER: DATE: 1999-09-24 APPLICATION NUMBER: DATE: 1999-03-10
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QPAPVAI : IIAWIWI : : QNQPSGI	36; 36; DLKVR : PDSNMIF	LUS SOMNUS 09/405,728 US 09/267,749
GVNTAHTPSPVAVQSSRPVQQHPAVQKFTPPVVVKKFTFTPVVQQPAPVAPPVTEAP 189	12.5%; Score 209; DB 9; Length 345; similarity 24.8%; Pred. No. 9.6e-09; 3; Conservative 49; Mismatches 106; Indels 36; Gaps YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISS : : :	749
189 229 249 268 307	6; 129	

RESULT 2 US-10-156-761-9179

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269

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PRIOR APPLICATION NUMBER: 2002-05-29

PRIOR PRIOR APPLICATION NUMBER: JP 2001-204009

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 9179

LENGTH: 301

TYPE: PTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptomyces avermitilis US-10-156-761-9179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: IKEDA HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                              Sequence 12234, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                  285 VRTGQR--IASMKNQPSGAAL-FEFRISRN-GVYVDPLTVLK 322
                                                                                                                                                                                                                                                                                                                                                193 HTGVDFVVPTGTTIKAVAAGTVVSAGWGGAYGNEVVVRHADGQYSQYAHMSQLSVSTGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AKTPASKTTTATRAADTTTGAG---YTLPVDG-----ATIGTAYKTAGSMWSSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 VQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSG- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 SAIGGDPTLIHPGLKLTIGAKSASSAATQSS-----TATKPATGVKSAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 SISSGVNT------AHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 EKSGTKTYAVRAGDSLSKIADEQSV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 -----YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRER 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GSHR-----TSGSGGLAI-----GSQVITDSQGVPNR-----
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83; Conserv
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APPLICANT: SAFAKI, YOSHIYUKI
APPLICANT: HATTORI, MSSAHIRA
TITLE OF INVERTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 12234
LENGTH: 203
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-12234
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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APPLICANT: OMURA, SI
APPLICANT: IKEDA,
APPLICANT: HISHIKAWI
APPLICANT: HORIKAWI
APPLICANT: SHIBA,
                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-14779
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US-10-156-761-14779
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Publication No. US20030119018A1
GENERAL INFORMATION:
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  252 ASSDR-
                                                                                                                                                                                 141 SGSATHTADRSTKRTVRDVKPQTTPQSQAGTAEMYTVLHGDTLSGIADSRHVRGGWEQLY 200
                                                                                        201 AANRGTIGADPDL-----ILPGORLHLRA---KATTRTDDASTST-HKSSTSSSKSSTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 AHLSRIDVRIGOVVATGOHIALSGNTGNSSGPHLHFEIRTTPNYGSGIDPVAFLR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 IHIKDAQVKTGDTVRTGQRIASMKN--QPSGAAL-FEFRISRN-GVYVDPLTVLK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 SNGMW----FSGRD-----GDLINASNAGTVIQADHN-----MDGASIVIQHTNGFVSSY
                                                                                                                                   89 GLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP 148
                                                                                                                                                                                                                            43 SGSGSHRTSGSGGLAIGS---QVITDSQ-GVPNRYQVKQGDTVSKIA------QRY 88
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                                                                                                                                                                                                                                                                    h 7.6%; Score 127.5; DB 9; Similarity 26.5%; Pred. No. 0.029; 79; Conservative 23; Mismatches 131;
                                        VQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGMWAHKHSGQDFAVPSGTEVLAAHGGTVVKAGGNGAGDGPAYGNAIVIKHGNGTYSQY
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HORIKAWA, HIROSHI
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-TEKATTSHSLV---APVNAGTGTQYHAAGSS--WSKGYHTGVDF 295
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US-09-468-147-166
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LENGTH: 1708
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Best Local (
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SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/173,141
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APPLICANT: Desai, Suresh M.
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EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1997-10-15
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                        200 FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASI 259
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                                                                                                          FCGEGTLYTRTWSTSGFSSDFSPPEAAAPASAAAPGLPYPT----PPVSDIWVLPPPS
                                                                                                                                     LNSSYTIYTGQWLTL-WSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV-----
                                                                                                                                                               XGGAPSAAPGEVXAFCSALYRYNRFTQRHSLTGGLWLHPEGLLGIFPPFSPGHIWESANP 693
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                                                                             -QQH-----PAVQKP---TPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199
                                                                                                                                                                                                                                               TCILAGC---ASKPTYNSTSGSGSHRTSGSGGLAI-----GSQVITDSQGVPNRYQVK 76
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Pred. No. 0.19
37; Mismatches
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Query Match
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Matches 52; Conserve
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US-09-738-626-6241
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                                                                                                                                                          APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
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SEQ ID NO 6241
LENGTH: 205
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
CURBER OF SEQ ID NOS: 4560
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND DIAGNOSIS OF PANCRES FILE REFERENCE: 210121.566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 AAGQEIAGMGSQGFSTGSHLHFEIHPDGVTPVDP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 RTGORIASMKNOP-SGAALFEFRISRNGVY-VDP 317
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIZOGUCHI
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Pred. No. 0.018;
                                                                                                                 PANCREATIC
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                                                                                                                 THE THERAPY
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RESULT 9
US-09-758-140-6
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US-09-789-386-2
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Patent No. US20020012965A1
GENERAL INFORMATION:
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SEQ ID NO 2
SEGO ID NO 2
SEGO ID NO 2
SEGO ID NO 2
TYPE: PRI
ORGANISM: HOMO SAPIENS
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LENGTH: 1192
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local (
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Patent No. US20020010324A1
GENERAL INFORMATION:
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Best Local &
APPLICANT: Strittmatter, Stephen M.

IITLE OF INVENTION: No. US20020012965A10 Receptor-Mediated Blockade of Axonal Growth
FILE REFERENCE: 44574-5073-US
CURRENT APPLICATION NUMBER: US/09/758,140
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/175,707
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/207,366
PRIOR APPLICATION NUMBER: US 60/207,366
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PRIOR APPLICATION NUMBER: U.K. 991698.1
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: U.K. 9816024.5
PRIOR APPLICATION NUMBER: U.K. 9816024.5
PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: US 09/359,208
PRIOR FILING DATE: 1999-07-22
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CURRENT FILING DATE: 2001-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MICHALOVICH, DAVID
APPLICANT: PRINJHA, RABINDER KUMAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185
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36; Conserv
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Larity 39.6%; Pred. No. 0.62; Indels 14
Conservative 8; Mismatches 33; Indels 14
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SEQ for Windows Version 3.0
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ilarity 39.6%;
Conservative
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Sequence 23, App-
Sequence 23, App-
Patent No. US20020072493AL

GENERAL IMPORMATION:
APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
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APPLICANT: MOSONEGO, Alon
APPLICANT: MOSCNEGO, Alon
APPLICANT: MOSCNEGO, Alon
APPLICANT: MOSCHWARTS-2A
CURRENT PILING DATE: 2001-66-28
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: WS 09/314,161
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: WS 09/218,277
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: WS 09/218,277
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: WS 09/218,277
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 1192
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US-09-972-599A-6
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Best Local Similarity 39.6%;
Matches 36; Conservative
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SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                             186 T-EAPFATGSSGVMQ---FRYPVGATNPVVR 212
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                                                                                                                                                                                                                                                                                                                                                  132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185
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Sequence 6, Application US/09972599A
Patent No. US20020077295A1
GENERAL INFORMATION:

APPLICANT: STRITTMATTER, STEPHEN M.
TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
FILE REFERENCE: C077 CIP US

CURRENT APPLICATION NUMBER: US/09/972,599A

CURRENT FILING DATE:

2001-10-06

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US-09-972-599A-6
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LENGTH: 1192
TYPE; PRT
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SEQ ID NO 4458
LENGTH: 237
TYPE: PRT
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                                                                                                                                               ORGANISM: Corynebacterium glutamicum 09-738-626-4458
                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/738,626
                                                                                                                                                                                                                                                                                                                                                                                                                           ILE REFERENCE: 249-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LICANT: OZAKI, AKIO
LE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                          Local
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APPLICATION NUMBER: 09/758,140
FILING DATE: 2001-01-12
APPLICATION NUMBER: 60/236,378
FILING DATE: 2000-09-29
FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                             FILING DATE: 2000-04-07
APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/207,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/01041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/175,707
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                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 TPAAPKRRGSSGSVDETLFALP-AASEPVIR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPA---PAPAAPPS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 T-EAPFATGSSGVMQ---FRYPVGATNPVVR 212
 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.1%;
1 Similarity 39.6%;
36; Conservative
                                                                                        Similarity
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                                  QNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGV 69
 QTTSPVTKGGVAFVAVAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Application US/09738626
o. US20020197605A1
                                                                    7.0%; Score 117; DB 9; Length 237;
22.2%; Pred. No. 0.1;
ive 44; Mismatches 93; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 118; DB 10;
Pred. No. 0.62;
8; Mismatches 33;
 --GAVSTAGAGG-AVAAQ--ASNQPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10155400 Publication No. US20030108988A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DING, SHI-YOU
APPLICANT: ADNEY, WILLIAM S.
APPLICANT: VINZANT, TODD B.
APPLICANT: HIMMEL, MICHAEL E.
TITLE OF INVENTION: THERMAL TOLERANT AVICELASE FROM ACIDOTHERMUS
TITLE OF INVENTION: CELLULOLYTICUS
FILE REFERENCE: NREL 01-36A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Acidothermus cellulolyticus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD_RES
LOCATION: (957)
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                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                      179
                                                                                                                                     794
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911 R-YWFT-RDG-----GSSTLV---YNCDWAAI 932
                                                                                                                                                                       121 KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTP---TPPVVQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                           80 T----VSKIAQRYGLNWRE--IGHINNLNSSYTIYTGQWLTLWSGDL------
                                                                                                                                                                                                                                                                                                                34 ASKPTYNSTSGSGSHR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 PNRYQVKQGDTVSKIAQRYG---LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERS
                                                                                                                                                                                                                                                                                                                                                 1 Similarity 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 957
                                NGMWFSGRDGDLINASNAGTVIQADHNMDGASI 259
                                                                   SPSSSPSSSPSPTPSSSPVSGGVKVQYKNNDSAPGDNQIKPGLQVVNTGSSSVDLSTVTV
                                                                                                    APVAPPVTE---APFATGSSGVMQFRYPVGATNP------VVRRFGTATVAGSTVTS
                                                                                                                                       PSASPSLSPSPSPSSSPSPSPSSSSPSSSPSPS---PSPSPSRSPSPSASPSPSSSSP
                                                                                                                                                                                                          TTWVLINDDQHQYG-NWGQAITGDHANLRRVYIGTNGRGIVY--GDIGGAPSGSPSPSVS
                                                                                                                                                                                                                                                                               ASSGLYHSTNGGSSWSAITGVSSAVNVGFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFEVYPAGGGA-VDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIDAGPASGFGNWVRLQHEDGTITVYGHMETVEVTVGQTVKAGERIAGMGSRGFSTGSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIQADHNMD-GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ--PSGAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVNFELTANDTTDLVAGSSAPQILSIAEFKPVVNL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                 38; Mismatches 104;
                                                                                                                                                                                                                                                                                                                -----TSGSGGLAIGSQ-----VITDSQGVPNRYQVKQGD
                                                                                                                                                                                                                                                                                                                                                                 Score 112; DB 9;
Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 957;
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Sequence 1, Application US/09917383
Publication No. US20030104522A1
SEMERAL INFORMATION:
APPLICANT: DING, SHI-YOU
APPLICANT: ADNEY, WILLIAM S.
APPLICANT: DECKER, STEPHEN R.
APPLICANT: HIMMEL, MICHAEL E.
TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FRC
TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FRC
TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FRC
CURRENT APPLICATION NUMBER: US/09/917,383
CURRENT FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
LENGTH: 1228
TYPER: PET
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US-09-917-383-1
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; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Segment of; OTHER INFORMATION: GuxA
US-09-917-384-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1228
TYPE: PRT
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Sequence 1, Application US/09917384
Publication No. US20030096342A1
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Best Local
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APPLICANT: DING, SHI YOU

APPLICANT: ADNEY, WILLIAM S.

APPLICANT: VINZANT, TODD B.

APPLICANT: UNCER, STEPHEN R.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: HIMMEL, MICHAEL E.

APPLICANT: OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS

TITLE OF INVENTION: CELLULOLYTICUS

FILE REFERENCE: 40,70.6US01

CURRENT APPLICATION NUMBER: US/09/917,384

CURRENT FILING DATE: 2001-07-28

NUMBER: 12.14
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Segment of
                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           992 SRGGVQPFGSQTATGVTVAGHTWNVWQGQQTS-----WKIISYVLTPGATSISNLD 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYVVNSDWGSGFTATVTVTNTGSRATNGWTVAWSFGGNQTVTNYWNTAL-----TQSGA 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNPVVRRFGTATVAGSTVTSNG------MWFSGRDGDLINASNAGTVIQADHNMDGA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-----SŚŚĠV-----ACRA 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VIQ----HTNGFVSSY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.7%; Score 112; DB 24.3%; Pred. No. 1.9; ative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSR 146
                                                                                                                                                                                                                                                                                   FROM ACIDOTHERMUS
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RESULT 16
US-10-101-464A-930
US-10-101-464A-930
; Sequence 930, Applicat
; Publication No. US200;
; Publication Procedure
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Pinus radiata US-10-101-464A-930
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US-09-917-383-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Ouery Match
Sept. Docal Similarity 21.5%; Pred: No. 0.47;
Matches 52; Conservative 20; Mismatches 51; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Ce
TITLE OF INVENTION: and Their Use in the Modification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1102
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                                                              140 VAVQSSRPPVQQHPAVQKPTPVVVVKKPTPTPVVVQQPAPVAPPVTBAPFATGSSGVMQ 199
                                                                                                                                               187 NLSSITKKFGSDLONFKSLNGMNSTLTAYT----
                                                                                                                                                                                                                                                                                              139 ANPTLNPTD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    992 SRGGVQPFGSQTATGVTVAGHTWNVWQGQQTS-----WKIISYVLTPGATSISNLD 1042
                                                                                                                                                                                                     81 -VSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSP 139
                                                                                                                                                                                                                                                                                                                                                                           51 SGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGH-----INNLN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 6.7%;
l Similarity 24.3%;
65; Conservative 2
VLVPVSQRPVLSQPVSSSPPPP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10101464A
o. US20030046728A1
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; Pred. No. 1.9;
20; Mismatches 92
                                                                                                                                                                                                                                                                                                       LQIGVQVIFPIRCKCPSQAQVKNGTKMLITYTVQPVDTH 186
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Sequence 1116, Application US/09925301

Patent No. US20020052308A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Ant
PILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR APPLICATION NUMBER: BOS/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694
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PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9957
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9957
                                                                                                                                                                                                                                                                         US-09-925-301-1116
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Best Local Similarity 25.2
Matches 55; Conservative
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, APPLICANT: IKEDA,
OFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: SHIBA, TÄDAYOSHI
PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                   155 DFHAASGTSVHAVGSGTVVEAGWGGAYGNNIVIKMNDGTYTQYGHLSSIGVSVGQTVTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 ATGSSGVMQFRYPVGATNPVVR----RFGT--ATVAGSTVTS-----NGMWFSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 ----RDGDLINASNAGTVIQAD-HNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 VNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPVVVQQPAPVAPPVTEAPF 190
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                                                                                                                                                                                                                                                                                                                                                       QQIGISGATGNTTGPHLHFEARTTAEYGSDIDPVAYLR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AARKKAAELAEKEHAAKARAAREAERKRLNTFVAPIAGSYVSTGYKSGGSLWSSGSHTGV 154
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                                                                                                                                                                                                                                                                                                                                                                                            QR--IASMKNQPSGAAL-FEFRISRN-GVYVDPLTVLK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 110; DB 9; Length 258, 25.2%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Mismatches 108; Indels
                                                                                                                                                                          Antibodies
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                ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3548
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                                                                     NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn ver.
SEQ ID NO 3548
LENGTH: 474
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3548, Application US/09738626 Publication No. US20020197605A1
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OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (29)
OTHER INFORMATION: X
NAME/KEY: SITE
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE LOCATION: (5)
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                                                                                                                                                                                                                                                                                                                                                                                      HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                   IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIZOGUCHI, HIROSHI
ANDO, SEIKO
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                           182 SG-GYRRTPSVTAQFSAQPHVNGGPLYSQNSISIAPPPPPMPQLTPQIPLTGFVARVQEN
                                                                                                                                                                                           145 -PSPPTIGPAAPGSAPGSQYGTMTRQISRHNSTTS-----
241 IADSPTPPPPPPDDIPMFDDSPPPPPPPPVDYEDEEAAVVQYNDPYADGDP 292
                                           164 VVKKETETEE-----VVQQEAEVAEEVTEAEFATGSSGVMQFRYEVGATNE 209
                                                                                                                                                                                                                                         69 VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS 128
                                                                                                                                                                                                                                                                                                                                       9 SQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQG
                                                                                                                                        SGVNTAHTPSPVAVQSSRPPVQQHP-----AVQKPTPPVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equals any of the
                                                                                                                                                                                                                                                                                                                                                                                                           Score 110;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                              6 L ;
                                                                                                                                                                                                                                                                                            SSGGSGSRENSGSSSIGIPIAVPT----
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                                                                                                                                                                                           STS
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CURRENT APPLICATION UNMER: US/09/932,183A
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION UNMERR: US 09/308,375
PRIOR FILING DATE: 1999-05-14
PRIOR PRIOR DATE: 1999-05-14
PRIOR PRIOR DATE: 1998-09-08
PRIOR PRIOR DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR PRIOR DATE: 1998-09-08
PRIOR APPLICATION NUMBER: E99719636.4
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT ; ORGANISM: Bacillius subtilis US-09-932-183A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-09-932-183A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Estell, David A. TITLE OF INVENTION: Proteases From Gram-Positive Organisms FILE REFERENCE: GC394C1-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                  1556 YTNNSA---FR
                                                                                                                                1515
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                                                                                                                                                                                                                                                                                                                      1398 YGIVTSTTSSGGTPSSTGGSYSGKYSSYINSAASKYNVDPALIAAVIQQESGF--NAKAR 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 RFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSY-
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                                                                                                                                                                                                                                                                                                                                                                       22 FGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGL----AIGSQVITDSQGVPNRYQVK 76
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 20.3
63; Conservative
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                                                                       ATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQA 250
                                                                                                                       -----PGNVIKYGGIPPFKETONYVKKIMANYSKSLSSATSSI------ASY
                                                                                                                                                                     VNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPF 190
                                                                                                                                                                                                                        SGVGAMGLMQLMPATAKSLG-VNNAYDPYQNVMGGTKYLAQQLEKFGGNVEKALAAYNAG
                                                                                                                                                                                                                                                                      QGDTVSKIAQRYGLNWREIGHINNLNSSY-----TIYTGQWLTLWSGDLKVRERSISSG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVQKPTPPVV-VVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LN-SSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPVQQH-----P 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOTCAGGGTTTLLTAFQLSCNTAFVETGIDVGADALRASAEDFGVGOTYSLGLDNVPGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSTPRGQISTGGQVLAESSQDDQGFYQRSYITNPTAYAPVVGYLSDVYGAAGLELGYNSI 107
                                                                                                                                                                                                                                                                                                                                                                                                                  6.5%; Score 108.5; DB 10;
20.3%; Pred. No. 7.6;
ative 51; Mismatches 149;
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; Pred. No. 1.1; 
49; Mismatches 123;
                            VSSKYGQQESGLRSSPHKGTDFAAKAGTAIKSLQSGKVQIA 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LENGYSADSTVTAE----AAVTLPGTNTTLTNYG 257
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NUMBER OF SEQ ID N
SEQ ID NO 90
LENGTH: 877
TYPE: PRT
ORGANISM: Homo Sa
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US-10-245-103-90
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION NUMBER: US/10/245,103
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
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PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR PELICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
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PRIOR FILING DATE: 1998-06-25
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                                                                                                                                                                     446 GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY 500
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                                                                                                                                                                                                                                                                      64;
----TLWSGDLKVRERSISSGVNT-AHTPSPVAV----QSSRPPVQQHPAVQKPTPPVVV 164
                                                                                                                    Q----TIYTGQWL-----
                                                                                                                                                                                                                   GVITTCILAGCASKPTYNSTSGSGSHRTSGSG-----GLAIGSQVITDSQGVPNRY 73
                                                                    QKILWIPAGALRLQİAQL-----
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Watanbe, Colin
Wood, William
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li, J. Christopher
                                                                                                                                                                                                                                                                   6.5%; Score 108; DB 9; 24.4%; Pred. No. 2.6; tive 28; Mismatches 94
                                                                       ----RPSSNYLALRGPGGRSIINGNWAVDPPGSY 548
                                                                                                                                                                                                                                                                      94;
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LENGTH: 877
TYPE: PRT
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Publication No.
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-10-245-107-90
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                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 116
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CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16
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APPLICATION NUMBER: 60/059114
FILING DATE: 1997-09-17
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
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FILING DATE: 1997-10-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-05-22
501 QKILWIPAGALRLQIAQL------RPSSNYLALRGPGGRSIINGNWAVDPPGSY 548
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                                                                      446 GAPDICVAGRCLS
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                                                                                                      23 GVITTCILAGCASKPTYNSTSGSGSHRTSGSG------GLAIGSQVITDSQGVPNRY 73
                                                                                                                                                                                                                                                                      877
                                                                                                                                           64; Conservative
                                                                                                                                                            Similarity
                                   Q----TKQGDTVSKIAQRYGLNWREIGHINNLNSSY-----TIYTGQWL-----
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Pred. No. 2.6;
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US-10-245-143-90
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US-10-245-143-90
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Best Local S
Matches 64
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NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
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CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090689
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FILING DATE: 1998-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/086478
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                                                       446 GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY 500
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74 Q----VKQGDTVSKIAQRYGLNWREIGHINNLNSSY-----TIYTGQWL-----
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-90
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION UNMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
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FILE REPERENCE: 95430R41298

CURRENT APPLICATION NUMBER: US/10/245,771

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR PPLICATION NUMBER: 60/059114

PRIOR APPLICATION NUMBER: 60/063046

PRIOR APPLICATION NUMBER: 60/063046

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-11-10

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1997-11-10

PRIOR FILING DATE: 1997-11-10
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                                 446 GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY
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                                                                            23 GVITTCILAGCASKPTYNSTSGSGSHRTSGSG------GLAIGSQVITDSQGVPNRY 73
                                                                                                                                        h 6.5%; Score 108; DB Similarity 24.4%; Pred. No. 2.6; 64; Conservative 28; Mismatches
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Stephan, Jean-Phillippe
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Grimaldi, J. Christopher
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No. US20030068781A1
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FILE REFERENCE: P3630R1C93
CURRENT PILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/05027
PRIOR APPLICATION NUMBER: 60/079689
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US-10-245-851-90
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Best Local Similarity 24.4%; Pered, No. 2.6;
Matches 64; Conservative 28; Mismatches
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PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data rei
NUMBER OF SEQ ID NOS: 116
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ENGTH: 877
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23 GVITTCILAGCASKPTYNSTSGSGSHRTSGSG------GLAIGSQVITDSQGVPNRY 73
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Grimaldi, J. Christopher
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To. US20030068782A1
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; LENGTH: 877
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-90
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US-10-245-883-90
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Publication No.
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                    Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/245,883
CURRENT FILING DATE: 2002-09-16
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
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APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                           LING DATE:
      64:
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Godmaldi, J. Christopher
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Watanbe, Colin
Wood, William
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      Conservative
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                                                                                                                                                                                    Application data removed - See File Wrapper or PALM
NOS: 116
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  6.5%; Score 108; DB 24.4%; Pred. No. 2.6; tive 28; Mismatches
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                                         DB 9; Length 877;
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CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
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PRIOR APPLICATION NUMBER: 60/063046
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DR FILING DATE: 1998-07-01
DR APPLICATION NUMBER: 60/091978
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/099803
DR FILING DATE: 1998-09-10
DR APPLICATION NUMBER: 60/106932
DR FILING DATE: 1998-11-03
DR FILING DATE: 1998-11-03
DR APPLICATION NUMBER: 60/115554
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090689
FILING DATE: 1998-06-25
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FILING DATE: 1997-11-10
APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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No. US20030073188A1
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Watanbe, Colin
Wood, William
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Grimaldi, J. Christopher
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124419 127796 129404 131836 131836 141992 146374 101054	80137 80138 103297 123741 109238 902706 912035	26642 6762 7439 8098 8212 8219 9058 8099	218371 222695 229896 230621 232887 235147 235147 261878 261910 261939 262150
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PRIOR APPLICATION NUMBER: 60/119342
PRIOR PILING DATE: 1999-03-02-09
PRIOR PILING DATE: 1999-03-12
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PRIOR PILING DATE: 1997-11-10
PRIOR PPLICATION NUMBER: 60/05027
PRIOR PILING DATE: 1998-03-27
PRIOR PELICATION NUMBER: 60/07669
PRIOR PILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/086478
PRIOR PILING DATE: 1998-05-22
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Best Local Similarity
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APPLICANT: Pong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMS
TITLE OF INVENTION: ACIDS ENCODING THE SJ
FILE REFERENCE: P363DR1C11
CURRENT APPLICATION NUMBER: US/10/238,183
CURRENT FILING DATE: 2002-09-09
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FILING DATE: 2002-02-20
APPLICATION NUMBER: 10/119480
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No. US20030073189A1
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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                                      NUMBER: 60/090689
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Pred. No. 2.6;
8; Mismatches 94
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OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/099803
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/106932
OR FILING DATE: 1998-11-03
                                                                      FILING DATE: 2000-01-20
APPLICATION NUMBER: 60/179851
FILING DATE: 2000-02-02
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APPLICATION NUMBER: 60/146222
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FILING DATE: 1999-06-23
APPLICATION NUMBER: 60/144732
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APPLICATION NUMBER: 60/140653
FILING DATE: 1999-06-22
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FILING DATE: 1999-05-25
APPLICATION NUMBER: 60/135729
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FILING DATE: 1999-04-27
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APPLICATION NUMBER: 60/123972
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FILING DATE: 1999-01-12
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APPLICANT: Eaton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Gridard, Audrey
APPLICANT: Gridardi, J. Christopher
APPLICANT: Gridardi, J. Christopher
APPLICANT: Gridardi, J. Christopher
APPLICANT: Gridardi, J. Christopher
APPLICANT: Gridardi, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Pong, Sherman
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APPLICANT: Pong, Sherman
APPLICANT: NUMBER: US/10/238, 283
CURRENT APPLICATION NUMBER: US/10/238, 283
CURRENT APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/05914
PRIOR APPLICATION NUMBER: 60/05968
PRIOR APPLICATION NUMBER: 60/05968
PRIOR APPLICATION NUMBER: 60/05027
PRIOR FILING DATE: 1997-01-24
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 60/05027
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Best Local S
Matches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
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PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/9411992
PRIOR APPLICATION NUMBER: 09/946374
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
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64; Conser
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No. US20030073190A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.5%; Score 108; DB 9; llarity 24.4%; Pred. No. 2.6; Conservative 28; Mismatches 9.
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DR APPLICATION NUMBER: 60/230621
DR FILING DATE: 2000-09-05
DR FILING DATE: 2000-09-05
DR APPLICATION NUMBER: 60/235147
DR APPLICATION NUMBER: 60/235147
DR FILING DATE: 2000-09-12
TR APPLICATION NUMBER: 60/261878
DR APPLICATION NUMBER: 60/261970
DR FILING DATE: 2001-01-16
DR APPLICATION NUMBER: 60/261939
DR APPLICATION NUMBER: 60/261939
DR APPLICATION NUMBER: 60/261939
DR FILING DATE: 2001-01-16
DR FILING DATE: 2001-01-16
DR APPLICATION NUMBER: 60/262150
DR APPLICATION NUMBER: 60/262150
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DR APPLICATION NUMBER: 60/262150
DR APPLICATION NUMBER: 60/262150

DR FILING DATE: 2000-06-05

BR APPLICATION NUMBER: 60/218371

BR FILING DATE: 2000-07-13

BR APPLICATION NUMBER: 60/222695

BR FILING DATE: 2000-08-02

BR PELICATION NUMBER: 60/229896

BR APPLICATION NUMBER: 60/229896

BR APPLICATION NUMBER: 60/229896

PILING DATE: 2000-05-23
APPLICATION NUMBER: 60/209832 APPLICATION NUMBER: 60/206368 FILING DATE: 2000-04-25
APPLICATION NUMBER: 60/206330

NUMBER: NUMBER: 60: 2000-04-

60/199614 60/198587

OR APPLICATION NUMBER: 09/80137
OR APPLICATION NUMBER: 09/380137
OR APPLICATION NUMBER: 09/380138
OR APPLICATION NUMBER: 09/380138
OR PILING DATE: 1999-08-25
OR APPLICATION NUMBER: 09/403297
OR FILING DATE: 1999-10-18
OR APPLICATION NUMBER: 09/4032741
OR FILING DATE: 1999-11-10
OR APPLICATION NUMBER: 09/802706
OR APPLICATION NUMBER: 09/802706
OR APPLICATION NUMBER: 09/872035
OR APPLICATION NUMBER: 09/872035
OR APPLICATION NUMBER: 09/972035
OR APPLICATION NUMBER: 09/972035
OR FILING DATE: 2001-06-01
OR APPLICATION NUMBER: 09/924419
OR APPLICATION NUMBER: 09/924419
OR APPLICATION NUMBER: 09/924419
OR APPLICATION NUMBER: 09/924419
OR APPLICATION NUMBER: 09/924419
OR APPLICATION NUMBER: 09/924419
OR APPLICATION NUMBER: 09/92440
OR FILING DATE: 2001-08-06
OR FILING DATE: 2001-08-06
OR APPLICATION NUMBER: 09/92404
OR FILING DATE: 2001-08-06
OR APPLICATION NUMBER: 09/92404
OR APPLICATION NUMBER: 09/92404
OR APPLICATION NUMBER: 09/931836

FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/290589
FILING DATE: 2001-05-09
APPLICATION NUMBER: 09/180997
FILING DATE: 1998-11-19
APPLICATION NUMBER: 09/267213

FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/282199
FILING DATE: 2001-04-04 FILING DATE: 2001-04-03 APPLICATION NUMBER: 60/282129 APPLICATION NUMBER: 60/274399 FILING DATE: 2001-03-09 APPLICATION NUMBER: 60/280982

APPLICATION NUMBER: FILING DATE: 2001-0 FILING DATE: APPLICATION NUMBER: FILING DATE:

2001-02-09 2001-02-02 2001-01-25

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Publication No.
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                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/238,370
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION
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                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
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OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/089801
OR APPLICATION NUMBER: 60/090557
OR APPLICATION NUMBER: 60/090689
OR APPLICATION NUMBER: 60/090689
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                                                                                                            APPLICATION NUMBER: 60/059114
FILING DATE: 1997-09-17
                                                                          APPLICATION NUMBER: 60/063046 FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-06-25
                                  APPLICATION NUMBER: 60/065027 FILING DATE: 1997-11-10
                  APPLICATION NUMBER: 60/079689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 ----TLWSGDLKVRERSISSGVNT-AHTPSPVAV----QSSRPPVQQHPAVQKPTPPVVV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 QKILWIPAGALRIQIAQL------RPSSNYLALRGPGGRSIINGNWAVDPPGSY 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAGGTVFRYNRPPREEGKGESLSAEGPTTQPVDVYMIFQEENPGVFYQYVISSPPP---I
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                                                                                                                                                                                                                                                                                           Fong, Sherman
                                                                                                                                                                                                                                                                                                                                               Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10238370 to. US20030073191A1
                                                                                                                                                                                                                                                                                                                                                                                                         Gurney, Austin
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DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                           Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                 Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                          Grimaldi, J. Christopher
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                                                                                                                                                      2002-07-18
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Pred. No. 2
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; LENGTH: 877
; TYPE: PRT
; ORGANISM: Homo S
US-10-238-370-90
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Publication No.
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NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                  CURRENT APPLICATION NUMBER: US/10/245,055
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
                                   PRIOR APPLICATION NUMBER: 60/063046
                                                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C88
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
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No. US20030073192A1
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Grimaldi, J. Christopher
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-055-90
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PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR PRIOR APPLICATION NUMBER: 60/089801
PRIOR PRIOR APPLICATION NUMBER: 60/090557
PRIOR PRIOR DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
                                              APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P563084/72
CURRENT APPLICATION NUMBER: US/10/245,147
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1097-09-17
PRIOR APPLICATION NUMBER: 60/063046
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Matches 64
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NUMBER OF SEQ ID NOS: 116
EQ ID NO 90
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Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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Grimaldi, J. Christopher
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APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Fong, Semin
APPLICANT: Fong, Semin
APPLICANT: Fong, Sterman
ITILB OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
ITILE OF INVENTION: ACIDS ENCODING THE SAME
ITILE OF INVENTION NUMBER: US/10/245,730
CURRENT APPLICATION NUMBER: US/10/245,730
CURRENT APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/059114
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PRIOR FILLING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR PRILING DATE: 1998-03-27
PRIOR PRILING DATE: 1998-05-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/090891
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
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APPLICANT: Baker, Kevin
APPLICANT: Eateon, Dan
APPLICANT: Grimaldi, Ju
APPLICANT: Grimaldi, Ju
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US-10-245-730-90
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Grimaldi, J. Christopher
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Filvaroff, Ellen
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US-10-245-730-90
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NUMBER OF SEQ ID
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                         Sequence 90, Ap
Publication No.
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                                                                                                                                                                                               APPLICANT:
              CURRENT APPLICATION NUMBER: US/10/245,739
                                                                                                                                                                                                                                APPLICANT:
                                                    FILE REFERENCE: P3630R1C86
                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITTLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                      APPLICANT:
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Local Similarity 24.4%;
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APPLICATION NUMBER: 10/197942
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/086478
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APPLICATION NUMBER: 60/090689
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                                                                                                                                        Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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                                                                                                                                                                                                                                  Grimaldi,J.
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                                                                                                                       Zhang, Zemin
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                                                                                                        Sherman
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NUMBER OF SEQ ID NOS:
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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-10-245-739-90
                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin
                                                                                                    APPLICANT:
                                                                                                                                                             APPLICANT:
       TURRENT APPLICATION NUMBER: US/10/246,210
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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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FILING DATE: 1997-11-10
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                                                                                     Fong, Sherman
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Pred. No. 2.6;
28; Mismatches
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Best Local
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, F
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-10-246-210-90
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OR FILING DATE: 2002-07-18
OR FILING DATE: 1997-09-17
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/063046
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/065027
OR FILING DATE: 1997-11-10
OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/086478
OR FILING DATE: 1998-05-22
OR APPLICATION NUMBER: 60/086678
OR FILING DATE: 1998-05-02
OR FILING DATE: 1998-05-07
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087607
OR APPLICATION NUMBER: 60/089801
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/090689
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/090689
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/090689
OR FILING DATE: 1998-06-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 ----TLWSGDLKVRERSISSGVNT-AHTPSPVAV----QSSRPPVQQHPAVQKPTPPVVV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 PVVRREGIATVAGSTVTSNGMW 230
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10239196
To. US20030074735A1
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    ON: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ON: ACIDS ENCODING THE SAME P3630RICB
                                                                                                               Sherman
                                                                                                                                                  Zemin
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24.4%;
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CURRENT APPLICATION NUMBER: US/10/239,196
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/065914
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/08667
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089801
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-25
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US-10-243-024-90
                                                                                                                                                                                                                                                    Sequence 90, Application Publication No. US2003007 (GENERAL INFORMATION: APPLICANT: Baker, Kevin APPLICANT: Eaton, Dan APPLICANT: Filvaroff, El APPLICANT: Goddard, Audr
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-239-196-90
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Grimaldi, J. Christopher
Zhang, Zemin
Fong, Sherman
                                                               Stephan, Jean-Phillippe Watanbe, Colin Wood, William
                                                                                                                                                      Gurney, Austin
Smith, Victoria
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No. US20030077741A1
                                                                                                                                                                                                                                                                                      Filvaroff, Ellen
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Pred. No. 2.6;
B; Mismatches 94
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INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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RESULT 38
US-10-243-409-90
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US-10-243-024-90
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local 9
                                                                                                                                                                                            GENERAL
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                                                                                                                                                      APPLICANT: Baker, Kevin APPLICANT: Eaton, Dan
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CURRENT FILING DATE: 2002-09-12
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                                                          PPLICANT:
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/079689
                                                                                                                                                                                              INFORMATION:
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                                                                                                                                                                                                                                                                                                                                 666 AYWKRVGHSACSAS--CGKGVW 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 RAGGTVFRYNRPPREEGKGESLSAEGPTTQPVDVYMIFQEENPGVFYQYVISSPPP---I
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Similarity 24.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             VKKPTPTPPVVQ-QP--APVAPPVTEAPFATGSSGVMQF------RYPVGATN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TLWSGDLKVRERSISSGVNT-AHTPSPVAV----QSSRPPVQQHPAVQKPTPPVVV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q----VKQGDTVSKIAQRYGLNWREIGHINNLNSSY------TIYTGQWL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAPDICVAGRCLS-PGCDGILGSG-RRPDGCGVCGGDDSTCRLVSGN--LTD-RGGPLGY 500
                                                                                                                                                                                                                                                                                                                                                                   PVVRRFGTATVAGSTVTSNGMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKILWIPAGALRLQIAQL------RPSSNYLALRGPGGRSIINGNWAVDPPGSY 548
                                                                                                                                                                                                              Application US/10243409 No. US20030077742A1
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
                                                          Gurney, Austin
Smith, Victoria
                                                                                            Goddard, Audrey
Grimaldi, J. Christopher
                                                                                                                                      Filvaroff,Ellen
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US-10-245-033-90
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; ORGANISM: Homo
US-10-243-409-90
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PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
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NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
                                                                                                                                                                                                   Sequence 90, Application US/10245033
Publication No. US20030078401A1
                                                                                                                                                                                    GENERAL INFORMATION:
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Best Local Similarity
                                                                                                  APPLICANT:
                                                            APPLICANT:
                                                                                                                                                              APPLICANT: Baker, Kevin
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CURRENT FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P3630R1C41
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                         APPLICANT:
                                        APPLICANT:
  PPLICANT:
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FILING DATE: 1998-06-02
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FILING DATE: 1998-06-18
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                                                                           Filvaroff,Ellen
Goddard,Audrey
Grimaldi,J. Christopher
Stephan, Jean-Phillippe
Watanbe, Colin
                                        Smith, Victoria
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24.4%;
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Pred. No. 2.6;
28; Mismatches
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RESULT 40
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TYPE: PTI
; ORGANISM: Homo Sapien
US-10-245-033-90
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Publication No. US200300
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
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Best Local S
Matches 64
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SEQ ID NO 90
LENGTH: 877
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PRIOR FILING DATE: 1998-06-25
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PPLICANT: FONG, Sherman
ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDS ENCODING THE SAME
ILE REPERENCE: P3630R1CR4
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                                                           Eaton, Dan
Filvaroff, Ellen
                                                                                                                      Application US/10245621 to. US20030077743A1
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Search completed: July Job time : 56 secs
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CURRENT APPLICATION NUMBER: US/10/245,621
CURRENT APPLICATION NUMBER: US/10/245,621
CURRENT APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 10/059114
PRIOR FILING DATE: 1997-09-17
PRIOR PFLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/079689
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR PHIOR DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086901
PRIOR APPLICATION NUMBER: 60/089801
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PRIOR APPLICATION NUMBER: 60/080807
PRIOR FILING DATE: 1998-06-02
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NUMBER OF SEQ ID NOS: 116
SEQ ID NO 90
LENGTH: 877
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Best Local Similarity
Matches 64; Conserv
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PRIOR FILING DATE: 1998-06-25
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Watanbe, Colin
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                              8, 2003, 11:17:11
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Result
No.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: pir1:*
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AH0855
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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7.6	7.7	7.7	7.8	7.8	7.8	7.8	7.9	8.0	8.1	8.2	8.3	8.4		8.8	8.8
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ALIGNMENTS

RESULT S55063

conserved hypothetical protein PA3623 [imported] - Pseudomonas (Species: Pseudomonas aeruginosa C;Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change C;Accession: S55063; E83193 R;Tanaka, K.; Takahashi, H. Gene 150, 81-85, 1994 A;Title: Cloning, analysis and expression of an rpoS homologue A;Reference number: S55062; MUID:95047554; PMID:7959068

#text_change 31-Dec-2000 Pseudomonas aeruginosa

gene from Pseudomonas aeru

A;Status: preliminary A;Accession: S55063

A; Gene: PA3623 C; Superfamily: A;Molecule type: DNA A;Residues: 1-297 <TANS A;Cross-references: EMBL:D26134; NID:g440375; PIDN:BAA05130.1; PID:g440377 A;Cross-references: EMBL:D26134; NID:g440375; PIDN:BAA05130.1; PID:g440377 A;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bridadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. ; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: E83193 S A;Residues: 1-297 <STO> A;Cross-references: GB:AE004782; GB:AE004091; NID:g9949772; PIDN:AAG07011.1; GSPDB:GN001: A;Experimental source: strain PAO1 S 뭐 맑 Ś 뮍 Ś 밁 Ş A;Status: preliminary
A;Molecule type: DNA Query Match
Best Local Similarity ;Superfamily: lipoprotein D ;Genetics: Matches 185 239 INASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN 296 133 TAHTESEVAVQ-SSREEVQQHEAVQKETEEVV--VVKKETETEEVVQ-----QEAEVAEE 184 69 73 25 20 LIFGVITTCILAGCASKP-----TYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNR 91; YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVN 132 VTEAPFATGSSGVMQ-----FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDL LLLGAVVCSLLAACSSSPPGGVKVVDRNGSAPAARRTPVTSG-----Q STTTPPSSGATPVVAGPAVGGWAWPASGT--LIGRF----ASNGSLNKGIDIAGQLGQP -----AIOFGGRASTO--ESVAKNTPVVAAPVATKPTPVPPAVSTSVPAKPAP-APA 156 YIVRRGDTLYSIAFRFGWDWKALAARNGIAPPYTIQVGQ----Conservative 17.8%; Score 298; DB 2; Length 297; 28.0%; Pred. No. 2.7e-14; tive 50; Mismatches 106; Indels 78; Gaps 107 83

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A;Reference number: Z
A;Accession: T50918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <NA
A;Cross-references: E
A;Experimental source
C;Genetics:
A;Gene: nlpD
   lipoprotein XF0855 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: A82754
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide
R; anonymous, The Xylella fastidiosa.
R; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:2035717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; A; Accession: A82754
A; A; Coses-ion: A82754
A; Molecule type: DNA
A; Residues: 1-242 <SIM:
A; CSSIM:
A; CSSIM:
A; CSSIM:
A; CSSIM:
A; CSSIM:
A; CSSPDB A; CYCOSS-references: GB:AE003925; GB:AE003849; NID:g9105758; PIDN:AAF83665.1; GSPDB
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Experimental source: strain IL144
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ce: strain 9a5c
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25.6%; Pred. No. 4.2e-12;
vative 43; Mismatches 161;
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65070
A;Atcession: A65070
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residuse: 1-259 <a href="https://doi.org/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.
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A65070
hypothetical protein b2865 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: A65070
C;Accession: A65070
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submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E. A.Authors: Martins, E.M.F.; Matkuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A., P.G.; Palmieri, D.A., A.Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Vettore, A.L.; Za, A.Confarte annoverica, A.S.; Vettore, A.L.; Za, A.Confarte annoverica, A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C.; A.C
16 KRĻGLIFGVITTCIĻAGCASKPTYNSTSGSGSHRŢSGSGGLAIGSQVITDSQGVPNRYQV
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                                                                                                                                          14.3%; Score 238; DB 2; 24.9%; Pred. No. 4.8e-10; tive 46; Mismatches 103
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VIYVS-

conserved hypothetical protein PA4924 [imported] - C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Accession: B83031

Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,

M.J.;

.; Br Lim,

15-Sep-2000 #text_change

31-Dec-2000

Pseudomonas aeruginosa

(strain

PAO1)

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A; Plance type: DNA
A; Molecule type: DNA
A; Residues: 1-259 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB37161.1; PID:g13363210; GSPDB:GN00154
A; Cross-references: strain O157:H7, substrain RIMD 0509952
RESULT
B83031
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B91096
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                                                             RYRATAIDPLRYL 250
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                                                                                                                                                                                                                                                                                                                   KRGDTLYRISRTTGTSVKELARLNGISPPYTIEVGQKLKL--GGAKSSSSTRKSTAKSTT 110
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Pred. No. 4.8e-10
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Shiba, T.; Hattori, I
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A;Gene: STY3194
C;Superfamily: lipoprotein
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Nature 413, 848-852, 2001
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A;Accession: AD0871
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C;Accession: AD0871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable lipoprotein (imported) - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi
                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-250 < PAR >
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                                                                                                                                                                                             A;Cross-references: GB:AL513382; PIDN:CAD02868.1; PID:g16504121; GSPDB:GN00176
                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004905; GB:AE004091; NID:g9951195; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-231 <STO>
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                                                                                                                                                                              ;Genetics:
                                                                                Query Match
Best Local
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1 Similarity 26.7%;
68; Conservative 3
                                                             76;
                                                                                Similarity
LGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIRQNGRPLDPLSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVNNMRGYGNLVIIQHGTSYTSTYAHNSRLLVKEGQMVGKGQKIAEAGSSDADRVQLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LRGWQWPM--KGPVIRRF----SSSDKLNKGIRIAGTLGQPVQASLAGKVV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRGEYRVKRGDTLYSIATRHGWNYKDLARANGIRPPYAVKVGQ-VVRFDGRKSTYVASSR
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                                                             Conservative
                                                                              13.9%;
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                                                           49;
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                                                   Score 232.5; DB 2,
Pred. No. 1.1e-09;
Pred. No. 1.99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 234; DB 2
Pred. No. 8e-10;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Davis, P.; Davies, R.M.; Dowd, L.; White, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ARKPPPPPPSVT------ 108
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                                                                                                250;
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RESULT 9
E75291
probable cell wall glycyl-glycine endopeptidase - Deinococcus
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipoprotein D homolog - Haemophilus influenzae (strain Rd Kw20)

C;Species: Haemophilus influenzae

C;Date: 1B-Aug-1995 #sequence_revision 1B-Aug-1995 #text_change 29-Sep-1999

C;Accession: F64087; T09410

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800
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Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: nucleic acid sequence not shown; translation not shown
Molecule type: DNA
Residues: 1-405 <TIGR>
Cross-references: GB:U32753; GB:L42023; NID:g1573701; PIDN:AAC22363.1; PID:g1573707;
                                                                                         370
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                                                                                                                                                                                                                                                                                                        VNTAHTESPVAVQSSREPVQQHPAVQKFTP------PVVVVKKPTPTPPVV 175
                                                                                                                                                                                                                                                                                                                                      NTYKVNKGDTMFLIAYLAĞIDVKELAALNNLSEPYNLSLĞQVLKISNCDIKTVTTTVS--
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                                                                                                                                            IŚĠSRĠQAVKAAAAĠRIVYAGNALRGYGNLIIIKHNDDFLSAYAHNDKILVADQQEVKAG
                                                                                                                                                                          FSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTG 288
                                                                                                                                                                                                          TSSTQVTSSVNNANSTPINSNVVA---PI-ASN-VVWQWPTSGNIIQGFSSTDGGNKGID 309
                                                                                                                                                                                                                                        QQPAPYAPPYTEAPFATGSSGVMQFRYPVGATNPVVRRFGTA--TVAGSTVT---SNGMW 230
                                                                                                                                                                                                                                                                      ----VKQPAVTASTATPVK--PAVTY-TPGANGTQIGSDGTIIGPIKSEAGTSPSVPVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDTLYRISRATGTSVKELARLNGISPPYTIEVGORIKV-RGSAKSSSSTRKTSNKTATKT
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 219.5; DB 2;
Pred. No. 1.8e-08;
6; Mismatches 114;
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                                                                                    402
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                                                                              Query Match
Best Local S
Matches 91
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A; Gene: DR2291
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       PMIRLRRVAACTVVSLWLVGCTND---NSTSAP----ISSVGGDRSGTMLSKANTDSSGG 58
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C;Genetics:
A;Gene: nlpD
C;Superfamily: lipoprotein D
                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92586.1; PID:g15981283; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., deno-Traga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of Yersinia pestis, the causative agent of plague
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0407
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: E75291
C;Accession: E75291
N; White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu A;Reference number: A75250; MUID:20036896; pMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipoprotein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Aate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C;Accession: AF0407
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A; Residues: 1-454 < WHI>
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:AE002061; GB:AE000513; NID:g6460095; Experimental source: strain R1
14 PIKRLGLIFG-VITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIG---SQVITDSQG- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 ARPSPAQPAPPRVAQATPEHHARVVVRQTSSHSLWQWPLPGYGRITSDFGWRVLDGEREK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 QQPAPVAPPVTEAPFAT------GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 LKVRERSISSGVNTAHTPSPVAVQSSRP-PVQ---QHPAVQKPTPPVVVVKKPTPTPPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 SQVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGD
                                                                    Similarity 25...
91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNGMWFSGRDGDLINASNAGTVIQADHNMD-----GASIVIQHTNGFVSSYIHIKDAQVK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HQGIDVAAPPGTPVIAARSGRVIQA--HLDETYGWGWTVVIQHPDGWQTRYAHLSRISVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGQLVRQGERVGAVGSTGRVTGPHL-HFGLYRNWDPHNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGDTVRTGQRIASM--KNQPSGAALFEFRISRNGVYVDPL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQLAAAKKPKPTTHRVEIGDTFYSVARRYGINPIALQEYNPRLAGQTLNVGAVLSLVAPP
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                                                                                               13.1%;
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                                                                ; Score 218.5; DB 2;
; Pred. No. 1.7e-08;
52; Mismatches 130;
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Pred. No. 2.1e-08;
0; Mismatches 116;
                                                                                                                          Length
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                                                             Gaps
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T.; Zalewski, C.; Ma
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AH0855
lipoprotein NlpD precursor [imported] - Salmonella enterica subsp. enterica serovar Typh C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002 C;Accession: AH0855
C;Accession: AH0855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; PMID:11677608

A;Accession: AH0855
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A; Residues: 1-373 < PAR>
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Best Local S
Matches 84
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                                                                   VIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNGVYVDPLT 319
                                                                                                                                                                              YSEGSGEQSANKMLPNNKPAGTVVTAPVTAPTVSTTEPNASSTSTSAP-----ISAWR
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                                                                                                                                                                                                                                                                                                                        QPVTEQPVQMENGRIVYNRQYGNIPKGSYTGGSTYTVKKGDTLFYIAWITGNDFRDLAQR 142
                                   IIKHNDDYLSAYAHNDTMLVREQQEVKAGQKIATMGSTGTSSTRLHFEIRYKGKSVNPLR
                                                                                                                                                                                                                                                                                                                                                        QVITDSQ-----GVP-----NRYQVKQGDTVSKIAQRYGLNWREIGHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHNDDYLSAYAHNDTMLVREQQEVKAGQKIATMGSTGTSSVRLHFEIRYKGKSVNPLRYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRFGTATVAGSTVTS-----NGMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVI
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 VL 321
                                                                                                      WP--TDGKVIENFG-ASEGG----NKGIDIAGSKGQAIVATADGRVVYAGNALRGYGNLI
                                                                                                                                        YPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS--I
                                                                                                                                                                                                               -----QHPAVQKPT--PPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFR 201
                                                                                                                                                                                                                                                 NSISAPYSLNVGQTLQVGNASGTPITGGNAITQADAAQQGVVTRSAQNSTVAVASQPTIT
                                                                                                                                                                                                                                                                                     NNLNSSYTIYTGQWL-----TLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV- 149
                                                                                                                                                                                                                                                                                                                                                                                             LAGCTSSSNPPAPVTSVDSGSSSNTNSGMLITPPPKMGATPQQAPQIQPVQRPVTQPMQT
                                                                                                                                                                                                                                                                                                                                                                                                                                   LAGCASK-----PTYNSTSGSGSHRTSG-----SGGL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AL513382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.6%; Score 210; DB 2 23.2%; Pred. No. 8e-08; tive 56; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAD06031.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --AQPPSNIQNTTTIQNTTTTVDSQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:g16503998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
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              A; Experimental source: strain
                               A;Cross-references: GB:AE008917; PIDN:AAL52260.1; PID:g17983047; GSPDB:GN00190
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C;Accession: AI3386
C;Accession: AI386
C;Accession: AI386
C;Accession: AI386
C;Accession: AI386
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, l., Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens. A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <KUR>
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A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, Fchardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Mature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: DNA Sequence of both chromosomes of the cholera pathogen A; Reference number: A82035; MUID:20406833; PMID:10952301
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C;Accession: H82311
                                                                                                                                                                                                                                                                                                                 AI3386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE004139;
A;Experimental source: serogroup
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                                                                                                                                                                                                                             ipoprotein nlpD [imported] - Brucella melitensis (strain 16M)
;Species: Brucella melitensis
;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: H82311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Vibrio cholerae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQRIASMKNQPSGAALFEFRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIAGQRGQAVVATADGTVVYSGNALRGYGNLIIIKHNEHYLSAYAHNDQLLAKEGQTVQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLGLL---LFCSLLFGCTA-PTPAPVSGLGKDYNKVERGSYRGSY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLGLIFGVITTCILAGCASKPTYNSTSGSGSGHRTSGSGGLAIGSQVITDSQGVPNRYQVK 76
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                                                                                                                                                                                                                                                                                                                                                                                                         GQKIATMGSSGTNSVRLHFEIRYQGKSVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGKQNVNVNVAKAKPSDEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVQQPAPV----APPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSTSASVAKAATTATVAQTVSKSSNTKNVQNGSTNSQNLTKKDPVKTVDQTKTKEYVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---RERSISSGVNTAHTPSPVAVQSSRPPVQ-----QHPAVQKPTPPVVVVKKPTPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGDTLYFÍAYLTDKDVNDLISYNDLAPPYTIHPGÓKIKLWLPNYTPPAYGGTGGAATVAV 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 208.5; DB 2
Pred. No. 8.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----IAKWLWP--TKGRVIKNFS----AGDQ-GNKGI
                                                                                                                                                                                                                                                                                                                                                                                                         306
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El Tor
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H.; Dragoi,
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I.; Sellers,
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C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: G81864
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81864
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G81864
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A; Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Status: preliminary
;Molecule type: DNA
;Rosidues: 1-415 <PARS
;Residues: 1-415 <PARS
;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84920.1;
;Cross-references: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                       185 HTIVRGDTVYNISKRYHISQDDFRAWNGMTDN-TLSIGQ-----IVKVKPAGYAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
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                                                                                                                                                                                                                                                                                                          73 YQVKQGDTYSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
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                                                                                                                                                                                                                                                                                                                                                   h 12.2%; Score 203; DB 2; Length 415; Similarity 27.3%; Pred. No. 2.9e-07; Indels 71; Conservative 42; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 26.2
79; Conservative
                                                                 NASNAGTYIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ
PSGAALFEFRISRNGVYVDP 317
                              LAAADGKVVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNT
                                                                                                                  PAPOSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG-
                                                                                                                                                PVTEAPFA----TGSSGVMQFRYFVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI
                                                                                                                                                                                          ----PKAAAVK-SRPAVP--AAVQTPV-----KPAAQPPVQSAPQPAAPAAENKAVPA
                                                                                                                                                                                                                               TAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RGRILASFGORE---GTSVSDGIDIMVPEGTPVKAAENGVVIYAGDGLKEFGOTVLIRH
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RESULT D91078

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A;Residues: 1-379 <ICH>
A;Residues: 1-379 <ICH>
A;Residues: 1-379 <ICH>
A;Residues: 1-379 <ICH>
A;Residues: 1-379 <ICH>
A;Residues: 1-379 <ICH>
A;Cross-references: GB:L07869; NID:g433183; PIDN:AAA17875.1; PID:g433185
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col.
A; Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Recission: B65055
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-379 <ALAT-
A;Cross-references: GB:AE000358; GB:U00096; NID:g2367156; PIDN:AAC75784.1; PID:g1789099;
A;Experimental source: Strain K-12, Substrain MG1655
A;Experimental source: Strain K-12, Substrain MG1655
R;Takayanagi, Y; Tanaka, K; Takahashi, H.
Mol. Gen. Genet. 243, 525-531, 1994
A;Title: Structure of the 5' upstream region and the regulation of the rpoS gene of Esch
A;Accession: S45580
A;Strains - x-1:--
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A;Molecule type: DNA
A;Residues: 99-138, A',140-379 <TAK>
A;Cross-references: EMBL:D17549; NID:g404097; PIDN:BAA04487.1; PID:g404099
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C;Species: Escherichia coli
C;Date: 25-Aug-1995 #sequence revision 25-Aug-1995 #text_change 01-Mar-2002
C;Accession: B55522; B65055, S45580
R;Ichikawa, J.K.; Li, C; Fu, J.; Clarke, S.
J. Bacteriol. 176, 1630-1638, 1994
A;Title: A gene at 59 minutes on the Escherichia coli chromosome encodes a: A;Reference number: A55522; MUID:94173096; PMID:8132457
A;Accession: B55522
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      341
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                                                     286 RTGQRIASMKNQPSGAALFEFRISRNGVYVDPLTVL 321
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72; Conserv
                                                                                                             GIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIKHNDDYLSAYAHNDTMLVREQQEV
                                                                                                                                                                                                                          TATTVIAPVTVPTASTTEPTVSSTSTSTPISTWRWP--TEGKVIETFG-ASEGG----NK 280
                                                                                                                                                                                                                                                                                                                                              ASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSANKMLPNNKP
                                                                                                                                                                                                                                                                                                                                                                                                   TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
KAĞQKİATMGSTGTSSTRLHFEİRYKĞKSVNPLRYL
                                                                                                                                                                     GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                                                                                                                                                                                                   TPPVVQQPAPVAPPVTEAPFATG---SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ--TLQVG---
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ilarity 26.1%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 202.5; DB 2;
; Pred. No. 2.8e-07;
42; Mismatches 113;
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C;Accession: E85923
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamon Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Molecule type: DNA
A;Rosidues: 1-379 <HAY>
A;Rosidues: 1-379 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37019.1; PID:g13363067; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipoprotein [imported] - Escherichia coli (strain 0157:H7, substrain EDL933) C;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; I
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
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A; Residues: 1-379 <STO>
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A;Experimental source: strain O157:H7, substrain EDL933
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Best Local S
Matches 72
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  168
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                                                                                                                                                                                                 12.1%;
Similarity 26.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSANKMLPNNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                     YTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ--TLQVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAGQKIATMGSTGTSSTRLHFEIRYKGKSVNPLRYL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTVKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ--TLQVG------N 167
                                        TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIIKHNDDYLSAYAHNDTMLVREQQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPPVVQQPAPVAPPVTEAPFATG---SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN 227
ASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSANKMLPNNKP
                                                                                                                                 YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTVTAPVTVPTASTTEPTVSSTSTSTPISTWRWP--TEGKVIETFG-ASEGG----NK
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                                                                                                                                                                            ; Score 202.5; DB 2
; Pred. No. 2.8e-07;
42; Mismatches 113
                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                              Indels
                                                                                                                                                                              49;
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Potamousis,
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  227
                                          170
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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eiser Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vymathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Complete genome sequence of Neisseria meningitidis
A;Reference number: A81000; MUID:20175755; PMID:10710307
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                     KAVPAPAPQSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG-----NNKGVDIAGN 324
                                                                                                                                                                                                                                                          VKVKPAGYAAPKTAAVESRPAVP--AAVQTPV-----
                                                                                                                                                                                                                                                                                                                                               HTIVRGDTVYNISKRY-----HISQDD-----FRAWNG---MTDNMLSIGQI
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LMGNTDASRTQLHFEVRQNGKPVNP
                                      SMKNOPSGAALFEFRISRNGVYVDP 317
                                                                                AGQPVLAAADGKVVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEGQQVKRGQQVA 384
                                                                                                                           DGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIA 292
                                                                                                                                                                                                              -----PVTEAPFA----TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGR 234
                                                                                                                                                                                                                                                                                                                                                                                      YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%;
27.2%;
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B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 198; DB 2; 1
Pred. No. 6.8e-07;
8; Mismatches 95;
                                                                                                                                                                                                                                                          - KPAAQPPVQSAPQPAAPAAEN
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strain MCS
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MC58.
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Ver

peptidase, M23/M37 family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: G87496
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249, MUID:21173698, PMID:11259647

RESULT G87496

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AF2785
Lipoprotein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
Lipoprotein: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Algrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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AFAUthors: AGMENTAL AGROUPT
AFAUthors: Young Agrobacterium tumefaciens (strain C58, Dupont)
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <STO>
A;Cross-references: GB:AE005673; NID:g13423465; PIDN:AAK23971.1;
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PGASTDAIKTASVPAKEA--AAAKPVE--TASIKPEPYKAPAAAATTAAPATPATASVSD
                                                                                ERSISSGVNTAHTESPVAVQSSRPPVQQHPAVQKPTP---PVVVVKKPTPTPPVVQQPAP
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23.6%; Pred. No. 1.5e-06;
tive 54; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                       -TPLRAPDGNVAVLPSQAAARDKLSSEAGKLTPPGGKPL
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43K antigen (AF157831) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: H97564
R;Goodner, B; Hinkle, G; Gattung, S; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; PMID:11743194
A;Accession: H97564
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A; Map position: circular chromosome
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A;Molecule type: DNA
A;Residues: 1-562 <KUR>
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MTGSAKRPQVHFEVRKDATPVNP
                                                                                                       NASNAGTYIQADHNMD--GASIVIQHTNGFYSSYIHIKDAQYKTGDTYRTGQRIASMKNQ 297
                                PSGAA---LFEFRISRNGVYVDP 317
                                                                      KAAENGVVIYAGNGLKOLGNTVLVRHDDGKVTVYGNAANLDVQRGQKVQRGQTIAT--SG
                                                                                                                                                                                                                                                         ERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQXPTP---PVVVVKKPTPTPPVVQQPAP 180
                                                                                                                                                                                                                                                                                             PPSGG----YKVQPGDSLAKIARANGVSVAALKAANGI-SNESIRVGQTLAM------
                                                                                                                                                                                                                                                                                                                                  TDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVR 123
                                                                                                                                              IEKKADMASIAPESTGIGKYRWÞVRGA---VINNÞGD-NVEGS--RNDGINISVÞEGTÞÍ
                                                                                                                                                                                 VAPPVTEAPFATGSSGVMQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI
                                                                                                                                                                                                                      PGASTDAIKTASVPAKEA--AAAKPVE--TASIKPEPYKAPAAAATTAAPATPATASVSD 422
                                                                                                                                                                                                                                                                                                                                                                         IALNRNGDQP-----TPLRAPDGNVAVLPSQAAARDKLSSEAGKLTPPGGKPL 319
                                                                                                                                                                                                                                                                                                                                                                                                            IAINSQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLA-IGSQVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%;
ilarity 25.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 188.5; DB 2;
; Pred. No. 4.8e-06;
64; Mismatches 131;
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probable secreted peptidase - Streptomyces coelicolor (;Species: Streptomyces coelicolor (;Species: Streptomyces coelicolor (;Species: Streptomyces coelicolor (;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000 (;Accession: T35413 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajanc submitted to the EMBL Data Library, March 1999 A;Reference number: Z21577 A;Accession: T35413 A;Status: preliminary; translated from GB/EMBL/DDBJ

B.G.; Rajandream,

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RESULT 22 T35413

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A;Gene:
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-223 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasriller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable lipoprotein Z4203 [imported] -
C;Species: Escherichia coli
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A; Residues: 1-312 < CUL'>
A; Cross-references: EMBL: AL049485;
A; Experimental source: strain A3(2)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: F85941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Dec-2001;Accession: F85941
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Best Local :
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                                  SSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFRYP 203
                                                                              GTSVKELARLNGISPPYTIEVGQKLKL--GGAKSSSSTRKSTAKSTTKTASVTPSSAVPK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GORI--ASMKNOPSGAAL-FEFRISRN-GVYVDPLTVLK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAVGSDPSLIHPGLKLSIDGQAAKPSAPSSAQSQKPA-----QKSAEKPAEKTAAKPA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSISSGVNTAHTPSPVAV--QSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKNSDSRTYTVKSGDYLSKIADEQDVD-
                                                                                                                   GLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGVNTAH-TPSPVAVQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RDGDLINASNAGTVIQAD-HNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRT
SSWPPVGQRCWLWPTTGKVIM----
                                                                                                                                                              LLAGC----SGSKSSDTGTYSG-----SVYTVKRGDTLYRISRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQQVGLSGATGNVTGPHLHFEIRTTPDYGSDIDPLAFLR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDFVVPTGTSLKAVGAGTVVSAGWGGAYGNQVVIQLADGHYAQYAHLSSLSVSAGQSVTA
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                                                                                                                                                                                                      ILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQRY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----NRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRE
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                                                                                                                                                                                                                                             10.1%; Score 169; DB 2; 1 24.0%; Pred. No. 3.8e-05; tive 35; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli (strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B.; Glasner,
imalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPDB:GN00070; SCOEDB:SC6A5.
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-PYSTADGG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.D.; Rose, Potamousis,
                                                                                                                                                                                                                                                 86;
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          Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduenc ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AH1387
A; Status: preliminary
                                                                                                                                                                           cell wall binding proteins homolog lmo2504 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AH1387 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
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Dominguez-Bernal, G.; Jones, L.M.; Karst, U

Madueno, E.; Boland, J.A.;

Voss, Maitournam,

Α..

F.; Berche, P.; ; Entian, K.D.; |

; Bloecker, Fsihi, H.

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8;Fittle: Complete genome sequence of Treponema pallida A;Fittle: Complete genome sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida professional sequence of Treponema pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida pallida palli
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A;Residues: 1-371 <COL>
A;Cross-references: GB.AE001200; GB.AE000520; NID:g3322419;
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein TP0155 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
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                                                                                                                                                                                                            TATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHN-MDGASIVIQHTNGFVSSYIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIAAAH-----QISLERLVLLNTPSSSKESPPSVRTLVSPFYNSAARESCVPFPFSSAKQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGD---LKVRERSISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVI
QTVLVSAGTRVTSATKIGLLGKTGRSTGPHLHFTIYKNGSAINPTSLLR
                                                                KDAQVKTGDTVRTGQRIASM-KNQPSGAALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                        SDPFTGARSFHNGLDMVSRRGTPVYSALGGIVRTVGYSAVYGNYLIVGHHAGYQTLYGHL
                                                                                                                                                                                                                                                                                        WRENTSFDAVQPLQPA----RVLFLPGAHLSARALQEINGDLFRAPLRSRYYVSSRYGWR
                                                                                                                                                                                                                                                                                                                                                            -----PVVQ--QPAPVAPPVTEAPFATGSSGVMQ-----FRYPVGATNPVVRRFG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 167; DB 2;
Pred. No. 0.0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NKGIDISAPRGTPIYAAGAGKVVYVGNQLRGYGNLIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:AAC65145.1; PID:g3322422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not
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A;Accession: r.,
A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <WHI>
A;Cross-references: GB:AE001939;
A;Cross-references: GB:AE001939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable lipoprotein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: F75467
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan; J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans HA;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75467
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A;Cross-references: GB:NC_003210; PIDN:CAD00582.1; PID:g16411992; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2504
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                               position: 1
           182
                                                                                                                        174
                                                                                                                                                                                         128 SSGVNTAHTPSPVAVQSSRP-PVQQHPAVQKPT--PPVV----VVKKP--TPTPP-----
                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408
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                                                                                                                                                                                                                                                                                                         h
9.5%; Score 158; DB 2; I
Similarity 21.7%; Pred. No. 0.00046;
74; Conservative 36; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 9.5%;
Similarity 24.8%;
56; Conservative 3
EVRLGGDVVRGQIPVGDLGQRVQHLNLPPSISKVLQDPAREAEDAAVEQAYQRRTPQQWQ
                                                                                                                                                      GEGAATPATPAPAAPTPATPAPAAPAPAPAPAPATKLPTVATAANVLKLPGVTITAPKALKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAGTVIQADHNMDGAS-----IVIQHTNGFVSSYIHIKDAQVK--TGDTVRTGQRIAS 293
                                                                            GDGFALRLSGEQAANVTVRFPSELGEDVRQPNEELRPLWSSGQYIVPGRVVLGKTTPVIY 181
                                                                                                                                                                                                                                ĠŸĀGĀŸTŸĸĸĠĎTĿŸSĿĀRGSĠĿTVDĀĿMRĿŊĠĿ-ŚTPĒĿRVĠQVIĶĹ-------P
                                                                                                                                                                                                                                                                      GVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGSTGQSTGQHL-HFEIHKNGIPVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M--KNOPSGAALFEFRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASGTVVFSGFGASGSGFGGYGYVVKIDHGNGFQTLYGHMRAGSLKVVTGQQVSQGQPIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKQEAAIKAAEEKRMQEAAAASSAKSAAVVK------QPSSSSNEATE----TVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGQFIKPASGILTSGFSERTNPVTGKYESHKGQDIAGGGTVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVMQFRYPVGA-----TNPVVRRF----GTATVAGSTVTSNGMWFSGRDGDLINAS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TESPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKNDLVMALANKKDLT-----KSEQTLLASE----QGALTDEEKRLASNIAGEK
                                                                                                                ---VVQQPAPVAPPVTE----APFATGSSGVMQFRYPVGATNPVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE000513; NID:g6458563; PIDN:AAF10427.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432
                                                                                                                                                                                                                                                                                                                                             Length 375;
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                                        -----RR-----
                                                                                                                                                                                                                                                                                                         Gaps
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  241
                                      213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g64585
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A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-437 <GLA>
A;Roseriduse: 1-437 <GLA>
A;Crose-references: GB:AL592022; PIDN:CAC97874.1; PID:gl6415184; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
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C;Bate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Bate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Aacession: ABI763
C;Accession: ABI763
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
;Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I
D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
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Science 294, 849-852, 2001
A;Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
A;Authors: Kreft, U.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.;
ck, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1763
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AB1763
cell wall binding protein homolog lin2647 [imported] - Listeria innocua (strain Clip1126;
C;Species: Listeria innocua
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Best Local
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  409
                                          294
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                                                                                                                                                                                                                                                                                                                                                          210 EKNDLVMALANKKDLT-----KSEQTLLTNE----QGALSDEQKKLASNIAGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 -- FGTATVAGSTVTSN------
                                                                                                                                                                                                                                                                                                                                                                                                       76 KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 62; Conserv
MGSTGQSTGQHL-HFEIHKNGIPVDP
                                                                                                                              NAGTVIQADHNMDGAS-----IVIQHTNGFVSSYIHIKDAQVK--TGDTVRTGQRIAS
                                       M--KNOPSGAALFEFRISRNGVYVDP 317
                                                                                       ASGRVVFSGFGATGSGFGGYGYVVKIDHGNGFQTLYAHMRAGSLKVVTGQQVSQGQPIGI
                                                                                                                                                                              GGGQFIKPASGMLTSGFSERTNPVTGKYESHKGQDIAGGGTIT------
                                                                                                                                                                                                                      GVMQFRYPVGA-----TNPVVRRF----GTATVAGSTVTSNGMWFSGRDGDLINAS
                                                                                                                                                                                                                                                                                                             TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRGGLVVIDHGAGVVSLYFHQSKVTAKVGQQIKRGQKVGEV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         35,
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Pred. No. 0.00092;
5; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GMWFSGRDGDLINASNAGTVIOAD-HN 253
                                                                                                                                                                                                                                                                     ---VAAQQPSSVTSSAGTGATDTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                         ----VSAA
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Voss, H.; Wehland,
                                                                                                                              293
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Fsihi, H.,
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probable peptidase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec.1999 #sequence_revision 03-Dec.1999 #text_change 03-C;Accession: T36379 D; Bentley, S.D.; Parkhill, J.; Barrell, B.G R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G submitted to the EMBL Data Library, April 1999 A;Reference number: Z21573 A;Accession: T36379 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Cross-references: EMBL:AL049628; PIDN:CAB40868.1; GSPDB:GN00070; A;Experimental source: strain A3(2)

03-Dec-1999 B.G.; Rajan

Rajandream,

3

SCOEDB:SCE94.19c

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R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA RES. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy:Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AB2225
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A;Residues: 1-760 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75052.1; PID:g17132448; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein alr3353 [imported] - Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SCOEDB: SCE94.19c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Nostoc sp.
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Best Local Similarity
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                                   646
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                                                                                                                                                                                                                                                                                                  406 SVPITVPTPGADSETPVDTIVPLESASAPAETQGVGGNVPIPKAFIEIQRPQQPGKRAAR 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 VAGSTVTSNGMW----FSGRD-----GDLINASNAGTVIQADHN------MDGASIVIQHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 20.1
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        LKVRERSISSGVNTAHTPS------
 AQVKTGDTVRTGQRIASMKNQPSGAALF---
                               GWRWGRMHRGIDIAAPVGTPVFAAADGVVEKSGWNRGGYGNLVDIRHPDGSLTRYAHNSR
                                                                                                  RLNASESLGRMRGTTVSPKLPPLAAVDQYLPQAIDESVPPPSDSTTAFIWPAKGVLTSGY 645
                                                                                                                                                                                                                                  AKGDRLRSLQAEIQRLQAKYRDQQTGNTPVPVVANQNNNTAIPIPVTSPNNFAVTRPISR 525
                                                                                                                                                                                                                                                                                                                                                                       -----AIDSSSTIAQAPAIISSNRVQYPGTPTVPNFPVDTARVNPSLPVAQPPSIANND 405
                                                                                                                                                                                                                                                                                                                                                                                                                                        QPLTETSASTANTYEVKPGDTLAAIASRYNTSVAELVKVNNLSNPNQLKISQQLIIPS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVITD-SQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSASFAQNGGMWAHKHSGQDFAVPIGTNVVAAHGGTVVKAGGNGAGDGPAYGNAIVIKHG 160
                                                                                                                                                                   QQEIAVPIAVPTPLAPNDSNHPVKPQFRATLPVNEALNPEFLPNNAPQNPSVRRVATPPV
                                                                                                                                                                                                    ---PAPVAPPVTEAPFATGSSGVMQFR--YPVGAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGTYSQYAHLSRINVKIGQIVKTGQSIAKSGNTGNSSGPHLHFEIRTTPNYGSAVDPVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAAL-FEFRISRN-GVYVDPLTV 320
                                                                                                                                 -----AGSTV-----TSNG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.1%;
                                                               --DGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 152; DB 2;
Pred. No. 0.0031;
1; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 153; DB 2;
Pred. No. 0.00055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                      TPTPPVVQQ
 -EFRISRNGV-YVDPLTVL 321
                                                                                                                                                                                                                                                                                                                                                                                                      ----PVAVQSSRP---PVQQHPAVQK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 224;
                                                                                                                                                                                                    ----NPVVRRFGTATV 219
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                                               A; Experimental C; Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1147
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Kesidues: 1-439 <STO>
A;Cross-references: GB:AB005176; PID:g12723133; PIDN:AAK04370.1;
A;Experimental source: strain IL1403
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AG1147
                                                                                                                                                                                                                                                                                                  R;Glaser, P.; Frangeul, L.;
; Dominguez-Bernal, G.; Duo
D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
AG1147
P60 extracellular protein, invasion associated protein Iap [imported] - Listeria monocyto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) [imported] - Lactococcus 1. C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: H86558 C;Accession: H86558 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbagenome Res. 11, 731-753, 2001
                          A;Cross-references: GB:NC_003210; PIDN:CAC98661.1;
                                                    A; Residues: 1-482 <GLA>
                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: acmA
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: H86658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 TAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVT----EA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 TAALTGKYATDPNYGASLNRIISQYNLTRFDGASSAGTSNSGG-STATNTNNNSNTSSTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOVKOGDTVSKIAORYGLNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSTSNSSAAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTV----RTGQRIASMK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYKTTIAQLKSWNHLNSDTIFIGQNLIVSQSAGSSSSSTG-----SSSAST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAGTTTPTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTVKSGDTLWGISQKYGISVAQIQSANNLKST-VIYIGQKLVLTTSSSSSNTNSSTSSGN
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  source:
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strain
                                                                                                                                                                                                                                                                                                                               Duchaud,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 146.5; DB 2; 23.6%; Pred. No. 0.0038; ative 39; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                  Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; chaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
  <u>6</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NTSIH----KVVKGDTLWGLSQKSGSPIASIK
                                                                                                                                                                                                                                                                                                                                                                                                                      27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SVTPAKPASQTTIKVKSGDTLWGLSV
                    PID:g16409958;
                                                                                                                                                                                                                                                                                                                                                                                                           #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
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                          GSPDB:GN00177
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Voss, H.; Wehland,
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8.8%;

Score

146.5;

BB

2

Length

482;

Ξ.

Qy 90 LINWREIGHINILIASSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSGVAVQSSRPPV 149	Pred. No. 0.0043; 46; Mismatches 121; SGSGSHRTSGSGGLAIGSQVI : : : ESNGWHKITYNDEKTGFVNGKYL	re number: A41487; MUID:90256283; PMID:21 n: A41487 n: A41487; MUID:90256283; PMID:21 n: A41487 s: 1-484 <koe> siferences: GB:X52268 nf: B41487 si 1-494 <koe> si 1-494 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe> si 28-49 <koe 28-49="" <ko<="" <koe="" si="" th=""><th>434 VFFDYGSGISHVGIYV 449 60 precursor - Listeria monocytogenes ste names: invasion-associated protein s: Listeria monocytogenes 10-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1996 10n: A41487; B41487 10n: A41487; B41487 10n: A41487; B41487 10n: A41487; B41487</th><th>Qy 150 QQHDAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199 </th><th>Best Local Similarity 20.6%; Pred. No. 0.0043; Matches 81; Conservative 46; Mismatches 121; Indels 145; Gaps 14; Oy 25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITD</th></koe></koe></koe></koe></koe></koe></koe></koe></koe></koe></koe></koe></koe></koe></koe></koe>	434 VFFDYGSGISHVGIYV 449 60 precursor - Listeria monocytogenes ste names: invasion-associated protein s: Listeria monocytogenes 10-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1996 10n: A41487; B41487 10n: A41487; B41487 10n: A41487; B41487 10n: A41487; B41487	Qy 150 QQHDAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQ 199	Best Local Similarity 20.6%; Pred. No. 0.0043; Matches 81; Conservative 46; Mismatches 121; Indels 145; Gaps 14; Oy 25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITD
RESULT 34 \$76492 Ilipoprotein nlpD - Synechocystis sp. (strain PCC 6803) N.Alternate names: protein slr0993 C;Species: Synechocystis sp. A;Variety: PCC 6803	Db 270 ENSNANTATTEKKETATEQCTTTKAPTQAAKPAPASTNINKTNITNNNTNAS 322 Qy 211 VRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHT 264	25 ITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITD	A; Reterence number: AB1077; MUID:21537279; PMID:11679669 A; A; Accession: AG1506 A; Status: preliminary A, Molecule type: DNA A; Residues: 1-465 < GLA> A; Cross-references: GB:AL592022; PIDN:CAC95823.1; PID:g16413031; GSPDB:GN00178 A; Experimental source: strain Clip11262 C; Genetics: A; Gene: iap Query Match Best Local Similarity 21.1%; Pred. No. 0.013; Matches 75; Conservative 51; Mismatches 143; Indels 87; Gaps 14;	RESULT 33 AG1506	Qy 200 FRYPVGATINDVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ 249 216 KTIVINTNITNITNITNITNSNITNINITNISNITNINGSSASAIIAE 375 Qy 250 ADHNWD

```
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Agripson, R.J.G.; Reinach, F.C.; Arruda, P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.; Perreira, A.J.S.; Bueno, M.C.; Facincani, A.P.; Franca, S.C.; Franco, M.C.; Frohm as Neto, E. C.; Aller, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrichado, M.A.; Madeira, H.M.F.; Marxino, C.L.; Marques, M.V.; Martins, E.A.; Machins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
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C82736
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C;Accessic
R;Kaneko,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein XR0987 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-2000 #text_change 20-Aug-20-Aug-20-Aug-20-Aug-20-Aug
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A;Molecule type: DNA
A;Residues: 1-285 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bei
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
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A; Residues: 1-715 < KAN>
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A;Accession: S76492
A;Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AE003937; GB:AE003849; NID:g9105920; PIDN:AAF83797.1; GSPDB:GN00:
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; Pred. No. 0.027;
44; Mismatches 128;
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A;Authors: da Silva, A.C.R.; d.
M.; Tsuhako, M.H.; Vallada, H.
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: D64158
A;Status: nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-410 <TICR>
A;Cross-references: GB:U32760; GB:L42023; NID:g1573764; PIDN:AAC22415.1;
A;Note: best homolog was a hypothetical protein from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: D64158
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ;
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.;
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein HI0756 - Haemophilus influenzae (strain C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #favt char
                                                                                                                                                                                                                                                                                                                                                                                                  Query
Best I
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                                                                                                                                                                                                          AHTPSPVAVQSSRPPV-QQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFAT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRVEYSGQVLRVDDKGQVVFGVGRNNIGPLILRIQSPEGTVKQVNITVTTRQW------
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QADH-NMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAALFE
                                                    STSGLGAAKKQYSLPVSGS--ILHTFG--SIQAGEVRWKGMVIGASAGTPVKAIAAGRVI
                                                                                                     GSSGV----MQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVI
                                                                                                                                                                                                                                                               QKKQQQALQKAQQEHQ-----STLNELNKNLALDQDKLNT-----LKANEQALRQEIQR 236
                                                                                                                                                                                                                                                                                                                QVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGAVGATGRATGPHL-HWGMNWFNVRIDPLLVLE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGTPVKAPAAGVITFAAPDLYLTGGTVLLDHGAGVSSNFLHLSRIDVKVGDHVDQGQV
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                                                                                                                                                         AEQAAREQEKREREALAQRQKAEEKRT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVAPPVTEAPFATG--SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IASM--KNOPSGAALFEFRISRNGVYVDPLTVLK 322
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25.0%;
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H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----PLEVVNGVPPKTVNP-----PPEIAAR-----ITREQA
                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 135;
Pred. No. 0
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Pred. No. 0.
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hypothetical protein HI0409 - Haemophilus influenzae (strain Rd KW20)
(,Species: Haemophilus influenzae
(,Species: Haemophilus influenzae
(,Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
(,Accession: F64151
R,Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
R,Fleischmann, Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A6400; MUID:9535030; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein PA5133 [imported] - Pseudomonas aeruginosa (strain P. C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep_2000 #sequence_revision 15-Sep_2000 #text_change 31-Dec_2000
C;Accession: A83005
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lorry, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Recession: A83005
A;Recession: A83005
A;Accession: A83005
A;Accession: A83005
A;Accession: A82950; MUID:20437337; PMID:10984043
A;Accession: A82950; MUID:20437337; PMID:10984043
A;Accession: A82950; MUID:20437337; PMID:10984043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .../Molecule type: DNA
;Residues: 1-428 «STO»
;Cross-references: GB.AE004926; GB.AE004091; NID:g9951424; PIDN:AAG08518.1;
;Experimental source: strain PAO1
                                                                Cross-references: GB:U32724; GB:L42023; NID:g1573378; PIDN:AAC22068.1; PID:g1573382; Note: best homolog was a hypothetical protein from Escherichia coli Superfamily: hypothetical protein HI0409
                                                                                                                                      Status: nucleic acid somolecule type: DNA Residues: 1-475 <TIGR>
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Best Local :
Query Match
Best Local
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larity 28.2%;
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                                                                                                                                                                                         acid sequence not shown; translation not shown
7.9%;
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; Pred. No. 0.02
28; Mismatches
Score 132;
Pred. No. 0
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  DB 2;
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K.; Lim,
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S71558
                                                                                                                                                                                                                                                                                                                                                                                                                  probable cell wall-plasma membrane linker protein PRP N;Alternate names: hybrid-proline-rich protein C;Species: Brassica napus (rape) C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #te C;Accession: S71558
밁
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                                                                                                                                                                                                               A;Cross-references: EMBL:X94976; NID:g1155067; PIDN:CAA64425.1; C;Superfamily: hydroxyproline-rich glycoprotein C;Superfamily: hydroxyproline-rich glycoprotein F;1-27/Domain: signal sequence #status predicted <SIG>F;28-376/Product: probable cell wall-plasma membrane linker prot
                                                                                                                                                                                                                                                                                                                          R;Goodwin, W.; Pallas, J.A.; Jenkins, G.I.
Plant Mol. Biol. 31, 771-781, 1996
A;Title: Transcripts of a gene encoding a putative cell
A;Reference number: S71558; MUID:96400032; PMID:8806408
A;Accession: S71558
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A; Residues: 1-376 < G
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Best Local Similarity
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                                SSGVMQFRYPVGATNPVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYI 272
                                                                      TPTPPVVTPPTPPTPPVVTPPTPAPPVVTPPTPPVVTPPTPPVVTPPTPPVVTPPTVVT-
                                                                                                    TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVT--EAPFATG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLSKSLVKAGQTVKKGERIALSGNTGISTGPHLHYEFHI--NGRAVNPLTV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIKDAQVKTGDTVRTGQRIASMKNQ--PSGAAL-FEFRISRNGVYVDPLTV
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-PPTPTPPVV
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243
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Pred. No. 0.041;
L; Mismatches
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probable cell wall protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: E75461
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75461
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-665 <WHI >
A;Residues: 1-665 <WHI >
A;Experimental source: strain R1
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 40
E75461
                                                  GB:AE000513; NID:g6458624; PIDN:AAF10484.1;
                                                                                                                                                                                                                                                                                                                                                                             J.D.; Dodson,
T.; Zalewski,
                                                                                                                                                                                                                                                                        radiodurans
                                                  PID:g645862
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Search o	망	δ	Ъ	Ş	дь	Ş	Db	δ	дь	Q	Query M Best Lo Matches	C;Genetics A;Gene: DR(A;Map posit
Search completed: July 8, 2003, 11:08:21 Job time : 44 весв	183 RVEQUERINGLIGDAL 198	290 RIASMKNOPSGAAL 303	140QRLNGLKGNTIAVGQVLRLTAPPTTYRVQPGDTLPKIGVKVGL 182	245 GTVIQADHNMDGASIVIQHTNGFVSSYIHIXDAQVKTGDTVRTGQ 289	110 LKPAPTTYTVRRGDTLTSIGKFVGLRVEQL 139	185 VTEAPFATGSSGVMQFRYFVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNA 244	71TPLVKLSPAPVKLVPAKPVPAPPVAAKPAPVKLVPVKPA 109	130 GVNTAHTESEVAVQSSREEVQQHEAVQKETEPEVVVVKKETETEPVVQQEAFVAFE 184	26 PQTVVVRPGQTLYRIALQNGLSVAELQRLNGLHST-TIEVGQVLRV 70	70 PNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISS 129	Query Match 7.8%; Score 130.5; DB 2; Length 665; Best Local Similarity 25.0%; Pred. No. 0.092; Matches 64; Conservative 25; Mismatches 62; Indels 105; Gaps 11;	C;Genetics: A;Gene: DR0910 A;Map position: 1

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Minimum DB
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No.
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Listing first 45 s
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GUNA_CALSA
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Q46798 escherichia
P44833 haemophilus
Q56131 salmonella
P39700 salmonella
               P36685
P00018337
P011171
P01171171
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P048664
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R R R R R R R R R R R R R R R R R R R	88888		RESULT NLPD P						
(1) SEQUI STRA: MEDL: Tanal "Clo	Pag Psel Bact Psel NCB	01-J 01-J 16-(444	41 42	40 40	35 36 37	34
[1] SEQUENCE FROM N.A. STRAIN=ATCC 15692 / PAO1; STRAIN=ATCC 15692 / PubMed=7959068; MEDLINE=95047554; PubMed=7959068; Tanaka K., Takahashi H.; "Cloning, analysis and expression Pseudomonas aeruginosa PAO1."; Gene 150:81-85(1994).	PA3623. Pseudomonas aeruginosa Bacteria; Proteobacter Pseudomonas. PSEUTAXID=287;	P45682; 01-NOV-1995 01-NOV-1995 16-OCT-2001 Lipoprotein	T 1 PSEAE NLPD PSEAE		106	107 107	107.5	108.5 108.5	108.5
M N.A. 15692 7554; akahas alysis aerugi	aerugi oteoba 87;	(Rel. 32, (Rel. 32, (Rel. 40, nlpD/lppB	STA		6.3		000 444		ი
/ PAO1; PubMed=7959068 shi H.; s and expressiones PAO1.";	nosa. cteria		STANDARD;		532	444 553 3176	671 777 2167	555 3591 1593	283
)1; ;d=7959 ; expres PAO1."	φ	Created) Last seq Last ann homolog	•					444	۲
of an rpoS	ion;	Created) Last sequence update) Last annotation update) homolog precursor.	PRT; 297 AA.	ALIGNMENTS	SPG7 DICDI HMW3_MYCPN	SLAP LACAC ODP2_ALCEU	ALYS_ENTFA FRZE_MYXXA SHK1_RAT	GP1_CHLRE FHAB_BORPE AT12_HUMAN	EXTN_SORBI
homologue gene from	Pseudomonadaceae;				P22698 dictyosteli Q50360 mycoplasma	P35829 lactobacill Q59098 alcaligenes P13111 homo ganien	P37710 enterococcu P18769 myxococcus Ogwv48 rattus norv		P24152 sorghum bic

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15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical lipoprotein ygeR precursor.
TGER OR B2865.
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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MEDILINE=97426617; PubMed=9278503;

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Bacteria, Proteobacteria,
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-i- SUBCELLULAR LOCATION: Attached to the membrane by a li
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SEQUENCE
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                                                                                                                                                        SEQUENCE FROM N.A.

STRAINARd / KW20 / ATCC 51907;

MEDLINE=95350630 / PubMed=7542800;

MEDLINE=95350630 / PubMed=7542800;

Fleischmann R.D., Adams M.D., Mitte O., Clayton R.A., Kirkness B.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Gocoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.,
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pfam; pP01551; Peptidase_M37; 1.
sMaRT; sM00257; LysM; 1.
pROSITE; pS00013; pROKAR_LIPOPRO
Rd.";
Science 269:496-512(1995).
-!- FUNCTION: MAY BE A VIRULENCE DETERMINANT.
-!- SUBCELLULAR LOCATION: Attached to the outer
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Haemophilus influenzae.
Bacteria, Proteobacteria;
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NCBI_TaxID=727;
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251 HYPOTHETICAL LIPOPROTEIN
26 N-ACYL DIGLYCERIDE (POTEN
26564 MW; FCD6235D39790475 CRC64;
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Pred. No. 9.4e
46; Mismatches
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Q56131;
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MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wai Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                            Salmonella typhi
                                                                                                                                                                                                                                                                                                                            Lipoprotein nlpD precursor.
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Pfam; PF01551; Peptidase_M37;
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InterPro; IPR002886; Peptidase_M37.
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                                                                                                                                                                                                                TaxID=601;
                                                                                                                                                                                                                                                                                                         OR STY3050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSSTQVTSSVNNANSTPINSNVVA---PI-ASN-VVWQWPTSGNIIQGFSSTDGGNKGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQPAPVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTA--TVAGSTVT---SNGMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VKQPAVTASTATPVK--PAVTY-TPGANGTQIGSDGTIIGPIKSEAGTSPSVPVA
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+ 42505 MW;
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27.8%;
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; 4134FB6B93EFE57F CRC64;
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Pred. No. 3e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robbe-Saule V., Coynault C., Norel F.; "The live oral typhoid vaccine Ty21a is a rpoS m susceptible to various environmental stresses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the live typhoid vaccine Ty21a.",
FEMS Microbiol. Lett. 170:141-143(1999).
-i- FUNCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIVAL.
-i- SUBCELLULAR LOCATION: Attached to the inner membrane by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krogh A., Larsen T.S., L
Quail M., Rutherford K.,
                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002482; LysM.
InterPro; IPR002886; Pept:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The rpoS mutant allele of Salmonella typhi Ty2 is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Inner
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                                                                                                                                                                                                                                                                                                                                       membrane;
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                                                                                                                                                                                                                                                                                                                                                 SM00257; Lysm;
E; PS00013; PRO
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                                                                                                                                                                                     Similarity
                                                                                                QVITDSQ------GVP----NRYQVKQGDTVSKIAQRYGLNWREIGHI
                                                  NNLNSSYTIYTGQWL--
                                                                         QPVTEQPVQMENGR I VYNRQYGN I PKGSYTGGSTYTVKKGDTLFY I AW I TGNDFRDLAQR
                                                                                                                                                  LAGCASK-----PTYNSTSGSGSHRTSG-----SGGL--
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----QHPAVQKPT--PPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGVMQFR
                       NSISAPYSLNVGQTLQVGNASGTPITGGNAITQADAAQQGVVTRSAQNSTVAVASQPTIT
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39183 MW;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                 LIPOPROTEIN NLPD.
N-ACYL DIGLYCERIDE
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                                               -TLWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPPV-
                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                     AA APPROXIMATE REPEATS
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EMBL; AJ006131; CAA06881.1; -.
EMBL; X82129; CAA57639.1; -.
MEROPS; M37, UPW; -.
InterPro; IPR002482; LysM.
InterPro; IPR002486; Peptidase_M37.
InterPro; IPR002486; Peptidase_M37.
InterPro; IPR000437; prok_lipoprot.
Pfam; PF01476; LysM; 1.
Pfam; PF0151; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Inner membrane; Lipoprotein; Repeat; Sig SIGNAL
Inner membrane; Lipoprotein; Repeat; Sig SIGNAL
CHAIN
25 37 LIPOPROTEIN
LIPID
DOMAIN
26 26 37 N-ACYL DIGL
REPEAT
203 209 1.
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P39700;
01-FEB-1995
16-OCT-2001
15-JUN-2002
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIVAL.
-i- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid
-i- SUBCELLULAR LOCATION: Attached to the inner membrane by a lipid
-i- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
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NLPD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-99138748; PubMed-9973354; Paesold G., Krause M.; Paesold G., Krause M.; "Analysis of rpos mRWA in Salmonella dublin: identification of "Nanlysis of rpos mRWA in Salmonella dublin: identification in transcript with growth-phase dependent variation in transcript stability."; [2]. Bacteriol. 181:1264-1268 (1999).
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NCBI_TaxID=98360;
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
nlpD precursor.
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      Repeat; 31gnal.
BY SIMILARITY.
LIPOPROTEIN NILPD.
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4 X 7 AA APPROXIMATE REPEATS.
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RESULT 6
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Best Local Similarity
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P40827;

01-FEB-1995 (Rel. 31, Created)

15-JUN-2002 (Rel. 41, Last some standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the
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SEROINT / SGSC1412 / ATCC 700720;

STRAIN=LTZ / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MCClelland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P.,

MCClelland M., Sanderson K.E., Spleth J., Du F., Hou S., Layman D.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium.
Bacteria; Proteobacteria;
        SEQUENCE OF STRAIN=C52;
                                                                                                         MEDLINE=94368857; PubMed=8086465;
Prince R.W., Fang F.C., Libby S.J.;
Prince R.W., Fang F.C., Libby S.J.;
"Cloning and sequencing of the gene encoding factor from Salmonella typhimurium 14028s.";
Biochim. Biophys. Acta 1219:198-200(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                      SEQUENCE OF 280-377 FROM N.A.
STRAIN=ATCC 14028S;
                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Complete genome sequence
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InterPro; IPR000437; Prok_lipoprot.
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PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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EMBL; U05011; -; NOT_ANNOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 176:6852-6860(1994).
-!- FUNCTION: MAY BE INVOLVED IN STATIONARY-PHASE SURVIV.
-!- SUBCELLULAR LOCATION: Attached to the inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kowarz L., Coynault C., Robbe-Saule V., Norel F.; "The Salmonella typhimurium katf (rpoS) gene: cloning, sequence, and regulation of spvR and spvABCD virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; M37.UPW;
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                         DPLTVL 321
                                                   GNLIIIKHNDDYLSAYAHNDTMLVREQQEVKAGQKIATMGSTGTSSTRLHFEIRYKGKSV
                                                                           S--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNGVYV
                                                                                                      SAWRWP--TDGKVIENFG
                                                                                                                              MOFRYPVGATNPVVRREGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGA
                                                                                                                                                                                  PPV-----QQHPAVQKPT--PPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFATGSSGV
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                                                                                                                                                                                                                                                                                                                                                LAGCASK-----PTYNSTSGSGSHRTSG-----SGGLA----
                                                                                                                                                          PTITYSEGSGEQSANKMLPNNKPAGTVVTAPVTAPTVSTTEPNASSTSTSAP
                                                                                                                                                                                                                                      IGHINNLNSSYTIYTGQWL-----TLWSGDLKVRERSISSGVNTAHTPSPVAVQSSR
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                                                                                                     -ASEGG----NKGIDIAGSKGQAIVATADGRVVYAGNALRGY
                                                                                                                                                                                                                                                                                                                                                                        Score 209; DB
Pred. No. 1.5e-
56; Mismatches
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N-ACYL DIGLYCERIDE (BY SIMILARITY).
4 X 7 AA APPROXIMATE REPEATS.
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27C29D77A145ABF0
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.5e-07;
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RESULT 7
NLPD_ECOLI
 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.T. Mau B., Shao Y.;
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                                                                                                                                 EcoGene; EG12111; nlpD.
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37
                                                                                                                                                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                          This
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Takayanagi Y., Tanaka K., Takahashi H
"Structure of the S' upstream region
gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ichikawa J.K., Li C., Fu J.C., Clarke S.;
"A gene at 59 minutes on the Escherichia coli chromosome
lipoprotein with unusual amino acid repeat sequences.";
J. Bacteriol. 176:1630-1638(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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NLPD OR B2742.
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                                                                                                                                                                                                      L07869; AAA17875.1; -. U29579; AAA69252.1; -. AE000358; AAC75784.1; -.
                                                                                                                                                                                              D17549;
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                                                                              Lipoprotein;
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                                                                                       PROKAR LIPOPROTEIN;
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                                                                           Repeat; Signal; Complete
                                N-ACYL DIGLYCERIDE.
4 X 8 AA TANDEM REPEATS
                        P-V.
                                                       LIPOPROTEIN NLPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Escherichia coli K-12.";
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STATIONARY-PHASE SURVIVAL.
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                                                                                                                                                                             STRAIN=H825;
STRAIN=H825;
Theisen M., Rioux C.R., Potter A.A.;
Theisen M., Cloning, nucleotide sequence, a
"Molecular cloning, nucleotide sequence, a
lmnB. encoding an antigenic 40-kilodalton
                                                                                                                                                                                                                                                                                                                                01-JUN-1994
01-NOV-1995
01-OCT-1996
This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                     LPPB_HAESO
P36685;
                                                                                                                                                                                                                                                                             Haemophilus somuus.
Proteobacteria;
                                                                                                                                                 CONCEPTUAL
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                               anchor.

SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THREE FRAMESHIFTS HAD
TO BE INTRODUCED IN POSITIONS 264, 266 AND 328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281
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                                                                                                                                                                      Immun. 61:1793-1798(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN 132
                                                                                                                                                                                                                                                                                                                                                                                                                            KAGOKTATMGSTGTSSTRLHFEIRYKGKSVNPLRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                RTGQRIASMKNQPSGAALFEFRISRNGVYVDPLTVL
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(Rel. 32, Last sequence u)
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Pred. No. 4.1e.
42; Mismatches
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A8E6A2B8456105FE CRC64;
                                                                                                                                                                                                                                                                                        subdivision;
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7 AA APPROXIMATE REPEATS
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B precursor
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.le-07;
les 113; Indels
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n lipoprotein of Haemophilus
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                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-IL1403;

MEDICINE-21235186; PubMed=11337471;

MEDICLINE-21235186; PubMed=11337471;

Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,

Weissenbach J., Ehrlich S.D., Sorokin A.;

"The complete genome sequence of the lactic acid bacterium L.

1actis ssp. lactis IL1403.";

Genome Res. 11:731-753 (2001).

Genome Res. 11:731-753 (2001).
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Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L10653; MEROPS; M37.UI
                       SIMILARITY).

CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between acety1-D-glucosamine and N-acetylmuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.

DOMAIN. THE LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-UNN-2002 (Rel. 41, Last annotation
Probable N-acetylmuramidase precursor
hydrolase) (Autolysin) (Lysosyme).
ACMA OR LL0272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACMA LACLA
Q9CIT4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
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1 16 PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
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                                                                                                                           SEQUENCE FROM N.A.,
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Bacteria; Firmicutes; I
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SMART; SM00047; LYZ2; 1.
SMART; SM00257; LysM; 3.
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InterPro; IPR000423; Flag_FlgJ.
InterPro; IPR002482; LysM.
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RA Glaser P., Frangéul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
A. Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A. Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
A. Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A. Madueno E., Maicournam A., Mata Vicente J., Ng E., Nedjari H.,
A. Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A. Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A. Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
A. Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
"Comparative genomics of Listeria species.",
Science 294:849-852(2001).
C. -I FUNCTION: THIS MAJOR EXTRACELULAR PROTEIN MAY BE INVOLVED IN THE
 Matches
               Query Match
Best Local
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VARIANT
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InterPro; IPR000064;
InterPro; IPR003646;
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use by non-profit institutions as long as its content
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entities requires a license agreement (See http://www.isb-
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                                                           SEQUENCE
                                                                                                                                                                                                                    Pfam; PF00877; NLPC P60; 2.
Pfam; PF01476; LysM; 2.
SMART; SM00257; LysM; 2.
SMART; SM00287; SH3b; 1.
                                                                                                                                                                                                                                                                                                                       ListiList; LMO00582; -. MEROPS; C40.UPW; -.
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MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural and functional properties different Listeria species.";
J. Bacteriol. 174:8166-8171(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Mackaness / Serovar 1/2a;
MEDLINE=93094153; PubMed=1459966;
Bubert A., Kuhn M., Goebel W., Koehler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- DOMAIN: LYSM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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                Similarity
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19 X 2 AA TANDEM REPEATS OF T-N.
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LYSM 2.
S -> T (IN STRAIN MACKANESS).
A -> V (IN STRAIN MACKANESS).
V -> I (IN STRAIN MACKANESS).
"""STRAIN MACKANESS).
 46;
               Score 146.5; DB Pred. No. 0.0038;
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of the p60 proteins
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P60 LISIV
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Q1-APR-1993
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16-OCT-2001
                                                                                                                                                                                                DISCUSSION OF SEQUENCE.

MEDLINE=93094153; PubMed=1459966;

Bubert A., Kuhn M., Goebel W., Koehler S.;

Bubert A., Kuhn M., Goebel W., Koehler S.;

"Structural and functional properties of the p60 proteins from different Listeria species.";

J. Bacteriol. 174:8166-8171(1992).

-!- PUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE INVOLVED IN THE INVASION OF MONPROPESSIONAL PHAGOCYTIC CELLS BY LISTERIA.

-!- DOMAIN: LYSM REPBATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN BINDING.
                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=92384582; PubMed=1514809;

Bubert A., Koehler S., Goebel W.;

"The homologous and heterologous regions within the iap genus- and species-specific identification of Listeria; polymerase chain reaction.";
                                                                                                                                                                     -i- SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA P60 FAMILY.
-i- SIMILARITY: CONTAINS 3 LYSM REPEATS.
                          EMBL; M80350; AAA25284.1;
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             C40.UPW;
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IPR002482; LysM
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[2]
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MEDLINE=33094153; PubMed=1459966;
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MEDLINE=92384582; PubMed=1514809;

MEDLINE=92384582; PubMed=1514809;

Bubert A., Koehler S., Goebel W.;

"The homologous and heterologous regions within the iap

genus- and species-specific identification of Listeria s

polymerase chain reaction.";

p gene spp. b

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Appl. Environ. Microbiol.

58:2625-2632(1992)

Listeria seeligeri. Bacteria; Firmicutes; NCBI_TaxID=1640;

Bacillales;

Listeriaceae;

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Pfam; PF00877; NLPC_P60; 1.
Pfam; PF00476; LysM; 3.
SMART; SM00287; LysM; 3.
SMART; SM00287; S43b; 1.
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precursor (Invasion-associated pr
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SMART; SM00287; SH3b; 1.
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InterPro; IPR000064; NIPC P60
InterPro; IPR003646; SH3 bac.
Pfam; PF00877; NIPC P60; 1.
Pfam; PF01476; Lysm; 3.
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- SIMILARITY:
- SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTVTIAINSQNQKPIKRLGL-----IFGVITTCILAGCASKPTYNSTSGSGSHR-TSG
                                                                                                                                  DTVRTGQRIASMKNQPSGAALFEF--RISRNGVYV
                                                                                                                                                          NTNOSSSNSSSASAIIAEAOKHLGKAYSWGGNGPTTFDCSGF-TSYVFAQSGITLPRTSG
                                                                                                                                                                                  -VIQADHNMDGASIVIQHT-----KTG
                                                                                                                                                                                                           LQVGDVLKVKGTVPATNT----NTAT-APTTNTNNN---
                                                                                                                                                                                                                                                         TSTTKAPAQAAKPAPAPAPTVNTNASSYTVKSGDTLGKI ASTFGTTVSKI KALNGLTSDN
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                                                  STANDARD;
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PROTEIN P60.
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Pred. No. 0.0
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-i- FUNCTION: THIS MAJOR EXTRACELLULAR PROTEIN MAY BE
-INVASION OF NONPROFESSIONAL PHAGOCYTIC CELLS BY LI
-i- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN
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"The homologous and heterologous regions within the iag
genus- and species-specific identification of Listeria
polymerase chain reaction.";
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InterPro; IPR000064; NLPC_P60.
InterPro; IPR003646; SH3_bac.
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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-1- SIMILARITY: CONTAINS 2 LYSM REPEATS.
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                                                                                                 T-----PAVDTNAATYKVQN----GDSLGKIASLFKVSVADLTNWNNLNATI
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                                                                                                                                                     TVKQAAPAKVAPKQEVKQTAPAKQEQAKPAAKETVKPAVSKPKAATPAPTAKPAVEQKAS
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X Marbit A., Chetouani F., Buchrieser C., Chakraborty T.,

X Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

X Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

X Domann K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

X Dones L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

X Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

X Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

X Madueno E., Maitournam A., Mata Vicente J., Perez-Diaz J.-C., Purcell R.,

X Madueno E., Movella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

X Machael B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Y Comparative genomics of Listeria species.";

X Verence 294:849-852(2001).
InterPro; IPR002482; Lysm.
InterPro; IPR00064; NLPC_P60.
InterPro; IPR00064; NLPC_P60.
InterPro; IPR00064; NLPC_P60.
Pfam; PF00877; NLPC_P60; 2.
Pfam; PF00476; Lysm; 2.
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SMART; SM00257; Lysm; 2.
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15-JUN-2002 (Rel. 41, I
Protein p60 precursor of IAP OR LINO591.
Listeria innocua.
Bacteria; Firmicutes; E
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Bubert A., Kuhn M., Goebel W., Koehler S.;
Bubert A., Kuhn M., Goebel W., Koehler S.;
"Structural and functional properties of the p60 prodifferent Listeria species.";
J. Bacteriol. 174:8166-8171(1992).
J. BUNCTION: THIS MAJOR EXTRACELULLAR PROTEIN MAY EINVASION OF MONPROPESSIONAL PHAGOCYTIC CELLS BY
-I- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED
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[3]
DISCUSSION OF SEQUENCE.
MEDLINE=93094153; PubMe.
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Bubert A., Koehler S., Goebel W.;
"The homologous and heterologous regions within the iap gene allow
genus- and species-specific identification of Listeria spp. by
polymerase chain reaction.";
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SEQUENCE
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"The homologous and heterologous regions within the iap gene
genus- and species-specific identification of Listeria spp. b
polymerase chain reaction."
[20.7278-2679/1999]
This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are nuse by non-profit institutions as long as its comodified and this statement is not removed. Usage entities requires a license agreement (See http://worsend an email to license@isb-sib.ch).
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MEDLINE=92384582; PubMed=1514809;
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
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49044 MW;
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(Invasion-associated protein)
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; Pred. No. 0.01
51; Mismatches
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SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMedd-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Gocayne J.D.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

""" Sudek D.M., Brandon R.C., Fuhrmann J.L., Geoghagen N.S.M.,
                                                                                                                                                                                                                                                                                                                                                                               P44864;
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01-NOV-1995
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InterPro; IPR000064; NIPC P60
InterPro; IPR003646; SH3_bac.
Pfam; PF00877; NIPC_P60; 1.
Pfam; PF01476; LysM; 3.
                                                                                                                                                                                                                                                                                                                        Hypothetical HI0756.
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SMART; SM00287; SH3b; 1.
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                                                                                                                                                                                                                                                                            Proteobacteria;
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22.9%;
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Pred. No. 0.017
37; Mismatches
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LYSM 2.
LYSM 3.
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RESULT 17
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Matches 63
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01-NOV-1995
01-NOV-1995
15-JUN-2002
    MEDLINE=95350630; pubMed=7542800;
MEDLINE=95350630; pubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness I Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick (Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Smith H.O.,
                                                                                                                         SEQUENCE F
STRAIN=Rd
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Pfam; PF01551; Peptidase_M37; 1.
Hypothetical protein; Complete prot
SEQUENCE 410 AA; 45983 MW; B28D
                                                                                                                                                                                                                                                                                                                      HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                          Haemophilus influenzae
                                                                                                                                                                                                                       Hypothetical HI0409.
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TIGR; HI0756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Venter J.C.
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(Rel.
 McDonald L.A.,
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32, Last sequence update)
41, Last annotation updat
                                                                                                                         ATCC 51907;
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25.0%;
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 Small
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Pred. No. 0.02;
6; Mismatches 111
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                                                                                 A., Kirkness E.F.,
B.A., Merrick J.M.,
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 H.O.,
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MBL outstation -
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RESULT 18
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Q48603; O52362;
Q48603; O52362;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable N-acetylmuramidase precursor (EC 3.2.1.17) (Peptidoglycan Probable N-acetylmuramidase precursor)
Probable N-acetylmuramidase precursor (EC 3.2.1.17) (Peptidoglycan Probable N-acetylmuramidase precursor)
Probable N-acetylmuramidase precursor (EC 3.2.1.17) (Peptidoglycan Probable N-acetylmuramidase precursor)
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"Whole-genome 1
Rd.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS;
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=MG1363;
                                                                                                                                                                                                                                                                                    NCBI_TaxID=1359;
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PF01551; Peptidase M37;
hetical protein; Cell wa
NCE 475 AA; 53255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U32724; AAC22068.1;
S; M37.UPW; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIKDAQVKTGDTVRTGQRIASMKNQ--PSGAAL-FEFRISRNGVYVDPLTV 320
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dase M37; 1.
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MW; 143C10F92233939D CRC64;
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; Pred. No. 0.0:
37; Mismatches
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                                                                                                                                                                                                                                                                                                                  (Streptococcus cremoris).
s; Streptococcaceae; Lactococcus
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RA Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;

Ra Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;

Ra Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;

Ra Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;

Ra Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;

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Ra Govindasamy-Lucey S., Gopal P.K., Sullivan P.A., Pillidge C.J.;

Race of the proteins of the autolysis of six commercial milk.";

Lictococcus lactis cheese starter bacteria grown in milk.";

Lictococcus lactis cheese starter bacteria grown in milk.";

Lictococcus lactis cheese starter bacteria grown in milk.";

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EMBL; AF036720; AAB33629.1; -.
InterPro; IPR002991; Amidase 4.
InterPro; IPR002991; Amidase 4.
Pfam; PF01476; LysM; 3.
Pfam; PF01832; Amidase 4; 1.
SMART; SM00047; LYZZ; I.
SMART; SM000257; LySM; 3.
SMART; SM000257; LySM; 3.
SMART; SM000257; LySM; 3.
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CHAIN
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SEQUENCE FROM N.A.
STRAIN=2250;
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                                                               187
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      WNHLSSDTIYIGQNLIVSQSAAASNP
                                                                                                                                                                         SGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPVVVVKKPTPT--PVVVQQPAPVAPPVT
                                                                                                                                                                                                                                  SSTTYTVKSGDTLWGISQRYGISVAQIQSANNLKST-IIYIGQKLVLTGS----ASSTNS
                                                           EAPFATGSSGVMQ---FRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASN
                                                                                                                                                                                                                                                                                    ---RYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS
                                                                                                                                                                                                                                                                                                                                                   TAALTGRYATDPSYGASLNRIISQYNLTRFDGASSAGNTNSGG---STTTITNNNSGTNS
                                                                                                                                                                                                                                                                                                                                                                                                  TTCILAGCASKPTYNST------SGSGSHRTSGSGGLAIGSQVITDSQGVPN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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LYSM 3.

LYSM 3.

A -> T (IN REF 2).

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I -> N (IN REF 2).

I -> A (IN REF 2).

I -> A (IN REF 2).

T -> A (IN REF 2).

T -> S (IN REF 2).

A -> T (IN REF 2).

39;

Mismatches

STGSGSTATNNSNSTSSNSNASIHKVV

398

243 345 186

128

240 71

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Score 130.5; Pred. No. 0.

.043

DB 1; 119;

Length 437; Indels

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Gaps

CRC64;

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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
STRAIN=M497-1;
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15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91035265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ne from Achromobacter lyticus.";

Bacteriol. 172:6506-6511(1990).

- CATALYTIC ACTIVITY: Cleavage of N-acetylmuramoyl-|-Ala, insulin B chain at 23-Gly-|-Phe-24 > 18-Val-|-Cys(SO(3))

- COFACTOR: BINDS ONE ZINC ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                               GWGSNQNGNWVSASAAGSFKR--HSSCFAEIV--HTGGWSTTYYHLMNIQYNTGANVSMN
                                                          MWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTG
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9 (Rel. 38, Last annotation update)
metalloendopeptidase precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orioka S., Sakiyama F.; cloning and nucleotide sequence
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BY SIMILARITY.
BY SIMILARITY.
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InterPro; IPR001956; CBD 3.
InterPro; IPR001701; GH \( \frac{1}{2}\).
InterPro; IPR001701; GH\( \frac{1}{2}\).
InterPro; IPR000556; Glyco_hydro_48.
Pfam; PF00759; Glyco_hydro_9; 1.
Pfam; PF00942; CBM 3; 3.
Pfam; PF00011; Glyco_hydro_48; 1.
PRINTS; PR00844; GLHYDRLASE48.
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Leuthi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;
Leuthi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;
"Cloning, sequence analysis, and expression in Escherichia coli of a
"cloning, sequence analysis, and expression in Escherichia coli of a
gene coding for a beta-mannanase from the extremely thermophilic
bacterium 'Caldocellum saccharolyticum'.";
happl. Environ. Microbiol. 57:694-700(1991).
-I- FUNCTION: THE N-TERMINAL DOMAIN OF CELLA ENCODES FOR AN
ENDOGLUCANASE ACTIVITY ON CARBOXYMETHYLCELLULOSE. THE C-TERMINAL
DOMAIN PROBABLY ACT SYNERGISTICALLY TO HYDROLYZE CRYSTALLINE
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MEDIJINE=95336703; PubMed=7612247;
Te'O V.S., Saul D.J., Bergquist P.L.;
TeclA, another gene coding for a multidomain cellulase extreme thermophile Caldocellum saccharolyticum.";
Appl. Microbiol. Biotechnol. 43:291-296(1995).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Endoglucanase A precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Cellulase A).
ProDom; PD001947; CBD_3; 2.

ProDom; PD011903; Glyconydro_48; 1.

PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.

PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.

Cellulose degradation; Hydrolase; Glycosidase; SIGNAL 1 23 POTENTAL.

CHAIN 24 1742 ENDOGLUCANASE A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS E (FAMILY 9 OF GLYCOSYL HYDROLASES). SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS L (FAMILY 48 OF GLYCOSYL HYDROLASES).
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STRAIN-ATCC 9790;

MEDLINE=893271.52; PubMed=2753858;

MEDLINE=893271.52; PubMed=2753858;

MEDLINE=893271.52; PubMed=2753858;

Molinger D.L., Daneo-Moore L., Shockman "The second peptidoglycan hydrolase of S covalently binds penticillin.";

Covalently binds penticillin.";

D. Bacteriol. 171:4355-4361(1989).
                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE C
STRAILAFICC 9790;
STRAILAFATCC 9790;
MEDLINE=921.65737; PubMed=1347040;
Chu C.-P., Kariyama R., Daneo-Moor
"Cloning and sequence analysis of
Enterococcuis hizae.";
J. Bacteriol. 174:1619-1625(1992).
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
Muramidase-2 precursor (EC 3.2.1.17) (1,4-b
acetylmuramoylhydrolase) (Peptidoglycan hyd
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(1,4-beta-N-
can hydrolase)
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                                                                 n G.D.;
Streptococcus
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 RESULT 22
LA17_YEAST
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AC Q12446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 9790;
Del Mar Lleo M.,
                                                                                                                                                                                                                                                      SIGNAL
CHAIN
                                                                                                                                                                                                                                                                              InterPro; IPR002901; Amidase_4.
InterPro; IPR002482; LysM.
Pfam; PP01476; LysM; 6.
Pfam; PP01832; Amidase_4; 1.
SMART; SM00047; LYZZ; 1.
SMART; SM000257; LysM; 6.
SMART; SM00257; LysM; 6.
Coll division; Septation; Repeat; Signal.
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HSSP; P22629; 1SWD.
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"Thermosensitive cell growth i
                                                   304
 353
                          88
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                                                                                                        1 Similarity 36; Conser
HGISMNQLIEWNNIKNNF-VYPGQQLVVSKGSSSA--SGSTSNTSTGNTSSNTA
                          YGLNWREIGHINNLNSSYTIYTGOWLTLWSGDLKVRERSISSGVNTAHTPSPVA
                                                   AGCASKPTYNSTSG---SGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSKIAQR
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70670 MW;
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LYSM 2.
LYSM 3.
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LYSM 5.
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LYSM 5.
LYSM 5.
LYSM 6.
LYSM 6.
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Pred. No. 0.21
1; Mismatches
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are stimulated to divide
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STANDARD;

PRT;

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(Rel. 35, Created)
(Rel. 35, Last sequence up
(Rel. 35, Last annotation
protein LAS17.

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EMBL; Z75089; CAA99390.1; -.
SGD; S0005707; LAS17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL
-!- SIMILARITY: TO S.POMBE WSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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InterPro; IPR003124; WH2.
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SM00246;
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                                                                                  GMWFSGRDGDLIN---ASNAGTVIQADHN-MDGASIVIQHTNG
                                                                                                                   AFLTQQPQSGGAPAPPPPPQMP-ATSTSG
                                                                                                                                          P-VVQQP----APVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
                                                                                                                                                                  QPAVPLPQNTQAPSQATNVPVAPPPPPPASLGQSQIPQSAPSAPIPPTLPSTTSAAPPPPP
                                                                                                                                                                                       DLKV-----RERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTP
                                                                                                                                                                                                               PPPRASRPTPNVTMQQNPQQYNNSNRPFGYQTNSNMSSPPPPPVTTFNTLTPQ-MTAATG
                                                                                                                                                                                                                                     -VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSS-----YTIYTGQWLTLWSG
                                                                                                                                                                                                                                                             PMRTTTEGSGVRLPAPPPPPRRGPAPPPPPHRHVTSNTLNSAGGNSLLPQATGRRGPAPP
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                                                                       DAGRDALLASIRGAGGIGALRKVDKSQLDKPSVLLQEARG
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STANDARD; PRT; 1192 AA. ; Q9H212; Q9H3I3; Q9BXG5; Q9Y2Y7;
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WH2; 1.
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329
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4; Mismatches
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POLY-PRO.
                                                                                                                                                                                                                                                                                                                     Score 118;
Pred. No.
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  Q9UQ42; Q9Y293;
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                                                                      584
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Q9Y5U6;
15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 3).

Gu J.R., Wan D.F., Zhao X.T., Zhou X.M.,

Qin W.X., Huang Y., Qiu X.K., Qian L.F.,

Yu J., Han L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
"A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 of endoplasmic reticulum and reduces their anti-apoptotic activity. Oncogene 19:5736-5746 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). MEDLINE=20129242; Pubmed=10667780; Prinjha R., Moore S.E., Vinson M., Blake S., Michalovich D., Simmons D.L., Walsh F.S.; "Inhibitor of neurite outgrowth in humans."; Nature 403:383-384 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
(Neuroendocrine specific protein) (NSP) (Neuroendocrine specific protein C homolog) (RYW-x) (Reticulon 5) (My043 protein).
RTN4 OR NOGO OR ASY OR KIAAO886.
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human
                                                                                                                  "Novel human cDNA clone with growth.";
                                                                                                                                                                                                                        Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y. Luo B., Hu R., Chen J.; Luo B., Hu R., Chen J.; "Human neuroendocrine-specific protein C (NSP) homolog gene. Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                            "Isolation of a cell
Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta, and Ito T., Schwartz S.M. "Cloning of a member Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Developmentally-regulated alternative splicing in a novel Nogo-A.", Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jin W.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Jin W.-L., Ju G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang J., Yu L., Bi A.D., Zhao S.-Y.;
"Assignment of the human reticulan 4 gene
2p14--2p13 by radiation hybrid mapping.";
Cytogenet. Cell Genet. 88:101-102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2
MEDLINE=20237542; PubMed=10773680,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                           MEDLINE=99156230; PubMed=10048485;
                                                             TISSUE=Brain;
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           Yutsudo M.;
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                                                                                                       ubmitted
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                                                                                                       (AUG-1999)
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to the EMBL/GenBank/DDBJ
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                                                                                                                                 inhibiting
                                                                                                                                                             Jiang H.Q., Zhang
He L.P., Li H.N.,
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Yu Y.,
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SEQUENCE FROM I
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**BEDLINE=20499367; PubMed=11042152;

Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen "Cloning and functional analysis of cDNAs with open reading fram 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.";

Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                   block the regeneration of the nervous central system in adults.

Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.

This is likely consecutive to their change in subcellular location, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.

Isognation, from the mitochondria to the endoplasmic reticulum, after binding and sequestration.

Isognative interacts with Bcl-xl and Bcl-2.

Isognative interacts and Bcl-2.

Isognative interacts membrane protein. Endoplasmic reticulum through 2 putative transmembrane of the endoplasmic reticulum through 2 putative transmembrane domains.

Internative produced to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains.

Internative produced to the membrane of the endoplasmic reticulum through 2 putative transmembrane domains.

Internative Africa Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Actions Acti
                                              EMBL;
EMBL;
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                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20129259; PubMed=10667797; GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.; "Identification of the Nogo inhibitor of axon regeneration Reticulon protein."; Nature 403:439-444(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
Sha J.H., Zhou
Submitted (JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4) TISSUE-Brain, Mao Y.M., Xie Y., Zheng Z.H.; Submitted (MAY-1998) to the EMBL/GenBank/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 186-1192 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequences of 100 large proteins in vitro."; Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                 SÎMILARITY: CONTAINS 1 RETICULON DOMAIN CAUTION: Ref.11 sequence differs from the frameshifts in positions 1149 and 1156.
                                                                                                                                                                                                                                                                                                                                                                           specific.
SIMILARITY: CONTAINS 1
CAUTION: Ref.11 sequence
     AJ251383;
AJ251384;
AJ251385;
AB040462;
AB040463;
AF148537;
AF148538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou Z.M.,
(JAN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xie Y., Zheng Z.H.;
(MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pancreas,
CAB99248.1;
CAB99249.1;
CAB99250.1;
BAB18927.1;
BAB18928.1;
BAB18928.1;
AAG12176.1;
AAG12177.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.M.;
the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Placenta,
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeletal muscle;
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J.-W.,
Z.;
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RESULT 24
HES1 MOUSE
ID HES1 MOUSE
AC P35428;
DT 01-JUN-1994
DT 15-DEC-1998
DT Transcription
GN HES1 OR HES-1
OS MLS musculus
OC Eukaryota; Mc
OC Mammalia; Eut
OX NCBI_TaxID=10
RN [1]
RN [1]
RN FROM MEDLINE-94144
RA Takebayashi F
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Best Local S
Matches 36
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                                                                   Mus musculus (Mouse)
Eukaryota; Metazoa; C
Mammalia; Eutheria; I
NCBI TaxID=10090;
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VARSPLIC
CONFLICT
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TRANSMEM
DOMAIN
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                             Transcription HES1 OR HES-1.
                                                                                                                                                          01-JUN-1994 (Rel. 29, Creat
01-JUN-1994 (Rel. 29, Last
15-DEC-1998 (Rel. 37, Last
Transcription factor HES-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro; IPR003388; Reticulon.
fam; PF02453; Reticulon; 6.
                                                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:14085; RTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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PS50845; RETICUL
                                                                                                                                                                                                                                                                                                                                                                     T-EAPFATGSSGVMQ---FRYPVGATNPVVR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                           NTAHTPSPV---AVQSSRPPVQQHPAVQKPTPPVVVVK---KPTPTPPVVQQPAPVAPPV 185
                                                                                                                                                                                                                                                                                                                                          TPAAPKRRGSSGSVDETLFALP-AASEPVIR
                                                                                                                                                                                                                                                                                                                                                                                                              STVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPA---PAPAAPPS
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1040
1134
1155
1005
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107
135
458
564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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993
1004
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1004
107
135
458
564
                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%;
39.6%;
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                                                                                                                                                                                                                   Created)
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                                                                                                                                                              sequence update)
annotation updat
(Hairy and enhan
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ALT_INIT.
ALT_INIT.
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MISSING (IN ISOFORM 2).

S -> C (IN REF 6).

E -> Q (IN REF 6).

P (IN REF 1).

N -> S (IN REF 1).

N -> S (IN REF 1).
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Pred. No. 0.90
3; Mismatches
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POTENTIAL.

POTENTIAL).
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MISSING (IN ISOFORM
ANTENABLISKTS -> MDGQN
3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ative splicing; Transmembrane CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IN REF. 5).
W; CDE239BBF31589CA CRC64;
                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                  update)
enhancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SEQUENCE FROM N.A.
MEDLINE=94148977; PubMed=7906273;
Takebayashi K., Sasai Y., Sakai Y.,

Watanabe

Η.,

Nakanishi

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RESULT 25
NLPD_BUCAI
ID NLPD_BUCAI
AC P57493;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001092; HLH basic.
InterPro; IPR003650; Orange.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T01649; -. MGD; MGI:104853; Hes1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D16464; BAA03931.1; -. PIR; A53336; A53336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure, chromosomal locus, and promoter analysis of the gene encoding the mouse helix-loop-helix factor HES-1. Negative autoregulation through the multiple N box elements.";

J. Biol. Chem. 269:5150-5156 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMĀIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50888; HLH_1; 1. PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR.

TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN UNDIFFERENTIATED NEURAL PRECURSOR CELLS, BUT THE LEVEL OF EXPRESSION DECREASES AS NEURAL DIFFERENTIATION PROCEEDS.

NEURAL DIFFERENTIATION FROCEEDS.

DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A HELLX-INTERCUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG), RATHER THAN THE CANONICLA E-BOX (CAUNTG).

RATHER THAN THE CANONICLA E-BOX (CAUNTG).

DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL REPRESSION DOWAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A REPRESSION DOWAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH PROTEIN FOR THEIR TRANSCRIPTION, MAY ACT AS A NEGATIVE REGULATOR OF MYOGENESIS BY INHIBITING THE FUNCTIONS OF MYOD AND ASH1. SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORWATION OF A COMPLEX WITH A CO-REPRESSOR PROTEIN (GROUCHO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAIRY-RELATED PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTIONAL CO-REPRESSOR RECRUITED
                                                                                                                                                                                                170
                                                                                                   241
                                                                                                                                                                 181
                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                AHSGPVIPVYTSNSGTSVGPNAVSPSSGSSLTSDSM
                                                                                                                                                              PFAPPPPPPLVPIPGGAAPPPGSAPCKLGSQAGEAAKVFGGFQVVPAPDGQFAFLIPNGAF
                                                                                                                                                                                              ----PTPPVVQQPAPVAPPVTEAPFATGS------SGVMQFRYPVGA-
                                                                                                                                                                                                                                                         SISSGVNT-----AHTPSPVA-VQSSRPVQQHPAVQKPTPPVVVVKKPT------
                                                                                                                                --TNPVVRRF---
                                                                                                                                                                                                                             STCEGVNTEVRTRLIGHLANCMTQINAMTYPGQAHPALQAPPPP-----PPSGPAGPQHA
                                                                                                                                                                                                                                                                                                                                                              282
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             n regulation;
35 47
48 92
                                                                                                                                                                                                                                                                                                                                                              AA;
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                              29749
                                                                                                                                                                                                                                                                                                           7.0%;
                                                                                                                               -GTAT-----VAGSTVTSNGMW 230
                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Nuclear protein; Repressor.
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY PRO-RICH.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                       Score 116.5; DE
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                           WRPW MOTIF (REQUIRED FOR ACTIVITY)
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                 PRT;
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                 334 AA
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01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, L
01-OCT-1996 (Rel. 34, L
36.4 kDa proline-rich p
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SEQUENCE
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37;
SMART; SM00257; LysM; 1.
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                                            TPRP-F1
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Nature 407:81-86(2000)
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Bacteria; Proteobacteria;
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16-OCT-2001 (Rel.
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e endocellular bacterial symbiont of
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on update)
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Embryophyta; Tracheophyta; edons; core eudicots;

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Matches 33
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01-FEB-1996
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15-DEC-1998
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EMBL; X57076; CAA40361.1; -:
EMBL; X57076; CAA40361.1; -:
HSSP; P24.337; 1HYP.
HSSP; P24.337; 1HYP.
InterPro; IPR001768; Try/amyl inhbtr.
InterPro; IPR001768; Try/amyl inhbtr.
                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=cv. VFNT Cherry; TISSUE-Fruit;
STRAIN=cv. VFNT Cherry; TISSUE-Fruit;
STRAIN=22119262; PubMed=1731999;
MEDLINE=92119262; PubMed=1731999;
Salts Y., Wachs R., Kenigsbuch D., Gruissem W., Barg R.;
Salts Y., Wachs R., Kenigsbuch D., Gruissem W., Barg R.;
TPRP-F1 reveals an intron within the 3 untranslated transcript.";
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STRAIN=cv. Arava;
STRAIN=cv. Arava;
MEDLINE=91329722; PubMed=1868217;
Salts Y., Wachs R., Gruissem W., Barg R.;
Salts Y., Wachs R., Gruissem W., Barg R.;
"Sequence coding for a novel proline-rich protein preferentially
expressed in young tomato fruit.";
Plant Mol. Biol. 17:149-150(1991).
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NCBI_TaxID=4081;
                                                                                                                                                                                                              Yersinia enterocolitica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                          Lipoprotein NLPD.
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 This SWISS-PROT entry is copyright.
                            -!- SIMILARITY: BELONGS TO THE E.COLI NLPD / HAEMOPHILUS LPPB FAMILY.
                                                                                                                                                                        NCBI_TaxID=630;
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NCE 346 AA; 36375 MW;
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33; Conser
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It is produced through a collaboration
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HUMAN
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Q92794;
15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
15-UTL-1998 (Rel. 41, Last annotation update)
15-UTN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=96376968; PubMed=8782817;

BOTTOW J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G.

BOTTOW J., Stanton V.P. Jr., Disteche C., Dube I., Frischauf A.

HOTSMAN D., Mitelman F., Volinia S., Watmore A.E., Housman D.B.

"The translocation t (8;16) (p11;p13) of acute myeloid leukaemia

a putative acetyltransferase to the CREB-binding protein.";

Nat. Genet. 14:33-41 (1996).

Nat. Genet. 14:33-41 (1996).
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InterPro; IPR002437; Prok_lipoprot.
Pfam; PF01551; Peptidase_M37; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; PARTIAL.
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                      EMBL; U47742; AAC50662.1;
Genew; HGNC:13013; ZNF220.
MIM; 601408; -.
InterPro; IPR001386; Histo
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the ENropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    - FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.
- SUBCELULAR LOCATION: Nuclear:
- DISEASE: PARTICIPATES IN A T(8;16) (P11;P13) CHROMOSOMAL
- TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMAERA OBSERVED IN THE
- M4/M5 SUBTYPE OF ACUTE MYZELOID LEUKRMIA.
- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Motazoa, Chordata, Craniata, Vertebrata,
Mammalia, Butheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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IPR001386; Histone_H1/H5 IPR002717; MOZ_SAS.

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01-JUN-1994 (Rel.
15-DEC-1998 (Rel.
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DOMAIN
       MEDLINE=93109293; PubMed=8417318; Feder J.N., Jan L.Y., Jan Y.-N.; "A rat gene with sequence homology
                                                           STRAIN=Sprague-Dawley; TISSUE=Embryo; MEDLINE=94040724; PubMed=1340473; Sasai Y., Kageyama R., Tagawa Y., Shigemoto "Two mammalian helix-loop-helix factors structure of split.";
                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                              HES1 OR HES-1 OR HL
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Pfam; PF01853; MOZ SAS; 1.
SMART; SM00526; H15; 1.
SMART; SM00249; PHD; 2.
                                                     Genes
                                                                                                         SEQUENCE FROM N.A.
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                                  SEQUENCE FROM N.A.
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induced
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growth
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Last annotation update,
HES-1 (Hairy and enhancer of
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homology to the Drosophila factors known to influence
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MANB_CALSA P22533; 01-AUG-1991

(Rel. 19, Created)

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Best Local S
Matches 42
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50888; HLH 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001092;
InterPro; IPR003650;
Pfam; PF00010; HLH;
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Mol. Cell. Biol. 1
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DOMAIN: THE CARBOXYL-TERRUIAL WRPW MOTIF IS A TRANSCRIPTIONAL REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Cell. Biol. 13:105-113(1993).
FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE PROTEIN FOR THEIR TRANSCRIPTION. MAY ACT AS A NEGATIVE RECOF MYOGENESIS BY INHIBITING THE FUNCTIONS OF MYOD AND ASHIOF MYOGENESIS BY THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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TISSUE SPECIFICITY: PRESENT IN ALL TISSUES I
IN EFITHELIAL CELLS AND IN MESODERM-DERIVED
EMBRYONAL MUSCLE CELLS.
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                                                                                                                                                                                181
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                                                                                           HSGPVIPVYTSNSGTSVGPNAVSPSSGSSLTADSMW
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48
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SER/THR-RICH.

SER/THR-RICH.

SER/THR-RICH.

(BY SIMILARITY).

K -> W (IN REF. 2).

R.-> W (IN REF. 2).
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6; Mismatches
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SUCH AS
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InterPro; IPR001547; GH 5.
Pfam; PP00150; cellulase; 1.
Pfam; PP00942; CBM 3; 2.
ProDom; PD001947; CBD 3; 2.
PROSITE; PS00659; GLYCOSYL HYI
Hydrolase; Glycosidase; Cellul
Multifunctional enzyme.
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SEQUENCE OF 1-346 FROM N.A.

SEQUENCE OF 1-346 FROM N.A.

MEDLINE=91247819; PubMed=2039230;

Luethi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;

Luethi E., Jasmat N.B., Grayling R.A., Love D.R., Bergquist P.L.;

"Cloning, sequence analysis, and expression in Escherichia coli of a
gene coding for a beta-mannanse from the extremely thermophilic

bacterium 'Caldocellum saccharolyticum'.";

bacterium 'Caldocellum saccharolyticum'.";

Appl. Environ. Microbiol. 57:694-700 (1991)

-i-FUNCTION: DEGRADATION OF HEMICELLICOSES, THE SECOND MOST ABUNDANT

-polysaccharides IN NATURE. CONTAINS TWO CATALYTIC DOMAINS WITH

MANNANASE AND ENDOGLICONASE ACTIVITIES.

-i- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic

linkages in mannans, galactomannans, glucomannans, and
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MEDLINE=93119139; PubMed=1476429;

Gibbs M.D., Saul D.J., Luthi E., Bergquist P.L.;

"The beta-mannanase from 'Caldocellum saccharolyticum'
multidomain enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
Caldicellulosiruptor.
NCBI_TaxID=44001;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-mannanase/endoglucanase A precursor [Includes: Mannan endo
beta-mannosidase A (EC 3.2.1.78) (Beta-mannanase) (Endo-1,4-
beta-mannanase); Endo-1,4-beta-glucanase (EC 3.2.1.4) (Cellulase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L01257; AAA71887.1; --
EMBL; M36063; AAA72861.1; --
PIR; B43745; B43745.
PIR; A48954; A48954.
HSSP; Q06851; INBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYDROLASES).

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY J (FAMILY 44 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   galactoglucomannans.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
linkages in cellulose.
MISCELLANEOUS: THIS ENZYME IS MOST ACTIVE AT PH 6 AND 80 DE
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325
361
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518
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162
257
338
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Cellulose degradation;
POTENTIAL.

BETA MANNANASE/ENDOGLUCANASE A.
BETA MANNANASE ACTIVITY).

PRO/SER/THR-RICH (PT BOX).

SUBSTRATE-BINDING (POTENTIAL).

PRO/SER/THR-RICH (PT BOX).

SUBSTRATE-BINDING (POTENTIAL).

PRO/SER/THR-RICH (PT BOX).

PRO/SER/THR-RICH (PT BOX).

CATALYTIC (ENDOGLUCANASE ACTIVITY).

PROTON DONOR (BY SIMILARITY).

NUCLEOPHILE (BY SIMILARITY).

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76; Conserv
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                                                                                                                        AEVKFKKDAPLSLNPDLNDNFVYMD
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llarity 23.4%;
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Pred. No. 2.2;
4; Mismatches 156;
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HES1 OR HRY OR HL.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; C.

Mammalia; Eutheria; Primates; C.

NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN STANDARD; PRT; 280 AA. Q14459; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Transcription factor HES-1 (Hairy and enhancer like) (HHL) (Hairy homolog).
WALBIADE K., KUNAGGAI A., ILAKURA S., YAMAZAKI M., TASHIYO H.,
SUZUKI Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
SUBMILTED HUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE
PROTEIN FOR THEIR TRANSCRIPTION. MAY ACT AS A NEGATIVE REG
OF MYOGENESIS BY INHIBITING THE FUNCTIONS OF MYOD AND ASHI
SIMILARITY)
SIBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A
WITH A CO-REPRESSOR PROTEIN (GROUCHO) (BY SIMILARITY).
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MEDILINE=94292187; PubMed=8020957;

Feder J.N., Li L., Jan L.Y., Jan Y.-N.;

"Genomic cloning and chromosomal localization of HRY, homolog to the Drosophila segmentation gene, hairy.";

Genomics 20:56-61(1994).
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"Functional analysis o
Submitted (MAY-2000) t
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of human HRY in Drosophila.";
to the EMBL/GenBank/DDBJ databases
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Catarrhini; Hominidae
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InterPro; IPR003650; Orange.
Pfam; PP00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00351; ORANGE; 1.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50888; HLH_2; 1.
             SEQUENCE FF
STRAIN=AX2;
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DOMAIN
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 MEDLINE=95348228; PubMed=7622596;
                                                                 Dictyostelium discoideum Eukaryota; Mycetozoa; Dic
                                                                                                     01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
16-OCT-2001 (Rel. 40,
Myosin IC heavy chain.
                                                                                                                                             P42522;
01-NOV-1995
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DNA_BIND
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EMBL; AF264785; AAF73060.1; --
EMBL; AK000415; BBA91149.1; --
TRANSFAC; T04892; --
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                                                    NCBI_TaxID=44689;
                                                                                           MYOC OR DMIC.
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DOMAIN: THE CARBOXYL-TERMINAL MERPW MOTIF IS A TRANSCRIPTIONAL REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                            FROM N.A
                                                                                                                                                                                                                                       PVYTSNSGTSVGPNAVSPSSGPSLTADSMW 275
                                                                                                                                                                                                                                                                 RRF----GTAT-----VAGSTVTSNGMW
                                                                                                                                                                                                                                                                                          PLVPIPGGAAPPPGGAPCKLGSQAGEAAKVFGGFQVVPAPDGQFAFLIPNGAFAHSGPVI
                                                                                                                                                                                                                                                                                                                   PVVQQPAPVAPPVTEAPFATGS------SGVMQFRYPVGA---TNPVV
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Dictyosteliida;
                                                                              (Slime
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                                                                                                                   sequence up
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Pred. No. 0.
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F93'42A88FC749E3C
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                                                                                                                              update)
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                                                                 Dictyostelium
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DOMAIN
SEQUENCE
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"Molecular genetic analysis of myoC, a Dictyostelium myosin I.";
J. Cell Sci. 108:1093-1103(1995).

-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.

-i- SUBUNIT: MYOSIN I HEAVY CHAIN. INSELLE-HEADED. DIMER OF A HEAVY AND A LIGHT CHAIN. INBALLITY TO SELF-ASSEMBLE INTO FILAMENTS.

-i- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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Pfam; PF00063; myosin_head; 2
PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as a use by non-profit institutions as a use by non-profit institutions as a modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed. Usage by and the statement is not removed.
                 SEQUENCE FROM N.A.
MEDLINE=84270667; PubMed:
Baer R., Bankier A.T., B:
Gibson T.J., Hatfull G.,
                                                                                                                          Epstein-barr virus (strain B95-8) (Human herpesvirus Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000066; SH3; 1.
ProDom; PD000355; myosin_head;
SMART; SM00242; MYSC; 1.
                                                                                                         NCBI_TaxID=10377
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Tuffnell P.S.,
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InterPro; IPR001609; myosin_head.
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36; Conser
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SM00326; SH3; 1.
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1181 AA;
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Barrell B.G.;
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Last annotation updat
GP340 (Membrane antig
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Pred. No. 3.6;
17; Mismatches
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NON ALPHA-HELICAL,
ATP (POTENTIAL).
SH3.
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               G.S.,
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               Deininger P.L., Farrell P.
., Satchwell S.C., Seguin O
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antigen)
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"DNA sequence and expression of the B95-8 Epstein-Barr virus genome."; Nature 310:207-211(1984). -!- FUNCTION: RESPONSIBLE FOR EBV BINDING TO THE CR2 RECEPTOR ON HUMAN

B-CELLUS.

B-CELLULAR LOCATION: MOST ABUNDANT COMPONENT OF THE VIRAL

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noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/

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PIR; A03762; QQBE21
PIR; A03763; QQBE22
PIR; S33008; S33008.
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                                                                                                                66;
                                                                                                                             Similarity
                                                                      SKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRY--QVKQGDTVSKIAQRYGLNW
                          REIGHINNLNSSYTIYTGQWLT----LWSGDLKVRERSISSGVNTAHTPSPVAVQSSRPP
--TADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPT
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RESULT 35 GP1_CHLRE

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RESULT 34
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ID EXTN_SORBI
AC P24152;
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Best Local S
Matches 27
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Hydroxylation.
SIGNAL 1
CHAIN 25
SEQUENCE 283
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Plant Mol. Bio
-!- FUNCTION:
-!- PTM: EXTEN
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Eukaryota; Viridiplantae; Streptophyta; Embr
Spermatophyta; Magnoliophyta; Liliopsida; Po
Panicoideae; Andropogoneae; Sorghum.
MCBI TaxID=4558;
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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01-MAR-1992 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Leaf;
MEDLINE=91370882; PubMed=1893107;
MEZER R., Cretin C., Puigdomenech P., Martinez-Izquierdo J.
"The sequence of a hydroxyproline-rich glycoprotein gene
                                                                                                                                                                                                                            EMBL; X56010; CAA39485.1; -.
PIR; S14449; S14449.
InterPro; IPR002965; P rich extensn.
PRINTS; PR01217; PRICHEXTENSN.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extensin
                                                                                                                                                                                                                                                                                                                                                                                                                               IT MOI. Biol. 16:365-367(1991).
FUNCTION: STRUCTURAL COMPONENT IN PRIMARY CELL WALL.
FUNCE EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE
SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
GLYCOSYLATED.
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174
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                                                                                                              l Similarity
27; Conser
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                                                                                 HTPSPVAVQSSRP--PVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP-
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                            PPVTEAPFATGS 194
 PPVTKPPTHTPS
                                                        YTPSPKPPATKPPTYPTPKPPATKPPTPPVYT---PSPKPPVTKPPTPKPTPPVYTPNPK 173
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25
283 AA;
                                                                                                               Conservative
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39, Last annotation update)
(Proline-rich glycoprotein)
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29593 MW;
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EXTENSIN.
; 8D7FCD0DA8ED2D90 CRC64;
                                                                                                                 Score 108.5;
Pred. No. 0.80
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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a; Poales; Poaceae; PACC clade;
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                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                          Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                        EMBL; M58496; AAA69706.1; ALT_SEQ.
GlycoSuiteDB; O9FPQ6; -.
InterPro; IPR002965; Prich extensn.
InterPro; IPR003882; Pistil_extensin.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF309494; AAG45420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding cell wall hydroxyproline-rich glycoproteins.", Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-i- FUNCTION: Major component of the outer cell wall W6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91017504; PubMed=1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glycosylated polyproline II rods-with-kinks plant hydroxyproline-rich glycoproteins."; Biochemistry 40:2978-2987(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Chlorophyta; Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                 BORPE
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                                                                                                                                                                      Similarity
                                                                                                           SPSPPVPPSPSPPPSPAPPSPTP----PSPSPPVPPSPAPPSPAPPSP
                                                                                                                                TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP--VAPPVTEAP 189
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(Rel.
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                                               STANDARD;
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Last sequence update)
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                                                                                                                                                        Score 108.5; | Pred. No. 1.8; 4; Mismatches
                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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VEGETATIVE CELL WALL PROTEIN GP1.

49 X 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
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                                                                 -AT12 HUMAN
P58397;
15-JUN-2002
15-JUN-2002
15-JUN-2002
ADAMTS-12 Pr
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M60351; AAA22974.1; --
EMBL; M60351; AAA22975.1; ALT_INIT.
EMBL; M60351; AAA22976.1; ALT_INIT.
                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow "Genetic characterization of Bordetella pertussis filamentous haemagglutinin: a protein processed from an unusually large
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           ADAMTS12.
Homo sapiens
                                                     metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence and crucial role in adherence."
Proc. Natl. Acad. Sci. U.S.A. 86:2637-26.
-!- FUNCTION: EVIDENCE FOR A ROLE IN HOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemagglutinin: a precursor.";
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MEDLINE=90355839; P
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3591 AA; 36
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02 (Rel. 41, Last sequence update)
02 (Rel. 41, Last annotation update)
02 (Rel. 41, Last annotation disintegrin
oteinase with thrombospondin motifs 12)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domenighini M., Tuomanen E., Rappuoli R., Falkow hemagglutinin of Bordetella pertussis: nucleotide
             (Human)
                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                              PVVVVKKPTPTPPVVQQPAPVAPPVTE 187
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Pred. No. 15;
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HML; AJ250725; CAC20419.1; -.
Genew; HGNC::4605; ADAWIS12.

MIM; 606184; -.
InterPro; IPR001762; Disintegrin.
InterPro; IPR001890; Reprolysin.
InterPro; IPR001590; Reprolysin.
InterPro; IPR001300; Zn_MTpeptdse.
InterPro; IPR001300; Zn_MTpeptdse.
Pfam; PF00090; tsp_1; 6.
Pfam; PF000421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; PGP0142B_propep; 1.
SMART; SM00209; TSP1; 8.
PROSITE; PS00142; DISINTEGRIN 1; FALSE_NEG.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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MEDLINE-21264577; PubMed-11279086;

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Cal S., Argueelles J.M., Fernandez P.L., Lopez-Otin C.;

"Identification, characterization, and intracellular processing of ADAM-7912, a novel human disintegrin with a complex structural organization involving multiple thrombospondin-1 repeats.";

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NCBI_TaxID=9606;
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DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTAN DOMAIN: THE SPACER DOMAIN: AND THE TSP TYPE 1 DOMAINS ARE IMPORTAN FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY SIMILARITY).

PIM: IS SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND TO A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AN THE C-TERMINAL REGIONS TO PARAMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1 DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.

SIMILARITY: CONTAINS 8 TSP TYPE-1 DOMAINS.
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                                  CYS-RICH.

SPACER 1.

TSP TYPE-1 2.

TSP TYPE-1 3.

TSP TYPE-1 4.

SPACER 2.

TSP TYPE-1 5.

TSP TYPE-1 7.

TSP TYPE-1 7.

TSP TYPE-1 7.

TSP TYPE-1 7.

TSP TYPE-1 8.
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DISINTEGRIN-LIKE.
TSP TYPE-1 1.
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       SWITCH (POTENTIAL).
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                X MEDITINE 91358349; PubMed=1679432;
A Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
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J. Bacteriol. 173:5619-5623 (1991)
G. J. Bacteriol. 173:5619-5623 (1991)
G. HUDROITSES THE CELL WALL OF E.FAECALIS AND
M.LYSODEIKTICUS. MAY PLAY AN IMPORTANT ROLE IN CELL WALL GRO
AND CELL SEPARATION:
G. J. SUNCELLULAR LOCATION: Secreted (Probable)
G. J. DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGL
G. J. SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
G. J. SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
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or (BC 3.2.1.-) (Peptidoglycan hydrolase)
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  McCleary W.R.,
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Myxococcales;
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1 53 POTENTIAL.
4 671 AUTOLYSIN.
    Zusman D.R.;
                                                                                                                                                                                                                                                                                       STANDARD;
                     PubMed=2165608;
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Last annotation updat
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                                                                                                                                                                                  protein
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WSAT
WSAT
WSAT
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Pred. No. 2.6
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                                                                                                    subdivision; Myxobacteria;
Myxococcaceae; Myxococcus.
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                                                                                                                                                                                                                                                                                           777
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                                                                                                                                                                                  2.7.3.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GSSN---
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Best Local
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Purification and characterization of the Myxococcus xanthus FrzE protein shows that it has autophosphorylation activity.";

J. Bacteriol. 172:6661-6668(1920)

-i- FUNCTION: FRZE IS INVOLVED IN A SENSORY TRANSDUCTION PATHWAY THAT CONTROLS. THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING
                                                                                                                                                                                                                                                                      MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M35192; AAA25396.1; -. PIR; A35966; A35966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01627; Hpt; 1.
Pfam; PF02518; HATPase_c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00072; response_reg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002570;
InterPro; IPR001789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCleary W.R., Zusman D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium.", Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION OF HIS-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "FrzE of Myxococcus xanthus is homologous to both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTROLS THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING DIRECTION. FRZE SEEMS TO BE CAPABLE OF AUTOPHOSPHORYLATING ON AN HISTIDINE RESIDUE AND THEN TO TRANSFER THAT GROUP TO ASPARTATE RESIDUE IN THE C-TERMINAL PART OF THE PROTEIN. SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN. SIMILARITY: SIMILAR TO BOTH CHEA AND CHEY. SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                            198
                                                                                   140
                                                                                                                                                                      110
 269
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                                                                                                                                          80
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                                                                                                                                                                                                                                                                                                                                                                                                               ; PD000039; Response_reg;
; PD003142; Hpt; 1.
SM00260; CheW; 1.
                                                                                                                                                                                                                                                                                                                                                                         SM00073; HPT; 1.
SM00448; REC; 1.
                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                SM00387; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                 transduction; Transferase; Kinase; Ph
270 509 HISTIDINE KINASE
660 776 RESPONSE REGULATO
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR00344; BCTRLSENSOR.
 SSYTHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISRNG
                                                                                                             VQKPTPPVVVVKKPTPTPPVVQQP-----APVAPPVTEAPFA-TGSSGVMQFRYPVGATN
                                                                                                                                          GKTATEVATDVLLRACDVLSDLNEDLSGANTGNPASEEMVRMLAEVSGQTPPAIAGARPV
                                                                                                                                                                    GQWLTLWSGDLKVRERSISSGVNT----AHTPSPVA-----VQSSRPP--VQQHPA
                                                      PVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADHNMDGASIVIQHTNGFV
                                                                                   APPPAPPPAPVAAPVVTPAAVAAPPAPVQAPVAPPPTQAPVAEPGAHAAAAAPHPAAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR004359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR004358;
                                                                                                                                                                                                                                                      130
777
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                                                                                                                                                                                                                                                         AA,
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                                                                                                                                                                                                                                                                      49
197
                                                                                                                                                                                                                                                         83189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATPbind_ATPase.
Bact_sens_pr_C.
                                                                                                                                                                                                              6.4%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Response_reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIS_KIN_sig.
                          -----HGRDEEAPSAAKSAV---ADRSI-RVNVEVLDALGLL
                                                                                                                                                                                                 30;
                                                                                                                                                                                                 Score 107.5;
Pred. No. 3.1;
30; Mismatches
                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (
ALA/PRO-RICH (POSSIBLE HI
, 9912BD40991C69E5 CRC64;
                                                                                                                                                                                                                                                                                                   RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                             Phosphorylation
                                                                                                                                                                                                 76;
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                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
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                                                                                                                                                                                                                             777;
                                                                                                                                                                                                                                                                        REGION).
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                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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RESULTA O
SHKL RAT

IN SHKL RAT

OGNUES, COMULS, OSWERS, OSOZEB;

PT 15-JUN-2002 [Rel. 41, Created]

PT 15-JUN-2002 [Rel. 41, Created]

PT 15-JUN-2002 [Rel. 41, Created]

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

PT 15-JUN-2002 [Rel. 41, Last amounts to update)

REL SHAMAN Experience [Rel. 41, Last amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to update amounts to upd
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                EMBL; AF102855; AAD04569.2; -
EMBL; AF131951; AAD29417.1; -
EMBL; AF159046; AADA2975.1; -
EMBL; AF159046; AADA2975.1; -
EMBL; AF141904; AAF02498.1; A
HSSP; P00519; IABL.
InterPro; IPR0012110; ANK.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM.
InterPro; IPR001452; SAM.
Pfam; PF000536; PDZ; 1.
Pfam; PF00536; SAM; 1.
Pfam; PF00018; SAM; 1.
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RA Sheng M., Kim E.;

RA Sheng M., Kim E.;

RT "The Shank family of scaffold proteins.";

RT J. Cell Sci. 113:1851-1856(2000).

CC 11- FUNCTION: Seems to be a an adapter protein in the postsynaptic CC density (PSD) of excitatory synapses that interconnects receptors CC of the postsynaptic membrane including NUMDA-type and metabotropic CC of the postsynaptic membrane including NUMDA-type and metabotropic CC of the postsynaptic membrane including NUMDA-type and metabotropic CC of the postsynaptic membrane including NUMDA-type and metabotropic CC of the postsynaptic function. Overexpression promotes CC maturation of dendritic spines and the enlargement of spine heads CC via its shilty to recruit Homer to postsynaptic sites, and considered to enhances presynaptic function.

CC enhances presynaptic function.

CC enhances presynaptic function.

CC enhances presynaptic function.

CC ente PDZ domain (By similarity).

CC enteronal cells. Colocalizes with aspart of a complex with CC proposition of the postsynaptic density of the PDZ domain (By similarity).

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

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CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-latrotoxin receptor 1.

CC enteronal cells. Colocalizes with alpha-l
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Sala C., Piech V., Wilson N
"Regulation of dendritic sp
Shank and Homer.";
Neuron 31:115-130(2001).
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Bockers T.M., Mreutz M.R.
Bockers T.M., Gundelfinger E.D.
Buck F., Richter D., Gundelfinger E.D.
"Synaptic scaffolding proteins in rat
"Synaptic scaffolding protein family inter
multidomain Shank protein family inter
protein alpha-fodrin.";
J. Biol. Chem. 276:40104-40112 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                            COEFEBELLUM.
SIMILARITY: BELONGS TO THE SHANK FAMILY.
SIMILARITY: CONTAINS 7 ANK REPEATS.
SIMILARITY: CONTAINS 1 PDZ/PHR DOWAIN.
SIMILARITY: CONTAINS 1 SAM DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n N.R.,
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PROSITE; PS50002; SH3; 1.
PROSITE; PS50105; SAM_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                               DTVSKIAORYGLNWREIGHINNLN------SSYTI-YTGQWLTLWSGDLKVRE 124
                                        FE 305
                                                                              ----STDSHHGGASYIPERTSSLQRQRLS-EDSQ-----
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SQEGROESRSDKAKRLFRHYTYGSYDSFDAPSLIDGIDSG
-> MALSAVGGGPGGALPQPPPALSSSWPALGPRRRSVWY
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Q93ag4 azotobacter
Q8y038 ralatonia s
Q9ra36 deinococcus
Q8zbd1 yersinia pe
Q9kul7 vibrio chol
Q8ygs9 brucella me
                                                                                                                                                                                                            Q9jp90 rhodocyclus
Q9pf23 xylella fas
Q9ckKl pasteurella
Q8x2t2 escherichia
Q9hup0 pseudomonas
Q8z3y0 salmonella
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136.5	138.5	139.5	141	141	145	147.5	152	152.5	153	153.5	155	158	158	158.5	165.5	167	169	171	171.5	172.5	174	174.5	188.5	196	196.5	198	202.5	203
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285	715	512	164	162	247	176	760	203	228	176	437	375	321	436	401	371	223	449	312	392	512	512	562	609	515	415	379	415
16	16	N	N	N	N	N	16	N		Ŋ		16	16	16	N	16	16	16	16	N	16	N	16	16	16	16	16	16
Q9PEP1	P74517	Q03491	Q9APL3	Q9R3D9	Q9S4T2	Q9F7X9	Q8YRU0	Q9X6S4	Q9X8M5	052606	Q927Y9	Q9RW21	Q8RG41	Q8Y4E2	Q9KJW8	083190	Q8X3L6	Q8R6U3	Q9X7W8	Q8RNB5	Q926D2	008251	Q8UEQ5	Q9A6T7	Q98LD1	Q9JYP9	Q8X7Z3	Q9JTP1 .
Q9pep1 xylella fas	7	Q03491 listeria gr				escherichia	\sim	<	íΠ	н	Q927y9 listeria in	Q9rw21 deinococcus	Q8rg41 fusobacteri	Q8y4e2 listeria mo			Q8x316 escherichia		Q9x7w8 streptomyce	Q8rnb5 bartonella	Q926d2 rhizobium m	н	Q8ueq5 agrobacteri	Q9a6t7 caulobacter	Q98ld1 rhizobium l	Q9jyp9 neisseria m	Q8x7z3 escherichia	Q9jtpl neisseria m

ALIGNMENTS

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RESULT 1
Q9JP90
 Q9JP90 PRELIMINARY;
Q9JP90;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                  gelatinosus.";

Graph G. (eds.);
                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=IL144;
MEDLINE=94132007; PubMed=8300574;
                                                                                                                                                                                                                       Nagashima K.V., Shimada K., Matsuura K.; "Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple bacteria.";
                                          Igarashi N., Shi
"Photosynthetic
                                                                   STRAIN-IL144;
                                                                             SEQUENCE FROM N.A.
                                                                                                               "Primary structure and transcription of genes encoding B870 photosynthetic reaction center appproteins from Rubrivivax gelatinosus.";
                                                                                                                                                                                                                                                                      STRAIN=IL144
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Rhodocyclus gelatinosus (F
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                       NIPD protein.
mechanisms and effects (Proceedings of the 11th international congress
        Photosynthesis:
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=28068;
                                                                                                                                                                                                            hotosyn.
                                                                                                      Biol.
                                                                                                      Chem.
                                                                                                                                                                                                            Res. 36:185-191(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                        Shimada
                                                                                                     269:2477-2484(1994).
                                          gene
                                          K., Matsuura K., Nagashima K.V.; cluster in purple bacterium, Rub
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15,
                                                                                                                                                                                                                                                                                                                             (Rhodopseudomonas gelatinosa).
1; beta subdivision; Comamonadaceae;
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                                             Rubrivivax
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Matches 84
STRAIN-9-5-C;
STRAIN-9-5-C;
STRAIN-9-5-C;
STRAIN-9-5-C;
STRAIN-9-5-C;
STRAIN-9-5-C;
SIMPSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Simpson A.J.G., Reinach F.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.N
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.
Colauto N.B., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PF23;
Q9PF23;
01-OCT-2000
01-OCT-2000
01-MAR-2002
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EMBL; AB034704; BAA94071.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=IL144;
MEDLINE=20031519;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylella fastidiosa.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas
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Dordrecht (1999).
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PF01551; Peptidase M37; 1.
; SM00257; LysM; 1.
:NCE 314 AA; 32355 MW; 8
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Peptidase_M37.
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.9e-12;
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RA HO P.L., Hoheisel J.D., Junqueira M.H.S., Gomes S.L., Gruber A.,
RA Lemos B.G.M., Lemos M.V.F., Laigret F., Lambais M.R., Leite L.C.C.,
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RA Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mond I.A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Metalon M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Ge Oliveira M.C., de Oliveira R.C., Palmieri D.A., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Santelli R.V., Sawasaki H.E.,
RA Ge Souza N.E., Jr., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
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RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.,
RA da Silva A.C.R., Meidanis J., Setubal J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RI MELL AGO132; AAP83665.1;
DR HSSP; P23931; 1E0G.
DR InterPro, IPR002482; LysM.
DR Pfam; PF01551; Peptidase M37; 1.

RXMART; SM00257; LysM; 1.

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Hypothetical protein PM161.
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EMBL; AE006198; AAK03698.1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 2.
Pfam; PF01551; Peptidase_M37; 1.
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01-MAR-2002
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy, Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8.11-22(2001)
                                                                                                 EMBL; AP002563; BAB37161.1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002488; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
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STRAIN=0157:H7 / RIMD 0509952;
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"Complete genomic sequence of Pasteurella multocida Pm70."; 
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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A9E8CDE70DD284A6 CRC64;
     8A1E89E01F9B72E8 CRC64;
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Tanaka M., Tobe T.,
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MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";
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01-MAR-2001
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InterPro; IPRO02886; Peptidase_M2
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                Hypothetical protein; Complete SEQUENCE 231 AA; 25174 MW:
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HSSP; P23931; 1E0G.
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VRGEYRVKRGDTLYSIATRHGWNYKDLARANGIRPPYAVKVGQ-VVRFDGRKSTYVASSR
                                           VPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSIS
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(TrEMBLrel. 21, 1
protein PA4924.
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26.7%;
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                                                                                                 37;
                                                                                                 Score 234; DB
Pred. No. 1.9e
37; Mismatches
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Pred. No. 1.1e-09;
6; Mismatches 103;
                                                                                                                                                                                                      proteome.
3FC8EAA8B2A42B91 CRC64;
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                                                                                                 DB 16;
1.9e-09;
nes 90;
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Q8Z3Y0;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                              EMBL; AL627277; CAD02868.1; InterPro; IPR002482; Peptidase_M37. InterPro; IPR002886; Peptidase_M37. Pfam; PF01476; LysM; 1. Pfam; PF01551; Peptidase_M37; 1. SMART; SM00257; LysM; 1.
                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413.848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhi.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                             GDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGVNT
                                                                                                                                      FÄVNNMRGYGNLVIIQHGTSYTSTYAHNSRLLVKEGQMVGKGQKIAEAGSSDADRVQLYF
                                      AHT-PSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFAT 192
                                                                                     GDTLYRISRATGTSVKELARLNGISPPYTIEVGQRIKV-RGSAKSSSSTRKTSNKTATKT
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(TrEMBLrel.
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250 AA; 26426 MW; 9A57CF6117BE76C4 CRC64;
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Last sequence update)
Last annotation update)
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Best Local S
Matches 76
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EMBL; AE008839; AAL21913.1; -.

InterPro; IPR002482; LysM.

InterPro; IPR002886; Peptidase_M37

Pfam; PF01476; LysM; 1.

Pfam; PF01551; Peptidase_M37; 1.

SMART; SM00257; LysM; 1.

Hypothetical protein; Complete pro
SEQUENCE 252 AA; 26652 MW; 6AD
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Q8ZM83;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; PubMed=11677609;

MEDLINE-21534948; PubMed=11677609;

MEDLINE-21534948; PubMed=11677609;

MICCOLITING M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porvollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium

"Complete genome sequence of Salmonella enterica serovar Typhimurium
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Putative metalloendopeptidase.
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76; Conser
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                                                              NGVYVDPLTVL 321
                                                                                                                                                                                                                                                                                                                              GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQADH 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLK----VRERSISSGVNT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQ 77
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RATAIDPLRYL 243
                                                                                                                                                                                            NMDGAS---IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRISR 310
                                                                                                                                                                                                                                                                   AEGG
                                                                                                                                                                                                                                                                                                                                                                                                         AHT-PSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDTLYRISRATGTSVKELARLNGISPPYTIEVGÓRIKV-RGSAKSSTSTRKTSNKTATKT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGIAVLLCTGLLLAGC-----SSNSGSGTY--SGS-------VYTVKR
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                                                                                                                             QLRGYGNLIMIKHNEDYITAYAHNDTMLVNNGQSVKAGQKIATMGSTDAASVRLHFQIRY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.9%; (larity 24.4%; Conservative 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.8e-09;
9; Mismatches 99;
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Pred. No. 2.1
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6ADB04D76BAEE61E CRC64;
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Best Local S
Matches 81
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Q9KI20;
01-OCT-2000
01-OCT-2000
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Q9L528;
01-OCT-2000
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"Sequence of Pseudomonas putida nlpD gene (complete sequence)
similar to E. coli pcm gene (partial sequence).";
submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF260132; AAF70311.1; -...
SEQUENCE FROM N.A.

MEDITINE=21140372; PubMed=11447163;

MEDITINE=21340372; PubMed=11447163;

Seshadri R., Samuel J.E.;

Characterization of a Stress-Induced Alternate Sigma Factor, RpoS, (
"Characterization of a Stress-Induced Alternate Sigma Factor, RpoS, (
"Characterization of a Stress-Induced Alternate Sigma Factor, RpoS, (
"Characterization of a Stress-Induced Alternate Sigma Factor, RpoS, (
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                                                                                                                                                                                                                                                           Lipoprotein precursor NlpD. coxiella burnetii.
Bacteria; Proteobacteria; g Coxiella group; Coxiella.
NCBI_TaxID=777;
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InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
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Bacteria; Proteobacteria;
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|:|:|:::||:||:||:||
YGELIIIKHSDTYVSAYGHNRRLLVREGQQVKAGQSI 229
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Pred. No. 5.8e-09;
"" matches 95;
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                                                                                                                                                                                                                                                                                                                                subdivision;
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EMBL; Y19122; CAB46190.1;
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InterPro; IPR002886; Pepti
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Kojic M., Degrassi G., Venturi V.,
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PF01551; Peptidase_M37; 1.
; SM00257; LysM; 1.
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  YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN
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                                          LVLALAMGTLLAGCSST---SSTS-----
                                                                                   LIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNR------
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                                                                                                                                                                                                                   244 AA; 25191 MW; 6F9B5BA39CD739AE CRC64;
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"The stationary phase sigma factor (rpoS) of Azotobacter vinelandii.";
Submitted (SEP-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AP421551; AAL16090.1; -.
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SEQUENCE 217 AA; 22675 MW; ASAAEB0F64886945 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                          202
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                                                                                                                                                                                                                                                                                                                                                                                                                                147 PPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVA-----PPVTEAPFATGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 RYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAHTPSPVAVQSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
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                                                                                                                                                                                                                                                             DHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRI 308
                                                                                                                                                                                                                                                                                                                                                   SGVMQFRYPVG----ATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYGWEWRELAAHNGIAAPYVIHPGQKIQL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RROGKPVDPLOYL 214
                                                                                                                                                                                                                                                                                                                 QPAVSARSPSGWAWPAEGPLVGRFSS---NGS--LNKGIDIGGQLGQPVLAASDGSVVYA
                                                                                                                                                                                                                                                                                                                                                                                          GPVRQ-AAASTAARPSVPAATPAPTVPATSQAAVAATPVKPDSGKVQPPPATKAPSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGG-----WTWP--ANGVLIGKF-----ASNGSLNKGIDIAGDLGQPVFAASGGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRD--GDL---INASNAGT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-AHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAPFA 191
                                                                                                                                                                                              SRNGVYVDPLTVL
                                                                                                                                                                                                                                    GGGLRGYGELIIIKHSDVYVSAYGHNRRLLVREGQQVKAGQVIAEMGSTGTDRVKLHFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVYDGSGLRGYAELITIKHSDTYVSAYGHNRRLLVREGQQVKAGQSIA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVVSSPS----SSSKTTVIRRPVGSAGSAPASTTKPATTAPTI---PAPVVATVPAAERA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel. 20, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.2%; Score 221; DE 28.9%; Pred. No. 1.5e tive 30; Mismatches
                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19,
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Created)
Last seq
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Last
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                                                          PRT;
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  sequence update)
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                                                             268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
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RESULT 13
Q9RS36
ID Q9RS3
AC Q9RS3
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MB
DT C011
GN DR229
OS Deino
OC Bacte
OC Deinc
OX NCBI-
RN [1]
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Best Local S
Matches 78
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X MEDLINE=21681879; pubMed=11823852;

X Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cantolico L.,

A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

A Siguier P., Thebault P., Woisan A., Robert C., Saurin W., Schiex T.,

A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

IN Mature 415;497-502(2002).

R Mature 415;497-502(2002).

R Interpro; IPR002482; LysM.

IN Interpro; IPR002482; LysM.

Interpro; IPR002486; Peptidase M37.

Interpro; IPR002886; Peptidase M37.

Interpro; IPR002886; Peptidase M37.

Interpro; IPR002886; Peptidase M37;

Pfam; PF01551; Peptidase M37; 1.

R Pfam; PF01551; Peptidase M37; 1.

R PFAN; PF01551; Peptidase M37; 1.

R PFAN; PF01551; Peptidase M37; 1.

R PROSITE; S000782; TFIIB; UNKNOWN_1.

Complete proteome.
OPRS36

PRELIMINARY; PRT; 454 AA.

C 09R836;
C 09R836;
T 01-MAY-2000 (TIEMBLrel. 13, Created)
T 01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
T 01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
C 011-Mali glycyl-glycine endopeptidase, putative.
B Cell wall glycyl-glycine endopeptidase, putative.
DR2291.
DR2291.
DR2291.
DR2291.
DR2291.
S Deinococcus radiodurans.
S Deinococcus radiodurans.
C Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcaeae; Deinococcus.
C Deinococcaeae; Deinococcus.
X NCBI TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Last annotation probable lipoprotein NLPD/LPPB homolog. RSC1206 OR RS02686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIKRLGLIFGVITTCILAGCASK----PTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                     RRNGKPVDPMRFL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGPLRGYGNLVIIKHNDTFLTAYGNNDKVLVTEQSTVKKGQKIAEMGSTDADRVKLHFEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAGATDGAIALAWP--AHGOVIGRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLINASNAGTVIQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAVATP-----VRPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAPPVTEAP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGYYRVKRGDTLYSIALRNGQAPRDLVTWNNIPNPNQIEVDQLIRV-----VPPNADAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARAGRLAVAMVSAALLAACASSGNQAPVLDRTSRAGS------APAAPLEPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRNGVYVDPLTVL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADHNMD-GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSGAALFEFRI 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 220;
Pred. No. 2
                                                                                         Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---DDKANKGIDIGGKRGDAVTAADDGKVIH 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NTTTOPIDAAPAATPPVVSSGA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
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Best Local Similarity
Matches 73; Conserv
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CO-92 / BIOVAR ORIENTALIS;

MEDLINE=21470413; PubMed=11586360;

RATCHINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8ZBQ1
Q8ZBQ1;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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STRAIN-RI;

MEDLINE=20036896; PubMed=10567266;

MIDLINE=20036896; PubMed=10567266;

White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,

Vamathevan K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.

Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein.
NLPD OR YPO3356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00257; LysM; 3. Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 286:1571-1577(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR2291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGDTVRTGQRIASM--KNQPSGAALFEFRISRNGVYVDPL 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNGMWFSGRDGDLINASNAGTVIQADHNMD-----GASIVIQHTNGFVSSYIHIKDAQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQPAPVAPPVTEAPFAT------GSSGVMQFRYPVGATNPVVRRFGTATVAGSTVT
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454 AA; 48550 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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26.1%;
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Pred. No. 5.2e
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                                                          [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEROTYPE 01;
STRAIN=EL TOR N16961 / SEROTYPE 01;
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam I Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson I Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., McDonald C., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
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SEQUENCE
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Pfam; PF01551; Peptidase M37; 1.
PRINTS; PR01561; EDGERECEPTOR.
                                                           EMBL; AE004139;
TIGR; VC0533; -.
                                                                                                  "DNA sequence cholerae.";
                                                                                                                                                                                                                                                                 Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                   01-DEC-2001
                                                                                                                                                                                                                                                                                                                               01-OCT-2000
                                                                                                                                                                                                                                                                                                                                          Q9KUI7;
01-OCT-2000
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SMART; SM00257; Lysm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002482; InterPro; IPR002886;
                                   InterPro; IPR002482;
InterPro; IPR002886;
                                                                                   Nature 406:477-483(2000)
                                                                                                                                                                                                                                                      NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                       Lipoprotein
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EMBL; AJ414156; CAC92586.1; -.
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                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                         of both chromosomes of
                                                                      AAF93701.1; -.
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                                                                                                                                                                                                                                                                  gamma
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Last
                                                                                                                                                                                                                                                                                                                                           Created)
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Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                   subdivision;
                                                                                                                                                                                                                                                                                                                   sequence up
                                                                                                         the
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                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                   Vibrionaceae;
                                                                                                                               ragoi I., Seller;
man W.C., White (
s J.J., Venter J
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Pfam; Pfam;

PF01476; LysM; 1. PF01551; Peptidase_M37;

Peptidase_M37.

SM00257; LysM;

SS

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366

264

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RESULT 16
08YGS9
ID Q8YGS
AC Q8YGS
DT 01-MA
DT 01-MA
DT 01-MB
DT 01-MI
DE Lipoi
GN BMEI
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RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;

RX MEDLINE=20020109; PubMed=11756688;

RX DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

RA DelVecchio V.G., Kapatral V., Redkar R.J., Lykidis A., Reznik G.,

RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Jablonski L., Kyrpides N., O'Callaghan D., Letesson J.-J.,

RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA Selkova R., Kyrpides N., O'verbeek R.;

"The genome sequence of the facultative intracellular pathogen

RT William melitensis.";

RA Brucella melitensis.";

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RKL Froc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

RKL Froc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

RKL Froc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

RKL Froc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

RKL Froc. 1PR002482; LysM.

DR InterPro; IPR002886; Peptidase_M37.

DR Ffam; PF01575; Peptidase M37; 1.

RK SMART; SM00257; LysM; 1.
                                                                                                                           Query Match
Best Local S
Matches 79
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01-MAR-2002
01-JUN-2002
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SEQUENCE
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Brucellaceae; Brucella.
NCBI_TaxID=29459;
       162
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                                                         30 LĄGCASKPTYNSTSGSGSHRTSGSGGLĄIGSQVITDSQGVPNRYQVKQGDTVSKIĄQRYG
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                                                                                                                                                           Similarity
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   IAGVPQAPAVNGKKSSPTNMASAGGAIA----TPPSVGGAYVVKSGDSLFSIAKKHN
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311 AA;
                                                                                                                                                                                                                                                  proteome.
427 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                      43604 MW; 48912D48846E6BD7
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                                                                                                                           12.3%; Score 205; DB 16; 26.2%; Pred. No. 5.4e-07; tive 45; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Mismatches 138; Indels
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Matches 71
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EMBL; AL162756; CAB84920.1; -.

InterPro; IPR002482; LysM.

InterPro; IPR002886; Peptidase_M37

Pfam; PF01476; LysM, 2.

Pfam; PF01551; Peptidase_M37; 1.

SMART; SM00257; LysM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
Nature Advance of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JTP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative membrane peptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 415 AA;
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   240 NASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNT---AHTPSPV-AVQSS 145
                                                                                                                                                                                                                                                  TAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVAP------
                                                                                                                                                                                                                                                                                                                   HTIVRGDTVYNISKRYHISQDDFRAWNGMTDN-TLSIGQ-----IVKVKPAGYAA---
                                                                                                                                                                                                                                                                                                                                                                  YQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPVDQLKAANGLTSG-AIRVGQSLVI-----PSAAAGAPTQVAAITPQPANPAKAA
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                                                                 PAPQSPAASPSGTRSVGGIVWQRP--TQGKVVADFGG-----NNKGVDIAGNAGQPV
                                                                                                                   PVTEAPFA----TGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLI
                                                                                                                                                                                        ----PKAAAVK-SRPAVP--AAVOTPV-----KPAAQPPVQSAPQPAAPAAENKAVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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Pred. No. 7
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7.2e-07;
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Matches 72
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EMBL; AP002562; BAB37019.1; --
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 1.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
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Q8X7Z3;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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NLPD OR Z4050 OR ECS3596.
NLPD OR Z6050 OR ECS3596.
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genome sequence of enterohemorrhagic Escherichia coli
Ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 379 AA;
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STRAIN=0157:H7 / F
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        281
                                                                                                                                                                                                                                                                                         133 TAHTPSPVAVQSSRPPVQQHPAVQKP--TPPVVVVKKPT---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 26.:
72; Conservative
                                                        GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                              TATTVTAPVTVPTASTTEPTVSSTSTSTPISTWRWP--TEGKVIETFG-ASEGG----NK
                                                                                                                                                                                                                                   ASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSANKMLPNNKP
                                                                                                                                                                                                                                                                                                                                               TYKKGDTLFYIAWITGNDFRDLAQRNNIQAPYALNVGQ-
  GIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIIKHNDDYLSAYAHNDTMLVREQQEV
                                                                                                                                                                       TPPVVQQPAPVAPPVTEAPFATG---SSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
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26.1%; Pred. No. 7e-07
tive 42; Mismatches
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01-JUN-2002
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Science 287:1809-1815(2000).
SMRI: AE002497; AAF41839.1; -.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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InterPro; IPR002886;
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PF01551; Peptidase_M37; 1.
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Pred. No. 1.7e-06;
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Matches 69; Conservative
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DNA Res. 7:331-338(2000).;
EMBL; AP002996; BAB48532.1;
InterPro; IPR002482; LysM.
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 2.
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Q9A6T7;
01-JUN-2001
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01-MAR-2002
SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub
Eisen J., Heidelberg J.F., Alley M.
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STRAIN=MAFF303099;

MEDLINE=21082930; PubMed=11214968;

MEDLINE=21082930; PubMed=11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamo Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Simura T.

Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
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Bacteria, Proteobacteria, alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
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Q8UEQ5;
01-JUN-2002
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                                           Nester E.W.;
"The genome C58.";
                                                                                                SEQUENCE FROM N.A.

MEDLINE=21608550; PubMed=11743193;

MODINE=21608550; PubMed=11743193;

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Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulisen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatharage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Jil M.-J., McClelland E., Palmieri A.,

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SEQUENCE
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DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
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BMBL; AE005873; AAK23971.1; -.
TIGR; CC1996; -.
    Science [2]
                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein.
ATU1700 OR AGR C_3124.
AGRODacterium tumefaciens
Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
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InterPro; IPR002886; Peptidase
Pfam; PP01476; LysM, 4.
Pfam; PP01551; Peptidase M37;
SMART; SM00257; LysM; 4.
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(TrEMBLrel.)
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                                                              natural genetic
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Peptidase_M37.
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Last sequence update)
Last annotation update)
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Pred. No. 3.8e-06;
4; Mismatches 110;
                                                              engineer
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                                                            Agrobacterium
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Rhizobiaceae
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                                                                 tumefaciens
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Best Local S
Matches 81
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01-JUL-1997
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                   008251;
           Mol. Plant Microbe Interact. 10:933-937(1997).
EMBL; U81296; AABB8077.1;
InterPro; IPR002482; LysM.
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01476; LysM; 2.
Pfam; PF01551; Peptidase_M37; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294:2323-2328 (2001).
EMBL; AB009126; AAL42700.1; ALT_INIT.
EMBL; AB008991; AAK87473.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Wollam C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
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                                                                                                           "A biotin-regulated | Rhizobium meliloti."
                                                                                                                                      Streit W.R., Phillips D.A.;
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               Lipoprotein.
                                                                                                                                                   MEDLINE=97449848; PubMed=9304864;
                                                                                                                                                                                                         NCBI_TaxID=382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11743194;
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                                                                                                                       locus, bioS,
 52431 MW;
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25.1%;
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Pred. No. 1.2e
64; Mismatches
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Last sequence up
0A870A76EBCE7D8B CRC64;
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                                                                                                                       possible
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                                                                                                                          survival
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C., Mullin L.,
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RESULT 24
Q926D2
ID 60926I
AC Q926I
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q926D2; PRELIMINARY;
Q926D2; U1-DEC-2001 (TrEMBLrel 19,
01-DEC-2001 (TrEMBLrel 19,
01-MAR-2002 (TrEMBLrel 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPPB OR R01536 OR SMC02060.
                                                                                                                                                        Ptam;
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                           InterPro; IPR002482;
InterPro; IPR002886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
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                                                                                                                                                    PF01476; Lysm; 2.
PF01551; Peptidase_M37; 1.
                                                   l Similarity 79; Conserv
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proteome.
512 AA; 52003 MW; 6BBADDD3290125D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVVQQPAPVA-PPVTEAPFATG-----SSGVMQFRYPV-GATNPVVRRFGTATVAGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGSQVITDSQGVPNRYQVKQGDTVSK 83
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                  10.4%;
                                                                                                                                                                            Peptidase_M37.
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                                                     60;
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Last sequence update)
Last annotation updat
                                                                   Score 174;
Pred. No. 0
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Pred. No. 0.00011;
8; Mismatches 128
                                                     Mismatches
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subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                  Length
                                                     Indels
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                                                   Gaps
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                                                     12;
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Fiskus W., Padmalayam I., Baumstark B.;

"Molecular cloning, sequencing, and characterization of the homolog in Bartonella henselae.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF48425; AAL897611;

EMBL, AF48425; AA, 42635 MW; CF71E6B91FDA206C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barronella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKPTYNSTSGSGSHRTSGSGGLAIG----SQVITDSQGVPNRYQVKQGDTVSKIAQRYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INASNAGTVIQADHNMD--GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVAPPVTEAPFATGSSGVMQFRYPV-GATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINSAGEGGGNGAYTVKPGDSINRIAKANGVSVAALKQANGI-STEAIRIGQKINIPSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMTGRATRPOVHFEVRKNATPVNPATYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPSGAAL---FEFRISRNGVYVDPLTVLK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKAAENGVVIYSGSSLKELGNAVLVRHDDGTVTVYGNAAELKVQRGQKVQRGQTLAS--S
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GVSGDVKTPRVYFEVRENSLPVDPIKYLE
                                                                                                                                                                                                                                                                                                                                   KYSSTEKAPITPKPSA-QINRSNGEQNSSAQMSSLNYEKGVLDTVMNKDNGVTPQ-----
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                                                QPSG---AALFEFRISRNGVYVDPLTVLK 322
                                                                                                           VKAAENGIVIYASDGLKELGNVVMIRHENNIITIYGCNSKLVVTRGQRIRRGDEIA--KS
                                                                                                                                                                                                                                                                                                                                                                                       SISSGVNTAHTPSPVAVQSSRPPVQQHPAVQ-----KPTPPVVVVKKPTPTPPVVQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WREIGHINNLNSSYTIYTGQWLTLWSGDL---------KVRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSPPQDGTSSPNS-RIMGTPPRNLGTLSRSQMRNDPLFRQNSYIVQTGDTLLSIARQRGV
                                                                                                                                                                INASNAGTVIQADHNMD--GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN
                                                                                                                                                                                                                                                                        APVAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                               SVEALKLVNGIRSN-SIYIGQVLMIPSGRTAETSNVRNNDWGASKQSLSQSQSASSIRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.3%; Score 172.5; DB 2; Length 24.0%; Pred. No. 0.00011; tive 49; Mismatches 130; Indels
                                                                                                                                                                                                                       ---ATGISKMRWPV--RGRLLSQFGQKR---GTTMSRGIDIAVPEGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequences
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391
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Best Local S
Matches 79
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative secreted peptidase.
SC06773 or SC6A5-22.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomyces.
Actinomycetales; Streptomycineae; Streptomycetales; Streptomyces.
NCBI TaxID=1902;
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STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Reeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:111-147(2002).
EMBL; A1049495; CAB39706.1; -.
InterPro; IPR002482; Lysm.
InterPro; IPR002482; Lysm.
InterPro; IPR002486; Peptidase_M37.
Pfam; PP01476; Lysm; 1.
Pfam; PP01551; Peptidase_M37; 1.
PRINTS; PR01574; TUBBYPROTEIN.
SMART; SM00257; Lysm; 31633 MW; 2D489B9B7C448206 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97000351; PubMed=88434336; Redembach M., Kieser H.M., Denapaite D., Eichner A., Rinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; Bentailed genetic and "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
Oliver K., Harris D.;
Submitted (MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley S.D., Parkhill J., I
Submitted (MAR-1999) to the
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Bentley S.D.,
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                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                               GSHR-----TSGSGGLAIGSQVITDS------
EAVGSDPSLIHPGLKLSIDGQAAKPSAPSSAQSQKPA-----QKSAEKPAEKTAAKPA
                                                    RSISSGVNTAHTPSPVAV--OSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVA
                                                                                                           EKNSDSRTYTVKSGDYLSKIADEQDVD---
                                                                                                                                                                                                                          GKHRTRAMRLTRTIAVAGTGGAALALPLMGAAAANAAPAHSVSEQAVQSVPASAKKAAA
                                                                                                                                                                -----NRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRE
                                                                                                                                                                                                                                                                                                                                   10.3%; Score 171.5; DB 16; Larity 23.3%; Pred. No. 9.5e-05; Conservative 43; Mismatches 118;
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e EMBL/GenBank/DDBJ databases
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RESULT QRENUES ID ROBE OF COMMENTS OF COMM

NCBI_TaxID=38323; SEQUENCE FROM N.A.

Q8RNB5; Q8RNB5; Q1-JUN-2002 01-JUN-2002 01-JUN-2002 01-JUN-2002 N1pD.

Query Match Best Local S Matches 79

Similarity

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Best Local S
Matches 74
            Q8X3L6;
Q8X3L6;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Membrane proteins related to metalloendopeptidases.
MLPD6 OR TTE2691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome Genome Res. 12:689-700(2002).
EMBL; AE013208; AAM25810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium
Thermoanaerobacteriales; Thermoanaerobactes
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 449 AA; 50731 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21992816; PubMed=11997336;
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STRAIN=MB4T / JCM11007;
  Putative
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                                                                                                                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
lipoprotein
                                                                                                                                  GATGHATGPHVHFEVRKNGVPIDPMRFL
                                                                                                                                                            QPSGAAL---FEFRISRNGVYVDPLTVL
                                                                                                                                                                                                          LINASNAGTVIQADHNMD-GASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN
                                                                                                                                                                                                                                                                  PPVTEAPFATGSSGVM-----QFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGD
                                                                                                                                                                                                                                                                                                                        S----SGVNTAHT-PSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAPVA
                                                                                                                                                                                                                                                                                                                                                   YEVKENDSLWSIAREHDMYIQDILKLNPGLTENLKPGQIIYLSKEVPLVT---VVTEKEV
                                                                                                                                                                                                                                                                                                                                                                             YOVKQGDTVSKIAQRYGLNWREIGHIN-----NLNSSYTIYTGQWLTLWSGDLKVRERSI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQRI--ASMKNQPSGAAL-FEFRISRN-GVYVDPLTVLK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKSTDAEKASSSDTGSQ---STGTTSGY-----TSPVAGGTVGTPYHQSGSMWSSGYHTG
                                                                                                                                                                                      PIYASDGGTVIFAGWESGYGYLVKIDHHNGYVTYYGHASKLLVKVGDKVEKGQKIALV--
                                                                                                                                                                                                                                          EPISKI-VAVGSRRVSYVATGYFSYPARGT--ITSRFGPRWGGFHT----GVDIAARYGS
                                                                                                                                                                                                                                                                                              TYKEEIPFNTKFTKDDKLFVNQSKVLVEGEKGL-KEIKAVVISHNGVEVKRDIKEERVLK
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            (TrEMBLrel.
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ilarity 27.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                         42;
            Created)
Last sequence update)
Last annotation updat
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Pred. No. 0.00017;
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Y., Ling
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EMBL; AB005516; AAG57994.1; -.

InterPro; IPR002482; LysM.

InterPro; IPR002886; Peptidase_M37

Pfam; PF01476; LysM; 1.

Pfam; PF01551; Peptidase_M37; 1.

SMART; SM00257; LysM; 1.

Lipoprotein; Complete protecome.

SEQUENCE 223 AA; 23472 MM; 774
                                                                                                                                                                                                                                                                                                                                                                                            083190;
01-NOV-1998
01-NOV-1998
01-JUN-2002
MEDLINE-98332770; PubMed=9665876;
MEDLINE-98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Dodson E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T
Khalak H., Richardson P., Bowman C., Cotton M.D., Fujii C., Garland
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland
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                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=NICHOLS;
                                                                                                                                                                                                                                                                                            Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 083190
                                                                                                                                                                                                                                                                     NCBI_TaxID=160;
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Escherichia
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Escherichia coli O157:H7.
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l Similarity 24.0%;
63; Conservative 3
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3 (TrEMBLrel. 08, 1
2 (TrEMBLrel. 21, 1
1 protein TP0155.
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Pred. No. 9.3e-05;
5; Mismatches 79;
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., Potamousis K.,
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Padmalayam I., Kelly T., Baumstark B., Massung R.;

Padmalayam I., Kelly T., Baumstark B., Massung R.;

Padmalayam I., Kelly T., Baumstark B., Massung R.;

Indecular cloning, sequencing, expression, and characterization of an immunogenic 43-kilodalton lipoprotein of Bartonella bacilliformis that has homology to NlpD/LppB.";

Infect Immun. 68:4972-4979(2000).

EMBL; AP157831; AAF80360.1;

InterPro; IPR002482; LysM.

InterPro; IPR002483; Peptidase_M37.

Pfam; PF01476; LysM, 1.

Pfam; PF01476; LysM, 1.

SMART; SM00257; LysM; 1.

SMART; SM00257; LysM; 1.

SMART; SM00257; LysM; 43418 MW; C5ABFB0E8575FBDE CRC64;
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Pfam; PF01476; LysM; 2.

Pfam; PF01551; Peptidase_M37; 1.

SMART; SM00257; LysM; 2.

Hypothetical protein; Complete proteome.

SEQUENCE 371 AA; 40664 MW; 8BB00CSE5E3A82A8 CRC64;
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TIGR; TP0155; -.
Interpro; IPR002482; LysM.
Interpro; IPR002886; Peptidase
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Bartonella bacilliformis.
Bartonella bacilliformis alpha subdivision; Rhizobiaceae group;
Bartonellaceae; Bartonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.;
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   31 AGCASKPTYN-STSGSGS----HRTSGSG------GLAIGSQVITDSQGVPNRYQV
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                                                                                      9.9%; Score 165.5; DB 2; 25.0%; Pred. No. 0.00036;
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         255 AKQEAAIKAAEEKRMQEAAAASSAKSAAVVK--
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                                                                                                                                                                                                                                       l Similarity
66; Conser
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RP SEQUENCE FROM N.A.

RP STRAIN-EGD-E / SEROVAR 1/2A;

RX MEDILINE-21537279; PubMed=11679669;

RX MEDILINE-21537279; PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

RA Glaser P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,

RA Baquero F., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Domann K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

RA Domann K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nadjari H.,

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

RT "Comparative genomics of Listeria species.";

RI Science 294:849-852 (2001).

RI Science 294:849-852 (2001).

RI Science 294:849-852 (2001).

RI InterPro; IPRO02806; Peptidase M37.

InterPro; IPRO02806; Peptidase M37.

RI InterPro; IPRO02017; Spectrin.—

DR InterPro; IPRO02017; Spectrin.—

PR Pfam; PP01551; Peptidase M37; 1.

RY Scoutence 436 AA; 47049 MW; 2D36B87C1098E167 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lmo2504.
LMO2504.
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Bacteria; Firmicutes; Bacillus/Clostridium
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                                               TPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPVVQQPAPVAPPVTEAPFATGSS
                                                                                                            EKNDLVMALANKKDLT-----KŚEQŤLLASE-----QGALTDEEKRLASNIAGEK 254
                                                                                                                                                                          KQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDLKVRERSISSGVNTAH
                                                                                                                                                                                                                                    ; Score 158.5; DB 16; ; Pred. No. 0.0013; 33; Mismatches 100;
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QPSSSSNEATE ---- TVSS
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Best Local 9
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J. Bacteriol 184:2005-2018(2002).
EMBL; AE010559, AAL94673.1; -. Complete proteome.
321 AA; 35455 MW; OF4158B077775777
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Q8RG41;
01-JUN-2002
01-JUN-2002
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Cell wall endopeptidase family M23/M37.
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Bacteria; Fusobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21886394; PubMed=11889109;
Kapatral V., Anderson I., Ivanova N.,
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                                                                                                                                                                                                                                                                                    -VRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP
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                                                               HVNKGDLIGKTGNSGRTTGAHL-HFEIRHNGVPKNPMKYLQ
                                                                                       TVRTGQRIASMKN--QPSGAALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                                      SGRDGDLI-----NASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGD
                                                                                                                                                                                         --PPDTGGGDDGGAPASYSGEG---FAFPVRYAGITSPFGNRY--HPVLKRYILHTGV--
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9; Mismatches
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Pred. No. 0.00093;
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                                             01-DEC-2001
01-DEC-2001
01-MAR-2002
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01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                   Q927Y9
Q927Y9;
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  Hypothetical LIN2647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00257; LysM; 1.
Lipoprotein; Complete proteome.
SEQUENCE 375 AA; 39107 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus Deinococcaceae; Deinococcus. NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20036896; PubMed=10567266;
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InterPro; IPR002886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M.;
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PF01551; Peptidase_M37; 1.
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                                                                                                                                                                                                                                                                                                             MDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASM
                                                                                                                                                                                                                                                                                                                                                               QPFASÁLASGKATSSSFGQPRTYVAGGKVAYHYGTDYPARSGTAVLÁINDGTVVIÁGRYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEGAATPATPAPAAPTPATPAPAAPAPAPAPAVPTKLPTVATAANVLKLPGVTITAPKALKM 121
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                      (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation updat)
protein lin2647.
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21.7%;
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21,
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Last sequence update)
Last annotation updat
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6; Mismatches
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group;
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                                             update)
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RESULT 35
052606
ID 05260
AC 05260
DT 01-JU
DT 01-JU
DT 01-JU
DT NOVell
GN NILPD.
OS Ralst
OC Bacce
OC Ralst
OC NCBI
RN N[1]
RN SEQUE
RC STRAIR
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RX Claser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Claser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Buchaud E., Durant L., Dussurget O.,

RA Antian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hauf J., Jackson D.,

JOHES L.-M., Kaerst U., Kreft J., Kunn M., Kunst F., Kurapkat G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

"Comparative genomics of Listeria species.";

RC Science 294 489-852 (2001).

RI Science 294 499-852 (2001).

RMBL; AL596173; CAC97874.1; -.

DR InterPro; IPR002866; Peptidase M37.

InterPro; IPR002867; -.

RMBL; AL596173; Cacgraft M37; 1.

RMBL; AL596173; Peptidase M37; 1.

RMBL; Poptibetical protein, Complete proteome.

RW Hypothetical protein, Complete proteome.
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Best Loc
Matches
                                                                                                                                                                                                           052606;
052606;
01-JUN-1998
01-JUN-1998
01-JUN-2002
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STRAIN-CLIP 11262 / SEROVAR 6A;
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Bacteria; Firmicutes; B
Listeriaceae; Listeria.
SEQUENCE FROM N.A.
STRAIN=AW1;
MEDLINE=98294041; PubMed=9632252;
Flavier A.B., Schell M.A., Denny T.D.;
"An RpoS (sigmaS) homologue regulates
                                                                                                     NCBI_TaxID=305;
                                                                                                                                        Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; beta subdivision; Ralst
                                                                                                                                                            Ralstonia
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                                                                                                                                                                                                                                                                                                                                                                                                           M--KNOPSGAALFEFRISRNGVYVDP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                              ASGRVVFSGFGATGSGFGGYGYVVKIDHGNGFQTLYAHMRAGSLKVVTGQQVSQGQPIGI 408
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%; Score 155; DB 16; Length 43; 23.3%; Pred. No. 0.0023; tive 35; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                           . 06, Created)
. 06, Last sequence update)
. 21, Last annotation update)
(Fragment).
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                          433
                                                                                                                                                                                                                                                                                   176
  acylhomoserine
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                                                                                                                                        Ralstonia group;
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lactone-dependent
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Best Local
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PUCATIVE peptidase.
SCC3368 OR SCE94.19C.
SCC3368 OR SCE94.19C.
Streptomyces coelicolor.
Bacteria, Firmicutes, Actinobacteria, Actinobacteridae;
Bacteria, Firmicutes, Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoinduction in Ralstonia solanacearum. Mol. Microbiol. 28:475-486(1998).
EMBL; AF042351; AAC38576.1; -
InterPro; IPR002886; Peptidase_M37.
Pffam; PF01551; Peptidase_M37; 1.
                                                                                                 Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Collins M., Eromin A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9X8M5;
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97000351; PubMed=8843436;
Redembach M., Kieser H.M., Denapate D., Eichner A.,
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and
the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oliver K., Harris D.;
Submitted (APR-1999)
                            "Complete genome sequence coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=A3(2) / M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bentley S.D., Parkhill J., Submitted (APR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                     Hopwood
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      417:141-147(2002)
                                                                                 D.A.;
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                                                                                                                                                                                                                                                                                                                                 M145;
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EMBL/GenBank/DDBJ databases.
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6; Mismatches
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Pred. No. 0.0
                                                           the model
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                                                           Streptomyces
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RESULT 38
Q8YRU0
ID Q8YRU
AC Q8YRU
DT 01-MA
DT 01-MA
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 Q8YRU0;
01-MAR-2002
01-MAR-2002
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01-NOV-1999
01-DEC-2001
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SEQUENCE
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Q9X6S4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "RNA polymerase sigma factor RpoS of Vibrio parahaemolyticus.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF144608; AAD3392.1; -.
InterPro; IPR002886; Peptidase M37.
Pfam; PF01551; Peptidase M37; I.
NON TER 1 1 1
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InterPro; IPRO02886; Peptidase M37.
Pfam; PF01551; Peptidase M37, T.
SEQUENCE 228 AA; 22817 MW; 2263
                                                          Q8YRU0
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|:
LR 222
                                                                                                                                                                                        RTGORIASMKNOPSGAALFEFRISRNGVYVDP
                                                                                                                                                                                                                           GIDIAGQRGQPIVSTAAGTVVYSGNALRGYGNLIIVKHNDNYLSAYAHNDKLLVTEGQSV
                                                                                                                                                                                                                                                                                                                                         ------VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSN
                                                                                                                                                                                                                                                                                                                                                                                                       NGFVSSYIHIKDAQVKTGDTVRTGQRIASMKN--QPSGAAL-FEFRISRN-GVYVDPLTV
                                                                                                                                                    KSGQKIATMGSSGAKSVKLHFEIRYQGKSVNP
                                                                                                                                                                                                                                                                  GMWFSGRDGDLINASNAGTVIQADHNMDGAS--IVIQHTNGFVSSYIHIKDAQVKTGDTV
                                                                                                                                                                                                                                                                                                     KEYVGSKDNQHTKPKPPTT----TVQNDKVSKWLWP--TKGRVIKNPS----AGEQ-GNK
                                                                                                                                                                                                                                                                                                                                                                              PVVVPVVTTTP-----PPVVKPTTTTKPVTSSKNSSQKPTTTPTKVAQKEPPKKVEQTKA
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   (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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(TrEMBLrel. 12, Last seq
(TrEMBLrel. 19, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Mismatches
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 Created)
Last sequence update)
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Pred. No. 0.0014;
6; Mismatches 42;
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Best Local S
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                                                    Q9F7X9;
01-MAR-2001
01-MAR-2001
01-JUN-2001
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MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing

"Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01476; LysM; 1.

Pfam; PF01551; Peptidase M37; 1.

SMART; SM00257; LysM; 1.

Hypothetical protein; Complete p:
SEQUENCE 760 AA; 80569 MW; FF
 Escherichia coli
                   Lipoprotein NLPD.
                                                                                                                                 Q9F7X9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
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95; Conserv
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                                                                                                                                                                                                                                                            AQVKTGDTVRTGQRIASMKNQPSGAALF-----EFRISRNGV-YVDPLTVL 321
                                                                                                                                                                                                                                                                                                   GWRWGRMHRGIDIAAPVGTPVFÄAADGVVEKSGWNRGGYGNLVDIRHPDGSLTRYAHNSR
                                                                                                                                                                                                                                                                                                                                                                              RLNASESLGRMRGTTVSPKLPPLAAVDQYLPQAIDESVPPPSDSTTAFIWPAKGVLTSGY
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(TrEMBLrel.
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16,
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; Pred. No. 0.0079;
41; Mismatches 11
                                                      Last sequence update)
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FB62A0DDFC6A573B
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A., Kawashima K., Kimura T.,
Matsuno A., Muraki A.,
                                                                                                                                 176
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219

276 645 465

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525

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157 351

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Q9S4TZ
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Query Match
Best Local S
Matches 78
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Q9S4T2;
Q9S4T2;
01-MAY-2000
01-MAY-2000
01-JUN-2001
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                                                                                           STRAIN=EHILADELPHIA-1;

MEDLINE=99369860; PubMed=10438758;

Hales L.M., Shuman H.A.;

"The Legionella pneumophila rpoS gene is required for growth within Acanthamoeba castellani;";

J. Bacteriol. 181:4879-4889(1999).

EMBL; AR117715; AAD51395.1; -.

InterPro; IPR002482; LysM.
InterPro; IPR002482; LysM.
Pfam; PF01476; LysM; 1.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Lipoprotein.
Lipoprotein.
SEQUENCE 247 AA; 27535 MW; 6C36631BD5BC9675 CRC64;
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"An Escherichia coli reference collection group B2- and uropathogen-
associated polymorphism in the rpoS-mutS region of the E. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Legionella pneumophila.
Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
Legionellaceae; Legionella.
NCBI_TaxID=446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 TSTPIST-----WRWP--TEGKVIETFG-ASEGG----NKGIDIAGSKGQAIIATADG
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1 Similarity 78; Conser
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8.7%; Score 145; DB 2; Length 247; llarity 24.3%; Pred. No. 0.0058; Conservative 43; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Last annotation update)
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Search completed: July 8, 2003, 11:07:35 . Job time: 85 secs

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225 WGVHFEIRRAGVPVNPLNYLQ 245

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Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of BASB110 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of othitis media in children and pneumonia in adults. The sequence is a translation of the BASB110 gene coding region (see AAF30046). It differs by 1 residue from the predicted polypeptide sequence (see AAB20107) of a BASB110 PCR product, having Ser rather than Gly at position 104. The invention provides BASB110 polypeptides, and polynucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB110 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB110 polypeptide, or a polypeptide, or a immunogenic fragment of a BASB110 polypeptide, or a polypeptide and sequence identity to BASB10 or comprising a polypuchide composition used a polypeptide. A claimed method of diagnosing a conding such a polypeptide. A claimed method of diagnosing a contribody. A claimed therapeutic composition useful in treating the manns with M. catarrhalis infection composition useful in treating catarrhalis in a polypeptide. BASB110 polypeptides also have utility in raising specific antibodies, and in screening for antibacterial drugs.
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Best Local S
Matches 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel BASB110 polypeptides of Moraxella catarrhalis, useful as vaccine for treating Moraxella catarrhalis infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112459/12.
N-PSDB; AAF30046.
                                                                          AAB20107 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 82-83; 88pp; English.
Moraxella catarrhalis BASB110 protein.
                       23-APR-2001
                                                  AAB20107;
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                                                                                                                                                                                                                                                                                                               KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP
                                                                                                                                                                                                          ASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSG
                                                                                                                                                                                                                                                           VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                                                                                                                                                                                                                                                                             QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDL
                                                                                                                                                                                                                                                                                                                                                              AALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                                                                                                                           VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                                                                                                                                                                                                                            KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP
                                                                                                                                          AALFEFRISRNGVYVDPLTVLK 322
                                                                                                                                                                                          ASNAGTVIQADHNMDGASIVIQHTNGFVSSYIHIKDAQVKTGDTVRTGQRIASMKNQPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 322; DB 22; llarity 100.0%; Pred. No. 1.2e-310; Conservative 0; Mismatches 0;
                         (first entry)
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Length Indels

322; 0;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel BASB110 polypeptides of Moraxella catarrhalis, useful vaccine for treating Moraxella catarrhalis infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
Misc-difference 104
                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASB110; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                             Local
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)B; AAF30047.
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                     VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                        KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP 180
                                                                                                                                                                                                                            MTVTIAINSQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGS
                                                                  KVRERSISSGVNTAHTPSPVAVQSSRPPVQQHPAVQKPTPPVVVVKKPTPTPPVVQQPAP
                                                                                                                                     QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSGYTIYTGQWLTLWSGDL
                                                                                                                                                                      QVITDSQGVPNRYQVKQGDTVSKIAQRYGLNWREIGHINNLNSSYTIYTGQWLTLWSGDL
                                                                                                                                                                                                        MTVTIAINSQNQKPIKRLGLIFGVITTCILAGCASKPTYNSTSGSGSHRTSGSGGLAIGS
 VAPPVTEAPFATGSSGVMQFRYPVGATNPVVRRFGTATVAGSTVTSNGMWFSGRDGDLIN
                                                                                                                                                                                                                                                                                                                                                  322
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                                                                                                                                                                                                                                                                                             68.6%;
99.7%;
                                                                                                                                                                                                                                                                             Score 221; DB 22;
Pred. No. 1.7e-210;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                             Length 322;
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RESULT 4
AAG90076
ID AAG9
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AAG90076 standard; Protein; 223

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217 ATVAGSTVT 225

ATVAGSTVT

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RESULT 3
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  Matches
                       Query Match
                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511).
                                              Sequence
                                                                                 The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                Disclosure; SEQ ID NO 11865; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB61691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB61691 standard;
                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE
             Local
                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                       2001-656860/75.
DB; ABL05794.
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  Similarity 9; Conser
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                                                968 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanogaster polypeptide SEQ ID NO 11865
                                                                                                                                                                                                                                                                                                                          Adams M,
  Conservative
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2000US-0614150.
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            2.8%;
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            Score 9;
Pred. No.
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  Mismatches
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                      Length 968;
  Indels
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                                                                                                                                                                               The invention
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RESULT 5
AAW94997
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AC AAW9
DT 12-M
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Best Local Similarity
Matches 8; Conserv
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                   The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coryneform bacterium; organic acid synthesi
                                               YAK-1 related
                                                                         12-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; SEQ ID NO: 3830; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-376931/40.
DB; AAH65295.
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                                                                                                                           standard;
                                                                                                                                                                                         HTPSPVAV 137
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2000JP-0159162.
2000JP-0280988.
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Senoh A,
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                                             serine/threonine protein kinase-HTLAR33.
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                                                                                                                         Protein;
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                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H, Ando S, Hayashi M, Ikeda M, Ozaki A;
         e protein kina
osteoporosis;
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Pred. No.
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kinase; HTLAK33; LULL ACCE, osis; Adult Respiratory Disease
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                                                                                                                                                                                                                                                         DB 22;
o. 18;
                      HTLAR33; bone loss; ARDS;
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inflammatory disorder;

Syndrome;

23-MAR-1998

(first entry)

AAW31599;

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RESULT 6
AAW31599
ID AAW3
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AC AAW3
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AC AAW3
XX
AC 23-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC This represents a YAK-1 related serine-threonine protein kinase
CC polypeptide (HTLAR33). Host cells transformed with an expression
CC comprising the HTLAR33 nucleic acid are used for the recombinant
CC production of the protein. HTLAR33 polynucleotides and polypeptides are
CC useful for are useful for diagnosing susceptibility to diseases and for
CC screening for antagonists, agonists. These can be used in treatment to
CC enhance (agonist) or block (antagonist) HTLAR33 activity. Diseases
CC diagnosed, prevented or treated include: bone loss and inflammatory
CC (ARDS), Rheumatoid arthritis, osteoarthritis, Inflammatory Bowel Disease
CC (IBD), psoriasis, dermatitis, asthma, allergies; bacterial, fungal,
CC septic shock; pain; injury, cancers, anorexia, bullimia, Parkinson's
CC disease, cardiovascular disease including restencies; atherosclerosis,
CC acute heart failure, myocardial infarction; hypotension; hypertension;
CC urinary retention, angina pectoris; ulcers; benign prostatic hypertension;
CC urinary retention, angina pectoris; ulcers; benign prostatic hypertension;
CC depression, anxiety; delirium, dementia, severe mental retardation and
CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
syndrome. HTLAR33 polypeptides are also useful for mapping genes to
CC cand psgis.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis; psoriasis; dermatitis; asthma; allergy; infection; HIV-1; HIV-2; cachexia; immunodeficient disorder, septic shock; pain; injury; cancer; anorexia; bulimia; Parkinson's disease; cardiovascular disease; neurological disorder; Huntington's disease; gene therapy; gene mapping Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New serine-threonine kinase (HTLAR33) polypeptides and polynucleotides - useful as diagnostic reagents and for prevention and treatment of bone loss, neurological and inflammatory disorders and cancer, HIV infections and angina pectoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-108353/10.
N-PSDB; AAX17774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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28-JUL-1997;
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                                                                                                                AAW31599
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                                                                                                                                                                                                                                                           APVAPPVT 457
                                                                                                                                                                                                                                                                                                                APVAPPVT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 557 AA;
                                                                                                                                                                                                                                                                                                                                                                        2.5%; So llarity 100.0%; F Conservative 0;
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97US-0053924.
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                                                                                                                Peptide;
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RESULT 7
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AC AAU1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in trans, all virion proteins required for packaging such a retroviral vector. The helper DNA sequence encodes a ecotropic Moloney murine leukaemia virus (MMLV) or gibbon ape leukaemia virus (GALV) gag and pol; and a xenotropic, amphotropic, ecotropic or polytropic envelope protein. The packaging plasmids, designated KAT plasmids, are used with a second retroviral vector encoding a foreign gene of interest to produce mammalian cells with retroviral supernatants that express, e.g. a hormone, lymphokine, growth factor or coagulation factor. The plasmids are useful in construction of stable cell lines that constitutively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This linker peptide is used to construct a plasmid pIK98.6-K/L/H which is used in the construction of a retroviral packaging plasmid used for the production of high titres of recombinant retrovirus in human cells. The retroviral packaging plasmid comprises a retroviral helper DNA sequence derived from a replication incompetent retroviral genome that encodes, the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retrovirus particles: gag, pol and env. The stable produce reels continue to produce high titre retrovirus indefinitely in the absence of drug selection due to the stable integration of both packaging function and virus vector. The retroviral vector plasmids are constructed with sequences enabling the episomal persistence without the need for stable integration of the vector plasmid. The Env gene determines the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                            Synthetic peptide linker for chimaeric antibodies
                                                                                   12-MAR-2002
                                                                                                                                         AAU11448
                                                                                                                                                                                          AAU11448 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     produce the retroviral proteins required in trans for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 27; 157pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High efficiency retroviral packaging system - used to transduce human cells, esp. haematopoietic stem cells, T or B cells with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-165307/15
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7; Conservative
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                                                                             (first entry)
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100.0%; Pr
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k; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zsebo KM
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Matches
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14-DEC-1990;
12-DEC-1991;
09-DEC-1992;
                                                                                                                                 The invention relates to treating viral or malignant diseases using modified T cells that express proteins comprising (in an N-terminal to C-terminal direction) single chain antibody binding domains (that bind to viral or tumour antigens), transmembrane domains and cytoplasmic signal transducing domains. When the single chain antibody domain binds to the viral or tumour antigen on the cell, the modified T cells kill cells expressing the antigens. The modified T cells are used for treating malignant diseases and viral infection especially by, human immunodeficiency virus (HIV), cytomegalovirus, hepatitis G, hepatitis B, and mycobacterium avium. The present sequence is peptide linker used to link together the functional peptides of the chimaeric antibody molecule
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virucidal; cytostatic; peptide linker; anti-HIV;
human immunodeficiency virus infection; viral disease; malignant disease;
T cell; single chain antibody; cytomegalovirus; hepatitis C; hepatitis B;
                                                                                                                                                                                                                                                                                                                       Example 3; Column 23; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                Treating viral infections, e.g. HIV, and malignancies using T cells that express proteins which bind virus/tumour antigens and kill cells presenting the antigens, via the activity of a cytoplasmic signal
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-074399/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capon DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                     transducing domain
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41 STSGSGS 47
                              Similarity 7; Conserv
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                                                                                          13 AA;
                              Conservative
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90US-0627643.
91WO-US09431.
92US-0988194.
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                                             2.2%;
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                                             Score 7; Pred. No.
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5. 12;
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                                                            Length 13
                               Indels
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RESULT 8
AAE10936
18-DEC-2001
                                                AAE10936 standard;
                                   (first entry)
                                                peptide;
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Mouse mass1 protein conserved amino acid repeat motif #11.

Mouse; monogenic audiogenic seizure-susceptible-1 gene; mass1; transgenic animal; genetic abnormality; seizure

WO200165927-A1.

13-SEP-2001.

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RESULT 9
ABPO408F
XX ABPO
XX ABPO
XX YA-J
DT 24-J
XX Huma
XX Huma
XX Huma
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to nucleic acid molecules designated monogenic audiogenic seizure-susceptible-1 (mass1) genes. The nucleic acid molecule may be used via recombinant DNA methodologies in the production of transgenic animal (especially mouse) models for studying genetic abnormalities related to mass1 which result in seizure susceptible phenotypes (mass1 is audiogenic seizures). The present sequence is mouse monogenic audiogenic seizure-susceptible (mass1) protein conserved amino acid repeat motif.

Note: The present sequence (SEQ ID NO:16) is incorrectly referred to as SEQ ID NO:15 in the sequence listing of the specification.
                                                                                                                                                                                                                                                                               Human; open reading frame; ORRX; gene thorapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                           30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                       29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                       WO200192523-A2
                                                                                                                                                                                                                                                 myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX protein sequence SEQ ID NO:8156.
                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-2002
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03-AUG-2000;
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                                             CURAGEN CORP.
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Similarity 100.0%;
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2000US-222898P
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Pred. No. 31;
0; Mismatches
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CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABNI5762 to ABNI7752 encode the human ORFX CC in the specification). ABNI5762 to ABNI7752 encode the human ORFX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a grathology associated with an ORFX-associated CC sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, CC osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious CC diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease, and autoimmune inflammatory eye disease. ORFX proteins are also cuseful for treating burns, incisions, vulcers, for treating osteoporosis, CC useful for treating burns, incisions, vulcers, for treating osteoporosis, CC useful for treating burns, incisions, vulcers, and for gut creperfusion injury in various tissues and conditions resulting from CC NB. The sequence data for this patent did not form part of the printed condition, but was obtained in electronic format directly from WIPO at figure in the later, and for condition, but was obtained in electronic format directly from WIPO at figure in the later, and for conditions resulting from wipo.
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Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106308/14.
N-PSDB; ABN19839.
        Similarity 7; Conserv
                                                                                                        54 AA;
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     2.2%;
|larity 100.0%
|Conservative
0;
        Score 7; DB:
; Pred. No. 46;
0; Mismatches
                                  DB 23;
o. 46;
                                                       Length 54;
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RESULT 10
AAM83197
ID AAM83
XX
AC AAM83
AC AAM83
XX
Human
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Human
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N-PSDB; AAK55978.
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
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2000US-0241221.
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S-0244617.

S-0246474.

S-0246475.

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                                                                                                                                                                                                                                                                           SCI
                                                                                                                 human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                                                                     Ruben
                                                                                                                                                                                                                                                                           INC.
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                                                                                                                 : antigen
                                                                                                                     polypeptides, and
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54590 and AAM82169 represent sequences used in the exemplification of the present invention.
               Ruben SM,
Wei Y, En
Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                                                                                                         19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                             WO9947540-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein encoded by gene 48 clone HWAAP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1999
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Similarity 100.0%; Pred. No. 56
7; Conservative 0; Mismatches
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                                                                        GENOME SCI INC.
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98US-0080313
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                              Feng P, Sc
R, Lafleur
                              Soppet DR;
ur DW;
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Matches 7
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acme; pustulosis; hypercosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne, vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                       Skeiky YAW, Persing DH, L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood
Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                   N-PSDB; AAS59618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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DB; AAZ24858.
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                                                                                                                                                                                                                           Mitcham JL, Wang SS, Jen S, Carter D;
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polypeptides. The proteins and

AAU39105-AAU68017 represent Propionibacterium acnes

their associated DNA sequences

immunogenic are used in

Example 1; SEQ ID No 22782; 1069pp; English.

CC the treatment, prevention and diagnosts of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, cC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and CC therefore treat P. acnes infections. The antibodies may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC where linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed can be used for the proper can be used to constitute the proper can be used as consecuted immunosorbent assay (ELISA).

S

178 PAPVAPP 184

Query Match

ftp.wipo.int/pub/published_pct_sequences.

72

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Local

Similarity 7; Conserv

Conservative

2.2%; but 100.0%; Pr

Score 7; DB 2;; Pred. No. 61; 0; Mismatches

DB 22; 5. 61;

Length 72;

<u>,</u>

Indels

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Gaps

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RESULT 13
AAU50707
ID AAU50C
XX AAU50C
XX AAU50C
XX AAU50C
XX X
XX SAPHO
XX Uveilt
XW infla
XX derma
XX derma
XX OC20C
YX WO20C
XX TO 01-W
YF 20-Ai
YF 21-Ai
PR 02-JI
PR 07-JI
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Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                       WPI; 2001-616774/71.
N-PSDB; AAS59549.
                                                                                                                                                                                                                                                                                                                                 Skeiky YAW,
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                                                                                                                                                                                                                                                                                           L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                  Persing DH,
e J, Zhang Y,
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                                                                                                                                                                                                                                                                                       Mitcham JL, Wang
, Jen S, Carter
                                                                                                                                                                                                                                                                                                                             Wang SS,
                                                                                                                                                                                                                                                                                                                                 Bhatia
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Example 6; Fig 1; 94pp; English

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ID AAY96
XX AAY96
XX T11-SE
XX Leafy
XX Leafy
XX Leafy
XX Selec
XX Arabi
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XX O9-NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                             New HAP3-type CCAAT-box binding transcriptional activators, particularly Leafy cotyledon 1 transcriptional activator, u inducing somatic embryogenesis or apomixis in a plant cell
                                                                                                                                                                                          (PION-)
                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2000 (first entry)
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                                                                                                             WPI; 2000-376568/32
                                                                                                                                           Sun X,
                                                                                                                                                          Lowe KS,
                                                                                                                                                                                                                                           09-NOV-1998;
10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                          WO200028058-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Leafy cotyledon 1 transcriptional activator; LEC1; apomixis; selectable marker; transgenic plant; transgenic seed; HAP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis LEC1 consensus region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96225 standard; Protein; 90 AA
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oerster GJ,
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98US-0107810.
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                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant;
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dimpalli R;
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Length 101;

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Query Match
Best Local S
Matches 7
The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB5521). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 [published 18-oCT-2001] which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the leafy cotyledon 1 transcriptional activator, LEC1 consensus sequence from Arabidopsis. This sequence is a HAP3-type CCANT-box binding protein, LEC1 expression initiates the formation of rembryo-like structures and improves growth and recovery of transformants. When appmixis occurs, i.e. the replacement of sexual reproduction by asexual reproduction, LEC1 expression in the muclellus integument, or cell specific expression in the megaspore mother cell would trigger embryo formation from maternal tissues only. This results in the production of seeds identical to the parent. Using LEC1, transgenic high yielding seeds could be developed. In addition, LEC1 could be used for positive selection of a transformed cell (transgenic plant), for increasing transformation efficiency and for increasing recovery of regenerated plants. The present sequence was used in the identification of the plant LEC1 consensus sequence (AAY96223).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; SEQ ID No 2144; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleotide sequence useful in lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-043418/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and interactions -
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N-PSDB; ABL10237.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                           standard;
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                           Protein;
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        cancer; cirrhosis;
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RESULT 19 ABG04226 ID ABG04 XX

ABG04226 standard; Protein; 126

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64 99

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Conservative

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The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 CC in the specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide CC sequences can be used in gene therapy. ORFX sequences can be used in the CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver, CC psoriasis, benign tumours, keloid, degenerative disorders related to organ CC transplantation, cardiovascular diseases, diabetes mellitus, systemic CC steoarthritis, neurodegenerative disorders, disorders related to organ CC transplantation, cardiovascular diseases, diabetes mellitus, systemic CC storage disease, various immune deficiencies and disorders, infectious CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host CC one degenerative disorders, or periodontal disease, and for gut correction or regeneration and treatment of lung or liver fibrosis, CC protection or regeneration and treatment of lung or liver fibrosis, CC systemic Cytokine damage.

CC N.B. The sequence data for this patent did not form part of the printed
  Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythemat hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                              N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000;
29-AUG-2000;
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DB; ABN16672.
Similarity 7; Conserv
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2000US-228716P.
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                       Score 7;
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RESULT 20
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Matches 7
                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                               and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
         AAC05078;
                        AAO05078 standard; Protein; 136
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 34585; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                  biodiversity
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #4217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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RESULT 21
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Best Local Similarity
Thes 7; Conserve
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                                     18-OCT-2000
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 Arabidopsis
                                                                      AAG58103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      of cancer, leukaemia, nervous system
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thaliana protein fragment SEQ
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5. 1.1e+02;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;

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RESULT 22
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Matches 7
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26-OCT-1999;
28-OCT-1999;
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22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
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25-OCT-1999;
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13-OCT-1999
14-OCT-1999
14-OCT-1999
14-OCT-1999
14-OCT-1999
14-OCT-1999
                                                         Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
      07-SEP-2001.
                     WO200164835-A2
                                                                                        Human polypeptide SEQ ID NO 19767.
                                                                                                        06-NOV-2001
                                                                                                                        AAO05875;
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                                    Homo sapiens.
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                                                                                                                                                                                                           Local Similarity nes 7; Conserv
                                                                                                                                                                             129
                                                                                                                                                                                            123
                                                   system disorders;
                                                                                                                                       standard; Protein; 147 AA.
                                                                                                                                                                             RERSISS 135
                                                                                                                                                                                            RERSISS 129
                                                                                                                                                                                                            Conservative
                                                                                                        (first entry)
                                                                                                                                                                                                                                          99US-0160980.
99US-0160981.
99US-0160981.
99US-0161404.
99US-0161406.
99US-0161159.
99US-0161359.
99US-0161361.
99US-0161920.
99US-0161920.
99US-0161923.
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99US-0160767.
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99US-0159637.
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99US-0157117.
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100.0%; Pr
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0; Mismatches
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5. 1.1e+02;
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                                                                        therapy;
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ARESULT 23
AAE02227
ID AAE02227
AC AAE02
XX Stapl
TX Stapl
XX Biofi
KW otiti
KW otiti
KW lung;
KW lung;
KW blepl
XX septi
XX Stapl
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                                                                                                                                                                                                      Biofilm A; antibacterial; bacteraemia; food poisoning; osteomyelitis; otitis media; tracheliis; epiglottis; thyroiditis; empyema; abscess; lung; splenic; retroperitoneal; endocarditis; cerebral; renal; diarrhoea; blepharitis; conjunctivitis; keratitis; endophthalmitis; darcryocystitis; cellulitis; epididymitis; impetigo; folliculitis; wound; myositis; septic arthritis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the encoded proteins (AAO00010-ĀAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                         Staphylococcus aureus 'WCUH 29'.
                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus biofilm protein, biofilm A.
                                                                                                                                                                                                                                                                                                                                                       31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    AAE02227
                                                28-OCT-1999;
                                                                              26-OCT-2000; 2000WO-US29460
                                                                                                                                             WO200130806-A1
                                                                                                                                                                                                                                                                                                                                                                                      AAE02227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing and treating disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 19767; 1399pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000;
18-MAY-2000;
(SMIK) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001WO-US04927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immuno
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                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                99US-0161984.
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0; Mismatches
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1.2e+02;
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ID AAU66
XX AAU66
XX AAU66
XX I3-FE
XX SAPHC
XW SAPHC
XW UVeli
XW infl
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XW OC20
PN WO200
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Best Local
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                                                                                                                 21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                   Skeiky YAW, Persing DH, L'maisonneuve J, Zhang Y,
                                                                                                                                                                                         20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                              01-NOV-2001.
                                                                                                                                                                                                                                                                WO200181581-A2
                                                                                                                                                                                                                                                                                                     Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New biofilm protein from Staphylococcus, useful e.g. antibacterial agents, and related nucleic acid -
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                                                                            (CORI-) CORIXA CORP.
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DB; AAD05669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%; Score 7; DB 22; Length 15:
larity 100.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                            2000US-199047P.
2000US-208841P.
2000US-216747P.
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                   Mitcham JL, Wang SS, Jen S, Carter D;
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ARBSULT 25
AAU43562
ID AAU43
XX AAU43
XX Propi
XX Propi
XX SAPHC
KW SAPHC
KW Infla
KW Infla
XX O1-NC
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N-PSDB; AAS59749.
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                                   Skeiky YAW, I
L'maisonneuve
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2000US-208841P.
2000US-216747P.
                                       Mitcham JL, Wang
, Jen S, Carter |
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2001-616774/71.

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Matches 7
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                 Telford J,
Tettelin H;
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N-PSDB; AAS59520
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RESULT 27
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09-OCT-1998;
25-FEB-1999;
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09-OCT-1998;
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                                                                                                                                                                                                                                                                                          02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABN66109
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                                                         CHIRON CORP.
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                                                            GENOMIC
                                                                                                                                          98US-0103794.
98US-0103796.
99US-0121528.
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98US-0094869.
98US-0098994.
98US-0099062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy.
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Pred. No. 1.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein sequence SEQ ID NO:2858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; vaccine;
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Matches 7
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Tettelin
                                                                genes from Drosophila
interactions -
                                                                                                                   New isolated nucleic
                                                                                                                                                                                                                                         Venter JC,
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                  2001-656860/75
DB; ABL05627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 1343; 1453pp; English.
                                                                                                                                                                                                                                                                                        CORP NY.
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                                                                                                                                                                                                                                         Adams M,
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Venter JC;
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2000US-0614150
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                                                                                         detection reagent
for elucidating co
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0; Mismatches
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No. 1.5e+02;
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                                                                                         nt for detecting cell signalling
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LEC1 polypeptide is encoded by the leafy cotyledon-1 (LEC1) gene (see ANV61022-24) of Arabidopsis thaliana. Full-length LEC1 polypeptide can act as a subunit of a protein capable of acting as a transcription factor in plant cells. The LEC1 gene is embryo-specific and can be used to modulate development (claimed) of embryos or other organs in plants. Inhibiting expression can be useful e.g. in weed control (by transferring an inhibitory sequence
                                                                                                                                                   New isolated plant leafy cotyledon-1 gene - used for, e.g. increasing storage protein content in producing fruit with small and non-viable seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                        19-FEB-1998;
21-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis leafy-cotyledon 1 (LEC1) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-1999
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                                                                                                                       Claim 15; Page 31; 55pp; English.
                                                                                                                                                                                                                                                             Fischer RL,
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DB; AAV61022-24.
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larity 100.0%;
Conservative
                                                                                                                                                                                                                                                             Goldberg
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97US-0804534.
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                                       LEC1 genes are thought to play a central role in late embryogenesis, in cospecifying cotyledon identity during embryo development. LEC1 polypucleotides may act as transcription factors. LEC1 polypucleotides are conserved to the polypucleotide are conserved to the polypucleotide are conserved to the polypucleotide is a seed development and for inducing ecotopic development of embryonic tissue in a plant. In both cases, the LEC1 colypucleotide is introduced into the plant through a sexual cross and conserved in an antisense orientation with a second heterologous polypucleotide selected from AP2 and RAP2 genes of Arabidopsis. The coll polypucleotide is also useful for targeting expression in a seed, and for preparing expression cassettes for suppressing or enhancing conditions. LEC1 gene expression, which is useful in weed control or for improving nutritional value of plant tissue respectively. LEC1 colypeptides and polypucleotides are especially used for increasing or decreasing storage protein content in cotyledons or leaves. LEC1 also increases reproductive tissue mass, e.g., increases fruit size, seed content is the protein or its oil mass.
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                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 53-54; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                New embryo-specific gene useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-160588/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                embryo development; transcription factor; seed development; ecotopic development; embryonic plant tissue; weed control; nutritional value; storage protein; cotyledon; seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leafy cotyledon 1 gene; LEC1 gene; embryogenesis; cotyledon identity
                                                                                                                                                                                                                                                                                                             The present sequence represents a Leafy Cotyledon 1 (LEC1) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1998;
17-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to a weedy species and allowing it to be transmitted through sexual crosses) or to produce fruit with small and non-viable seed. Enhanced expression of LEC1 can be used to increase storage protein content in plant tissues to improve nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reproductive tissue mass; fruit size;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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98US-0193931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of an Arabidopsis leafy cotyledon 1 polypeptide.
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fischer
                                                                                                                                                                                                                                                                                                                                                                                transgenic
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Sequence

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CC sequence that encodes LEC-1 protein comprising a subsequence that comprising a subsequence that compression are used for modulating considerable in the induction of embryonic characteristics core seed development in a plant. Polynucleotide sequences from LEC1 combryos, to modulate the development of embryos or the characteristics core an embryo on other organs (e.g., by enhancing expression of the gene core in a transgenic plant). Modulation of the expression of LEC1 gene is core to manipulate a number of useful traits, such as increasing or confect sexpression is useful in weed control or to produce fruit with small and non-viable seed. Enhanced expression of LEC1 genes is competent content in control or to produce fruit competent gene promoters are useful for directing gene expression of LEC1 genes is competent gene product is located in embryos or seeds. Expression of CEC-1 genes in plant reproductive or vegetative tissue induce ectopic expression of cells and tissues, together with another plant nucleic
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Best Local
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Kwong R;
                                                                                                                                                                                                                                                                                The patent discloses novel leafy cotyledon 1 (LEC1) polypeptides polynucleotides encoding them. The invention also provides expres cassettes comprising a promoter operably linked to a heterologous
                                                                                                                                                                                                                                                                                                                                                                                               Novel leafy cotyledon 1 polynucleotide encoding leafy cotyledon polypeptide for modulating transcription resulting in seed developmen in plant comprises providing in an expression cassette linked to LEC1
                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 53-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD16914, AAD16915, AAD16916.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leafy cotyledon 1; LEC1; transcription modulator; seed development;
embryonic characteristic; transgenic plant; storage protein content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leafy cotyledon 1 (LEC1) protein
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                                                                                                                                                                                                                                                                                                                                              73pp;
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1.6e+02;
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                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG187) and the encoded proteins (ABB57037-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic a genes from Drosophila interactions -
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
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)B; ABL13439.
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting for elucidating cell signalling
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                                                                            Score 7; DB 22; L
Pred. No. 1.7e+02;
0; Mismatches 0;
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Pred. No. 1.0
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> 2000US-0229513. 2000US-0230437.

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                                                                                                                                 The invention relates to isolated nucleic acid molecules encoding CC novel human secreted extracellilar matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased CC expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules CC may be administered to down regulate expression of SPs by binding with CC the cells own genes and preventing their expression. The polynucleotides CC may also be used as DNA probes in diagnostic assays. The SPs may also be used as SNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. malanomas, neoplasms of the breast or liver, Sezary syndrome and CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses cinclude wound healing, maintenance of organs before transplantation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus yogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                      27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus polypeptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP30505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP30505 standard; Protein;
                                                                                                                                                                                                                                                                                                                                29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200234771-A2
(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
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298

Ö 10186.

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CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are considered from a range of human tissues disclosed in the specification. Crime nucleic acids, proteins, antibodies and (ant) agonists are useful cin the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adranal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (C) immune disorders e.g. Addison's disease, allergies, autoimmune chaestoyatese, multiple sclerosis, rhewmatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (C) disease, multiple sclerosis, rhewmatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (C) dispay; and (f) infectious diseases such as viral, bacterial, fungal cand parasitic infections.

CC Note: The sequence data for this patent did not form part of the corimon useful and seguination, but was obtained in electronic format directly from USPFO at segdata.uspto.gov/sequence.html?DocID=999909764870.
                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 300; 235pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding human proteins, useful for diagnosis, treatment and prevention of e.g. osteoporosis, also related polypeptides and antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-470713/50
N-PSDB; ABQ66545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ROSE/)
(RUBE/)
(BARA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUBEN S M.
BARASH S C.
KPTPTPP 217
                               KPTPTPP 173
                                                                                                                                                251 AA;
                                                                         Conservative
                                                                     2.2%; Score 7; DB:
100.0%; Pred. No. 2e-
tive 0; Mismatches
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o. 2e+02;
                                                                         0;
                                                                                                        Length 251;
                                                                         Indels
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                                                                         Gaps
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RESULT 36
ABB08497
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Telford J, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus sequences (S1), given in (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for
STABILISED RECOMBINANT ANIMAL CELL OF HCV
                                                                                                                                                                                                                                                                                                                                                                                           ABB08497 standard; Protein; 300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus proteins..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 4148; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-352536/38.
N-PSDB; ABN71136.
                                        N-PSDB; ABL41548.
                                                    WPI; 2000-144176/13.
                                                                                                                                                                   30-JUL-1994;
                                                                                                                                                                                              30-APR-1998
                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                             Envelope 2 protein;
                                                                                                                                                                                                                                                                                                         Envelope 2 protein of HCV
                                                                                                                                                                                                                                                                                                                                                                ABB08497;
                                                                                Ryu W,
                                                                                                           (GLDS )
                                                                                                                                       30-JUL-1994;
                                                                                                                                                                                                                       KR138597-B1.
                                                                                                                                                                                                                                                                                                                                      23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for detecting a compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100 7; Conservative
                                                                                Yang J,
                                                                                                           LG CHEM CO LTD.
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                                                                                                                                                                                                                                                                                                                                   (first entry
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100.0%; Pr
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0; Mismatches
             LINE
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b. 2.3e+02;
ches 0;
             EXPRESSING ENVELOPE
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              PROTEIN
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80 TVSKIAQ 86

Conservative

<u>,</u>

Mismatches

Indels

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Gaps

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RESULT 37
AAR98460
Query Match
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Matches 7; Conserve
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Best Local
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                                                                                                        The present sequence is that of the IlaIIC gene product, an endonuclease, part of a Lactococcus lactis restriction/modification (R/M) system. The LlaII R/M system is similar to the MboI system which recognises the sequence 5'-GATC-3' and cleaves it before the guanine. A plasmid contg. the DNA (AAT30440) encoding the R/M system can confer phage resistance to a bacterium, such as providing resistance to phage-sensitive dairy cultures. The DNA and proteins can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to stabilised recombinant animal cell line expressing envelope 2 protein of HCV. The present sequence represents the envelope 2 protein of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                             DNA encoding restriction and modification confers phage resistance to bacteria, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LlaIIA; LlaIIB; LlaIIC; m6A-methyltransferase; endonuclease; restriction;
modification system; phage resistance; milk; dairy product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR98460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 7; 8pp; Korean.
                                                           Sequence
                                                                                                                                                                                                          Claim 2; Fig 4; 48pp;
                                                                                                                                                                                                                                    additive
                                                                                                                                                                                                                                                                                     N-PSDB; AAT30400.
                                                                                                                                                                                                                                                                                                WPI; 1996-333992/33.
                                                                                                                                                                                                                                                                                                                      Moineau S,
                                                                                                                                                                                                                                                                                                                                                                       19-APR-1995;
30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactococcus lactis SMQ-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endonuclease LlaIIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR98460 standard; Protein; 304
                                                                                              improving fermentation of a dairy prod. and
                                                                                                                                                                                                                                                                                                                                               (UNIL ) QUEST INT BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9621017-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 TPSPVAV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPSPVAV 147
                                                           304 AA;
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                                                                                                                                                                                                                                                                                                                        Vandenbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                       95US-0424641.
94US-0366480.
                                                                                                                                                                                                                                                                                                                                                                                                             95WO-NL00448
                     2.2%;
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100.0%;
                                                                                                                                                                                                          English.
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                       Score 7;
Pred. No.
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Pred. No.
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                       DB 17; Le
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). 2.3e+02;
                                                                                                                                                                                                                                                                                                                        ER,
                                                                                                                                                                                                                                               enzymes from L. lactis - use in milk and as a food
                                                                                              proteins can be used as additives in food
                                                                                                                                                                                                                                                                                                                        Walker SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>;
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                                 Length 304
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171

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RESULT 39
ABP28875
ID ABP28
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AC ABP28
XX
DT 02-JU
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                                                                                                                                                                                Query Match 2.2%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                        This AA sequence encodes a restriction endonuclease, R. IlaAI, with the recognition sequence 5'-*GARC-3' (* indicating point of cleavage) from the plasmid-derived type-II restriction-modification system from Lactococcus lactis subsp. cremoris W9, LlaAI. R. IlaAI is one of 3 proteins in this restriction-modification system, along with a 284 AA methylase (M.IlaAIA, AAW02160), and a 269 or 257 AA methylase (M.IlaAIB, AAW02162, respectively). This restriction-modification system may be used in a method for conferring increased virus resistance, more specifically phage resistance, to a L. lactis errain resistance, more specifically phage resistance, to a L. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JOSE/)
(MADS/)
(NYEN/)
            02-JUL-2002
                                      ABP28875;
                                                             ABP28875 standard;
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                virus resistance, more specificali
strain used in cheese manufacture
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 65-66; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Type I restriction-modification systems obtd. from Lactococcus lactis - for conferring phage resistance on lactic acid bacteria. useful as starter cultures for cheese and fermented milk prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-393404/39.
N-PSDB; AAT36391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Josephsen J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis subsp. cremoris W9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactic acid bacterium; Danish starter culture; cheese; enzyme; restriction endonuclease; methylase; fermented milk; phage resistance
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                                                                                                                                171
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NYENGAARD N R.
VOGENSEN F K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOSEPHSEN J.
                                                                                                                                TVSKIAQ 177
                                                                                                                                                         TVSKIAQ 86
                                                                                                                                                                                                                                      304 AA;
            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-DK00076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95DK-0000179
                                                               Protein;
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                                                               321
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Pred. No. 2..
0; Mismatches
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                                                                                                                                                                             DB 17; L., io. 2.3e+02; 0;
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                                                                                                                                                                                                            Length 304;
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                                                                                                                                                                                   Indels
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RESULT 40
AAG38356
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                                                                                                                                                                                                                                                                                     Query Match
Best Local
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24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                         AAG38356;
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3855; 4525pp; English.
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N-PSDB; ABN69506.
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1.6 79 2 US-08-554-840-14 5 1.6 79 3 US-08-554-840-14 5 1.6 79 3 US-08-554-840-14 6 79 4 US-08-925-339-14	0 1.6 // 4 US-09-246 9 5 1.6 77 4 US-08-803 0 5 1.6 78 2 US-08-053 1 5 1.6 78 4 US-08-134	7 5 1.6 76 4 US-08-851 7 5 1.6 76 4 US-08-851 8 5 1.6 77 4 US-09-246	5 1.6 76 4 US-08-444 5 1.6 76 4 US-08-851	2 5 1.6 74 4 US-09-513-057C-1 3 5 1.6 76 3 US-08-956-307B-1	0 5 1.6 74 4 US-08-478 1 5 1.6 74 4 US-09-134	5 1.6 74 4 US-08-475-411A-6	7 5 1.6 73 4 US-08-858-207A-	5 1.6 72 3 US-08-338-579A-100 6 5 1.6 72 3 US-08-338-579A-105	5 1.6 71 4 US-09-134-001C-	2 5 1.6 70 4 US	1 5 1.6 70 3 US-08-554-840-9	0 5 1.6 69 4 US-09-205-426-1	8 5 1.6 69 4 US-09-082-514-21 9 5 1.6 69 4 US-09-324-542-18	7 5 1.6 69 4 US-09-095-855-1	6 5 1.6 69 3 US-08-467-976-2	4 5 1.6 69 2 US-08-997-362-1	3 5 1.6 69 2 US-08-467-536-21	2 5 1.6 69 2 US-08-997-080-1	0 5 1.6 69 2 US	9 5 1.6 69 1 US-08-480-750-4	8 5 1.6 69 1 US-08-487-174-4	6 5 1.6 69 1 US-08-137-800-4	5 1.6 68 5 PCT-US95-12686-1	4 5 1.6 68 4 13-09-134-6	3 5 1.6 68 2 US-08-511-485-1	1 5 1.6 68 1 US-08-180-761B	0 5 1.6 67 1 US-08-358-160-1	9 5 1.6 66 6 5252466-1	8 5 1.6 66 4 IIS:08-961-0	6 5 1.6 65 2 US-08-273-1	5 1.6 64 4 US-08-352-902D-	4 5 1.6 64 4 US-08-961-810-128	3 5 1.6 64 2 US-08-209-521-1	2 5 1.6 64 2 US-08-765-179B-1	0 5 1.6 62 4 US-09-134-0	9 5 1.6 62 4 US-09-402-668-10	8 5 1.6 62 2 05	7 5 1.6 62 1 113-08-473-0	5 1.6 59 4 US-09-670-827-41	4 5 1.6 59 4 US-09-100-0	3 5 1.6 59 2 US-08-733-505A-5	2 5 1.6 59 2 US-08-733-505A-5	1 5 1.6 59 2 US-08-733-5	0 5 1.6 59 2 US-08-733-505A-5	9 5 1.6 59 1 US-08-542-3	8 5 1.6 58 3 US-08-812-1	7 5 1.6 56 3 US-09-029-4	5 1.6 56 00-00-00-005-069-54	5 1.6 56 2 US-08-630-8

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COUPUTER READABLE FORM:

MEDIUM TYPE Diskette

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,064

FILING DATE: 20-FEB-1998

CLASSIFICATION UMBER: 60/053,924

FILING DATE: 28-UUL-1997

ATPORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-70172

TELEPHONE: 610-407-0700

TELEPHONE: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-027-064-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATENT NO. 6133006
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
APPLICANT: BERGSMA, DERK
TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASE-HTLAR33
NUMBER OF SEQUENCES: 6
NUMBER OF SEQUENCES: 6
                                                                                                                    TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
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US-08-480-750-41
US-08-53-501A-85
US-08-765-783A-104
US-08-554-840-13
US-08-554-840-13
US-08-554-840-13
US-08-554-840-13
US-08-894-017-5
US-08-894-017-5
US-08-818-111-117
US-08-818-111-117
US-08-818-111-117
US-08-818-111-117
US-08-818-111-117
US-08-818-111-117
US-08-925-339-13
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APPLICANT: BERGSMA, DERK
APPLICANT: SHABON, USMAN
TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
FILE REFERENCE: GH-70172-1
CURRENT APPLICATION NUMBER: US/09/271,815
CURRENT FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 09/027,064
EARLIER FILING DATE: 1998-02-20
EARLIER FILING DATE: 1998-02-20
EARLIER FILING DATE: 1998-02-20
SEATLIER FILING DATE: 1997-07-28
NUMBER OF SEQ ID NOWER: 09/027,07-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATE TO NOS: 6
SEQ ID NO 2
LENGTH: 557
TYPE: PRT
ORGANISM: Homo sapiens
US-09-271-815-2
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US-09-271-815-2
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US-08-258-152-9
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FINER, MITCHELL H.
APPLICANT: ROBERTS, MARGO R.
APPLICANT: ROBERTS, MARGO R.
APPLICANT: DULL, THOMAS J.
APPLICANT: ZSUBO, KRISZTINA M.
APPLICANT: QIN, LU
TITLE OF INVENTION: VIRUS AND HIG
TITLE OF INVENTION: OF MAMMALIAN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS: INC.
STREET: 322 LAKESIDE DRIVE
CITY: POSTER CITY
STATE: CALLEDON:
CIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPARTIVE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,152
FILING DATE: 10-UN-1994
FILING DATE: 10-UN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.5%; Score 8;
Best Local Similarity 100.0%; Pred. No.
Matches 8; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bequered No. 56802, OR PATENT INFORMATION:
GENERAL INFORMATION: FINER, MITCHELL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09271815
Patent No. 6297036
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.5%;
Best Local Similarity 100.0%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 APVAPPVT 186
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                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MAMMALIAN CELLS
32
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; Pred. No. 20;

0; Mismatches
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Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/08/076,299A
FILING DATE: 11-UN-1993
CLASSIFICATION #35
PRIOR APPLICATION UNUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08076299A Patent No. 5834256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO:
                                                                           TELEFAX: 415-349-7392 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.358-9600 X131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROBERTS, MARGO R. APPLICANT: DULL, THOMAS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEFAX: 415-349-7392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: QIN, LUTITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/076,299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94404
                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION INVENTION: OF MAMMALIAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FINER, MITCHELL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZSEBO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRISZTINA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHOD FOR PRODUCTION OF HIGH TITER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34,647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1; Pred. No. 5.6; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                               Matches
                                            Best
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                                                          Query Match
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/258,152
PRIOR APPLICATION NUMBER: US 08/258,152
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                   TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CEL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 00 FILING DATE: 11-JUN-93 ATTORNEY/AGENT INFORMATION: KRUPEN, KAREN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                   TOPOLOGY: 1i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                             Local Similarity nes 7; Conserv
                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01 FILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                             ENGTH:
  41 STSGSGS 47
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T: 322 LAKESIDE DRIVE
FOSTER CITY
                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08438582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALIFORNIA
                                                                                                                                                            13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                               Conservative
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                                                                                                                  linear
                                                                                                  peptide
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                                         2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MANWALIAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/438,582
                                                                                                                                                                                                                                              CELL
                               0,
                                            Score 7; DB 2; 
; Pred. No. 5.6;
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Pred. No.
                               Mismatches
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                             Gaps
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RESULT 7
US-08-479-737-44
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Best Local S
Matches 7
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SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
-09-266-596-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/517,488
APPLICATION UNMBER: 08/258,152
APPLICATION NUMBER: US 08/258,152
PILING DATE: 10-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/076,299
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
                                                                       tent No. 6319494
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GENI
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STATE: CALTERTY

CALTERT CALTERTY

STATE: CALTERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/266,596 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JCANT: FARSON, DEBORAH A.

E OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER

E OF INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION

E OF INVENTION: OF MAMMALIAN CELLS

EER OF SEQUENCES: 48
                                                            APPLICANT:
                                                                                                               44,
                                                                                                                                                                                                                                                41 STSGSGS 47
                                                                                                                                                                                                               2 STSGSGS 8
                                                                                                                                                                                                                                                                                      h 2.2%; Score 7; DB of Similarity 100.0%; Pred. No. 5.0 7; Conservative 0; Mismatches
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                                                                                                                 Application US/08479737
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FINER, MITCHELL H.
DULL, THOMAS J.
ZSEBO, KRISZTINA M.
COOKE, KEEGAN
                                                                                                                                                                                                                                                                                                                                                                                        single
linear
E:
Capon, Daniel J
Weiss, Arthur
Irving, Brian A
Roberts, Margo R
                                                                                                                                                                                                                                                                                                                                                                               peptide
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/479,737

FILING DATE: 07-Un-1995

FILING DATE: 07-Un-1995

PRIOR APPLICATION NUMBER: 08/238,405

FILING DATE: 05-MAY-1994

ATTORNEY/ACENT INFORMATION:
NAME: Mandel, SaraLynn
REGISTRATION NUMBER: 08/238,405

FILING DATE: 05-MAY-1994

ATTORNEY/ACENT INFORMATION:
NAME: Mandel, SaraLynn
REGISTRATION NUMBER: 06115.3

TELEPHONE: (415) 358-9600

TELEPHONE: (415) 358-9600

TELEPAX: (415) 358-0803

INFORMATION OR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids

LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-475-442A-44
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6407221 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                    NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
                                                                                                                                                                                                                                             APPLICANT: WEISS, ARTHUR
APPLICANT: IRVING, BRIAN A
APPLICANT: ROBERTS, MARGO R
APPLICANT: ZSEBO, KRISZTINA
APPLICANT: ZSEBO, KRISZTINA
TITLE OF INVENTION: CHIMERIC CHAINS FOR
TITLE OF INVENTION: RECEPTOR-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
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TITLE OF INVENTION: CHAMERIC CHAINS FOR RECEPTOR ASSOCIATED
SIGNAL TRANSDUCTION PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 STSGSGS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Foster City
STATE: California
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 STSGSGS 8
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                                                                                    94404
                                                                                                                                                                                                                                                                                                                                                                                                                    4, Application US/08475442A
6407221
                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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100.0%; Pred. No. 5.
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
o. 5.6;
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                                                                                                                                  US-09-029-424-15
                                                                Query Match
Best Local S
Matches 7
                                                                                                                                                                                   APPLICANT: Saitch, Masao
APPLICANT: Miyazono, Kohei
APPLICANT: IChijo, Hidenori
APPLICANT: IChijo, Hidenori
APPLICANT: ICHijo, HIDENORI MOLECULE ENCODING TGF RECEPTOR HAVING MODIFIED
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING TGF RECEPTOR HAVING MODIFIED
TITLE OF INVENTION: GROWTH INHIBITION, AND ITS USE
FILE REFERENCE: L0461/7027
CURRENT APPLICATION NUMBER: US/09/029,424A
CURRENT FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/GB96/02179
EARLIER FILING DATE: 1996-09-04
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 15
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415)358-960
TELEFAX: (415)349-7392
INFORMATION FOR SEQ ID NO:
                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                   LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CEL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 05-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,442A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                              Local Similarity nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0' FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/627,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    15, Application US/09029424A
5. 6030795
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35
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STSGSGS 41
                               STSGSGS 47
                                                                Conservative
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100.0%; Pr
                                                              2.2%; Score 7; DB 3;
100.0%; Pred. No. 21;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 7; DB 4
%; Pred. No. 5.6
0; Mismatches
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                                                                                              Length 56;
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US-09-193-931C-19
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US-09-103-478-19
                                                                                                                                                                      Sequence 19, Application US/09193931C Patent No. 6320102 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Appli
Patent No. 6235975
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.2%; Score 7; Best Local Similarity 100.0%; Pred. No.
              APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: LEAFY COTYLEDONI Genes and Their Uses
FILE REFERENCE: 023070-077620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/193,931C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/804
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR OPPOSITION NUMBER: US 09/026,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/103,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
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Ohto, Masa-aki
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CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24

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; LOCATION: (1)..(90)
; OTHER INFORMATION: LEC1 HAP3 subunit of CCAAT box-binding factor
; OTHER INFORMATION: (CBF) protein B domain homolog
US-09-193-931C-19
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Best Local Similarity
7, Conserv
INFORMATION FOR SEQ ID NO.

SEQUENCE CHARACTERISTICS:
LENGTH: 208 Aming
                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 09/026,221
FILING DATE: 19-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/804,534
FILING DATE: 21-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-077611US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
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PRIOR TILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 08/804,534
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/103,478
FILING DATE: 24-JUN-1998
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ENGTH: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLICANT: Lotan, Tamar
PLICANT: Ohto, Masa-aki
PLICANT: Goldberg, Robert B.
PLICANT: Fischer, Robert L.
TLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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Calofornia
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                                             5) 5/6-0300
576-0300
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FILE REFERENCE: 023070-077620

CURRENT APPLICATION NUMBER: US/09/193,931C

CURRENT FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: US 09/103,478

PRIOR APPLICATION NUMBER: US 09/026,221

PRIOR PILING DATE: 1998-06-24

PRIOR PILING DATE: 1998-02-19

PRIOR PILING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: US 09/026,221

PRIOR APPLICATION NUMBER: US 08/804,534

PRIOR FILING DATE: 1997-02-21

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENT ON SEQ ID NO 2

SEQ ID NO 2

LENGTH: 208
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US-08-424-641B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Arabidopsis thaliana US-09-193-931C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-193-931C-2
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Best Local Similarity
Thes 7; Consert
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Best Local Similarity
7; Conserve
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                                                                                                                       APPLICANT: Sylvain Moineau, Shirley A. APPLICANT: Walker, Ebenezer R. Vedamuthu, APPLICANT: and Peter A. Vandenbergh TITLE OF INVENTION: Isolated DNA Encoding TITLE OF INVENTION: Enzyme For Phage TITLE OF INVENTION: Resistance NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ohto, Masa-al
APPLICANT: Goldberg, Robe
APPLICANT: Fischer, Robe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
                                                                     STREET: 2190
CITY: Okemos
STATE: Michig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                   COUNTRY: U
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Goldberg, Robert B.
Fischer, Robert L.
The Regents of the University of California
                                                                                                                                                                                                                                                                                                                           Application US/08424641B
                                                                       Michigan
                                                                                                           E: Ian C. McLeod
2190 Commons Parkway
                                                      USA
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100.0%; Pred. No.
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o. 69;
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CURRENT APPLICATION DATA:

SOFTWARE:

Wordperfect 5.1

COMPUTER: Acer
OPERATING SYSTEM: MS-DOS

MEDIUM TYPE:

storage

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US-08-820-980-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5925388
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,64
FILING DATE: April 19, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: NO. 5824523e INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
                                                                                                                                  COMPUTER READABLE FORM:
MEDLIM TYPE: Diskette, 5.25 inch, 360 Kb
MEDLIM TYPE: storage
COMPUTER: Acer
COMPUTER: Acer
COMPUTER: Macana
COMPUTER: Morgarfect 5.1
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: MT 4.1-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                         STREET: 2-
STREET: 0kemos
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APPLICATION NUMBER: (
FILING DATE: December
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                   STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/4
FILING DATE: April 19, 1995
                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 TVSKIAQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08820980
                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Sylvain Moineau, Shirley A.
Walker, Ebenezer R. Vedamuthu,
and Peter A. Vandenbergh
TVENTION: Isolated DNA Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 Amino Acids
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                                                                                                                                                                                                                                                                                                                                                                                         Resistance
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                                                    08/424,641
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Query Match
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                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,64
FILING DATE: April 19, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: IAN C. MCLeod
REGISTRATION NUMBER: 20,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: NO. 5925388e INFORMATION FOR SEQ ID NO:
                                                                                           TELEPHONE: (517) 347-4103
TELEFAX: (517) 347-4103
TELEX: No. 5972673e
INFORMATION FOR SEQ ID NO: '
                                                                                                                                                                                                                                                                                                                                       COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDEPEFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                         REFERENCE/DOCKET NUMBER: Quest 4.1-155 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: and Peter TITLE OF INVENTION: I TITLE OF INVENTION: E TITLE OF INVENTION: R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenbergh
TITLE OF INVENTION: Isolated DNA Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Peptide
MOLECULE TYPE:
                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (517) 347-410
TELEFAX: (517) 347-4103
               TOPOLOGY:
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TOPOLOGY: Linear
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                                                            LENGTH:
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                                           Rmino Acid
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             Linear
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Pred. No.
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5.98;
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RESULT 18
US-09-147-236-11
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Best Local S
Matches
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                                                                                              APPLICANT: TONOUCHI, Naoto
APPLICANT: TONOUCHI, Takayasu
APPLICANT: TONOUCHIDA, Tumhhiro
APPLICANT: YOSHINAGA, Fumhhiro
APPLICANT: THARAA, Naoki
APPLICANT: THARAA, Naoki
APPLICANT: HAYASHI, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
TILE REFERENCE: 6537-011-0PCT
CURRENT APPLICATION NUMBER: US/09/147,236A
CURRENT APPLICATION NUMBER: US/09/147,236A
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/JP97/03633
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin Ver. 2.1
150 ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Patent No. 6316251
                               ORGANISM: Acetobacter xylinum FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Pla
TITLE OF INVENTION: res
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy of
COMPUTER: IBM PC comp
OTHER INFORMATION: n at positions 15741 and 15767 may be a, OTHER INFORMATION: {\sf t}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DK 01
FILING DATE: 17-FEB-1995
NFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                     ENGTH: 344
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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TOPOLOGY: 11--
LECHT-
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Similarity 100.0%;
7; Conservative 0;
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larity 100.0%;
Conservative
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0; Mismatches
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Mismatches
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US-08-909-828-2
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US-08-909-828-1
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local
                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                        APPLICATION NUMBER: US/08/909,828
FILING DATE:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 350 amino acid
                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                           STRANDEDNESS
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                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 TPPVVVV 165
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), 6060646
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                                        amino acids
TYPE:
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Pred. No.
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No. 1.1e+02;
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Best Local Similarity
""" hes 7; Conserve
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APPLICANT: Gimeno, Ruth E.

APPLICANT: Tartaglia, Louis A.

ITITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS

FILE REFERENCE: WH197-21p3MB

CURRENT APPLICATION NUMBER: US/09/232,200A

CURRENT FILING DATE: 1999-01-14

EARLIER APPLICATION NUMBER: 60/071,374

EARLIER FILING DATE: 1998-01-15

EARLIER APPLICATION NUMBER: 60/093,491

EARLIER APPLICATION NUMBER: 60/093,491
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Patent No. 6284487
GENERAL INFORMATION:
                                                                                SEQ ID NO 4
LENGTH: 356
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 Query Match
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Best Local :
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CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hirsch, David J. APPLICANT: Lodish, Harvey F.
                                                                                                                                                                                                                                                                                                                                                                                                             equence 4, Application US/09232200A
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stahl, Andreas
                                                TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Saccharomyces cerevisiae
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ARLIER FILING DATE: 1998-12-04
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Length 356;
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Query Match
Best Local Similarity
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                                                                                                                                   FILE REFERENCE: WHI97-21p3MC
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/93,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 356
TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-232-197-4
; ORGANISM: Saccharomyces cerevisiae
US-09-232-201-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-232-201-4
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EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ 1D NOS: 105
SOFTMARE: FastSEQ for Windows Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
US-09-232-197-4
                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartagdia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09232201A Patent No. 6348321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Appli
Patent No. 630009
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/232,197A CURRENT FILING DATE: 1999-01-14
                                      LENGTH: 35
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: WHI97-21p3MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 TEAPFAT 151
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                                                           356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Sequence 15, Patent No. 5

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; TOPOLOGY: linear US-08-149-105-15
                                         Sequence 15, Application US/08317847
Patent No. 5547854
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.2%; Score 7; DB 4; Ler Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Query Match 2.2%; Score 7; DB Best Local Similarity 100.0%; Prod. No. 1. Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: "U.S.A."
COUNTRY: "U.S.A."
COUNTRY: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WOXIGNERECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,105
FILING DATE: MS-DOS (VERSION 5.1)
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/029,673
FILING DATE: MSTCh 11, 1993
APPLICATION NUMBER: 07/853,396
FILING DATE: MSTCh 18, 1992
APPLICATION NUMBER: 07/853,396
FILING DATE: MSTCh 18, 1992
APPLICATION NUMBER: 007/853,396
FILING DATE: MSTCh 18, 1992
APPLICATION NUMBER: 007/853,396
FILING DATE: MSTCH 18, 1992
APPLICATION NUMBER: 007/853,396
FILING DATE: MSTCH 18, 1992
APPLICATION NUMBER: 007/86/211001
TELEPHONE: C121K, PSU1
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gustafson, Michael
APPLICANT: He, Wei W.
APPLICANT: Wang, Xiao-Fan
TITLE OF INVENTION: TGF- TYPE I
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
APPLICANT: Donahoe, Patricia K. APPLICANT: Gustafson, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 501
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 TEAPFAT 192
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                                                                                                                                                                                                                                         41 STSGSGS 47
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ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.49 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,847
FILING DATE: MAYCH 11, 1993
APPLICATION NUMBER: 07/83,396
FILING DATE: MAYCH 11, 1993
APPLICATION NUMBER: 07/83,396
FILING DATE: MAYCH 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTRATION NUMBER: 07/86/127002
FREFERENCE/DOCKET NUMBER: 07/86/127002
FREIERENCH/DOCKET NUMBER: 07/86/127002
FILIEFAX: 1617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 501
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                                                                                                                                                                                                                                    Sequence 8, Application US/09382256A
Sequence 8, Application US/09382256A
PATENT NO. 6207814

PATENT NO. 6207814

GENERAL INFORMATION:

APPLICANT: MIYAZONO, Kohei

TEN DIJKE, Peter

FRANZEN, Petra

YAMASHITA, Hidetoshi

HELDIN, Carl-Henrik

TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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TITLE OF INVENTION: FOUR NOVEL RECEPTORS OF THE TGF-B
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                    NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 STSGSGS 47
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225 Franklin Street
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ilarity 100.0%;
Conservative
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     3.25 inch, 1.44mb
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1.5e+02;
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RESULT 26 US-08-317-847-15

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OPERATING SYSTEM: PC-DOS

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RESULT 28
US-09-382-256-16
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: NO. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                 TITLE OF
                                                                                                                                                                                                                                                                                                                                              APPLICANT: MIYAZONO, Kohei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 STSGSGS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
                                                                                         ADDRESSEE: Pulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/382,256A FILING DATE: 24-Aug-1999
                                                                           COUNTRY:
                                                                                                                                                                                    TEN DIJKE, Peter
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PRO
HAVING SERINE THREONINE KINASE DO:
AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/GB99/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LING DATE: March 8, PLICATION NUMBER: G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2%; Sur
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; I
; Pred. No.
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                 3.25 inch, 1.44mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 505; 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09395115
Patent No. 6271365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16:
                                                 OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                         APPLICANT: Miyazono, APPLICANT: Franzen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
                                                                                                                                                             STATE: New
ZIP: 10022
                                                                                                                                                                                           ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 7; Conserv
CLASSIFICATION:
                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 STSGSGS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/382,256A FILING DATE: 24-Aug-1999
                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 5:
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Lity 100.0%;
Conservative
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                                                                                                          IBM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: (212) 318-30
(212) 752-5958
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                                                                                                                                                                                                                                                                                                                           Petra; Yamashita,
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                                US/09/395,115
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Pred. No.
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                                                                                                                                                                                                                                                                                        Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                                Peter Ten;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Len
o. 1.6e+02;
                                                                                                                                                                                                                                                                                                                           Hidetoshi; Heldin, Carl-Henrik
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PRIOR APPLICATION DATA:

US/08/436,265

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RESULT 30
US-09-395-115-16
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MOLECULE TYPE: protein
US-09-395-115-8
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                                                                                                                                                                                                                                                                      PATENT NO. 6271365
GENERAL INFORMATION:
APPLICANT: Miyazono,
APPLICANT: Franzen, P
TITLE OF INVENTION: H
TITLE OF INVENTION: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
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FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION NUMBER: 9313763.6
APPLICATION NUMBER: 9313763.6
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 9136099.2
FILING DATE: 3-AUGUST-1993
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-OCLOBE-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
Application variation
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FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
9304677.9
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                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kohlei, Vineet
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER
                                                     OPERATING SYSTEM:
                                                                                                                                     STATE: New York
ZIP: 10022
                                                                                                                                                                        MBER OF SEQUENCES: 29
RRESSCONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 STSGSGS 193
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WARE: Wordperfect
WI APPLICATION DATA:
JICATION NUMBER: US/09/395,115
                                                                                                                                                                                                                                                                                                                                                                       6, Application US/09395115
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17-No. 6271365ember-1992
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17-No. 6271365ember-1993
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                                                                                         Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                         , Kohei; Dijke, Peter Ten;
Petra; Yamashita, Hidetoshi; Heldin,
Activin Receptor-Like Kinase, Protein
Having Serine Threonine Kinase Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,003
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                                                                                                                                                                                                                                                                                                                     Carl-Henrik
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-395-115-16
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US-08-123-934A-8
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TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
TENGTH: 505 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.2%; Score 7; DB 4; Ler Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 17,003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION UMBER.
FILING DATA:
FILING DATA:
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PRIOR APPLICATION NUMBER: 9311047.6
APPLICATION NUMBER: 9913913
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321:
FILING DATE: 15-October--
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                          ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 9224057.1
FILING DATE: 17.No. 6271365ember-1992
IOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
                                                                                                    ADDRESSEE: Genet
STREET: 87 Cambi
CITY: Cambridge
                                                      COUNTRY: US
ZIP: 02140
                                                                                                                                                                                                  TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                 187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 STSGSGS 47
                                                                                                                                                                                                                                                                                        INFORMA
                                                                                                                                                                                                                                                                                                                       Application US/08123934A
                                                                                       MA
                                                                                                                       E: Genetics Institute Inc.- Legal Affairs
87 CambridgePark Drive
                                                                       USA
                                                                                                                                                                                                                                                                       OZNEY, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBER: 9304680.3
8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: 9321344.
15-October-1993
                                                                                                                                                                                                  No. 6291206oru
RECEPTOR PROTEINS
                                                                                                                                                                                                                                                    Anthony J.
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6271365ember-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9
FILING DATE: 8-March
                                                                                                                                                                     APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 30-Octobe:
CLASSIFICATION: 435
                   PRIOR APPLICATION DATA:
                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOPTWARE: FALLER DATA:
CURRENT APPLICATION DATA:
US/08/123,934A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617 876 1170
                                     APPLICATION NUMBER: FILING DATE: 28-May
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
OPERATING WORDERFECT
SOFTWARE: WORDERFECT
                                                                                                                                    APPLICATION NUMBER: FILING DATE: 8-Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 17-SEP-1993
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: LAZAR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 STSGSGS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 STSGSGS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617 876 5851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felfe & Lynch
                                                                                                                                    UMBER: 9304677.9
8-March-1993
                                                                                    8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                             MBER: US/08/436,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%; Score 7; DB 4; Length 505; 100.0%; Pred. No. 1.6e+02;
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Having Serine Threonine Kinase Domains And Their Use
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n_Release #1.0, Version #1.25
                                                    9311047.6
                                                                                                    9304680.3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-D
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                        APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
FILING DATE: 28-May-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: 9313
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                          FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93046
                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15-October-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 30-Oct CLASSIFICATION: 435
                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 37,003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 9136099.2
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New York City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 amino acids
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                                                                              8-March-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Kohei; Dijke, Peter Ten;
Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                          US/08/436,265
9313763.6
                                                                                             9304680.3
                                                                                                                                             9304677.9
                                               9311047.6
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To. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                           CURRENT APPLICATION DATA:

APPLICATION UNMER: US/09/679,187

FILING DATE: 03-OCT-2000

PRIOR APPLICATION UNMERR: US/08/436,265

APPLICATION NUMBER: US/08/436,265

FILING DATE: 30-October-1995

PRIOR APPLICATION NUMBER: PCT/CB93/02367

FILING DATE: 17-No. 6331621ember-1993

PRIOR APPLICATION NUMBER: 9224057.1

FILING DATE: 17-No. 6331621ember-1992

PRIOR APPLICATION NUMBER: 9204677.9

FILING DATE: 17-No. 6331621ember-1992

PRIOR APPLICATION NUMBER: 9304677.9

PRIOR APPLICATION NUMBER: 9304677.9

PRIOR APPLICATION NUMBER: 9304677.9

PRIOR APPLICATION NUMBER: 9304677.9

PRIOR APPLICATION DATA: 9304680.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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APPLICATION NUMBER: 9136099.2
FILLING DATE: 3-AUGUSE-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILLING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOALE: Vineet
REGISTRATION NUMBER: 37,003
REGISTRATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
APPLICATION NUMBER: 930468U.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 805 Third Avenue CITY: New York City STATE: New York CITY: New York COMPUTER 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashitat, Hidetosh; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 2.2%; Score 7; DB Local Similarity 100.0%; Pred. No. 1. les 7; Conservative 0; Mismatches
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; MOLECULE TYPE: protein US-09-679-187-8
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US-09-679-187-16
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Query Match
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Query Matches
                                     NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb
COMPUTER: 1BM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 03-OCT-0500
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 924057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FRIING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FRIING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FRIING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION DATE: 9-March-1993
PRIOR APPLICATION DATA:
APPLICATION DATE: 9-March-1993
PRIOR APPLICATION DATE: 9-March-1993
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APPLICATION NUMBER: 9136099.2

FILLING DATE: 3-AUGUST-1993

PRIOR APPLICATION NUMBER: 9321344.5

APPLICATION NUMBER: 9321344.5

FILLING DATE: 15-October-1993

ATTORNEY/AGENT INFORMATION:

NAME: Kohle: Vineet

REGISTRATION NUMBER: 37,003

REFERENCE/DOCKET NUMBER: LUD 5

TELECHONUNICATION INFORMATION:

TELECHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Miyazono,
APPLICANT: Franzen, I
TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 9313763.6 FILING DATE: 2-July-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 ŚTŚGŚGŚ 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Kohei, Dijke, Peter Ten;
Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
Activin Receptor-Like Kinase, Proteins
9311047.6
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PRIOR APPLICATION DATÁ:

FILING DATE:

28-May-1993

APPLICATION NUMBER: 9313 FILING DATE: 2-July-1993

9313763.6

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PCT-US94-10080-8
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                       TELEFAX: (617) 876-58
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
TYPE: amino acid
TOPOLOGY: 1:--
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,934
FILING DATE: 17-SEP-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                      SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10080
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-October-
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 87 Cambi
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD
                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 9136099.2 FILING DATE: 3-August-1993
                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B: Genetics Institute Inc.- Legal Affairs87 CambridgePark Drive
                                                                      (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                      (617) 498-8260
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NO: 8:
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RESULT 38

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US-08-469-412A-7
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                                                               Matches
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                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-UN-1995
                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER OF SEQUENCES:
                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                           ropology:
398 SGSGGLA 404
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                              51 SGSGGLA 57
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                                                              7;
                                                                              Similarity
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                                                                             2.2%;
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(first 8 amino acids from first exon not
included)"
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%; Pred. No. 1.7
0; Mismatches
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o. 1.6e+02;
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b. 1.7e+02;
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US-09-021-715-7; Sequence 7, Application US/09021715; Patent NO. 6194547; GENERAL INFORMATION: APPLICANT: Mayrothalassitis, George J.

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                                                                                                                                                                                                                                       US-09-232-200-89
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                           Sequence 89, Appl
Patent No. 628821
                              APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION
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Athanasiou, Meropi A.
Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATE: US/09/021,715

APPLICATION NUMBER: US/09/021,715

FILING DATE: 10-Feb-1998

CLASSIFICATION: CURRENTION:

AND DATE: TO-FEB-1998

CLASSIFICATION: THORNOWN:

ATTORNEY/AGENT INFORMATION:

ANTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
RMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                              398 SGSGGLA 404
APPLICATION NUMBER: US/09/232,200A
                                                                                                                                                                                                                                                                                                                                                                     51 SGSGGLA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..543
OTHER INFORMATION: /note= "murine ERF amino acid sequence (first 8 amino acids from first exon not included)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                  Application US/09232200A
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ilarity 100.0%;
Conservative
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Pred. No.
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). 1.7e+02;
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Search completed: July 8, Job time : 42 secs

2003, 11:22:01

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APPLICANT: Stath! Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTITILE REFERENCE: WHI97-21p3MB
CURRENT APPLICATION NUMBER: US/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER APPLICATION NUMBER: 60/10,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 50/110,941
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 50/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PASSEGQ for Windows Version 3.0
SEQ ID NO 98
LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Saccharomyces cerevisiae US-09-232-200-89
B
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EARLIER APPLICATION UNMBER: 60/07
EARLIER APPLICATION UNMBER: 60/07
EARLIER APPLICATION UNMBER: 60/09
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 89
LENGTH: 623
TYPE: PRT
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Best Local Similarity 100.0%;
Matches 7; Conservative
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• PRT
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398 TEAPFAT 404
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                                          186 TEAPFAT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACID TRANSPORT PROTEINS
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                                                                                     Score 7; DB; Pred. No. 1. 0; Mismatches
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0; Mismatches
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1.9e+02
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Title:
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Sequence:
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Maximum DB seq length: 2000000000
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322
1 MTVTIAINSQNQKP
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Match
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: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright
                                                                                                                                                                                                                                                                                                      Length
    Applications AA:*
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      US-09-738-626-3830
US-09-944-411-9
0 US-09-53-44
US-09-53-029-70
US-10-286-264-72
US-10-180-375-195
US-10-180-375-195
US-09-771-161A-109
US-10-156-761-14239
0 US-10-156-761-1366
US-10-156-761-1366
US-10-156-761-1366
US-09-771-161A-200
0 US-09-771-161A-200
0 US-09-738-626-5890
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Sequence 3830, Ap
Sequence 9, Appli
Sequence 44, Appl
Sequence 70, Appl
Sequence 72, Appl
Sequence 195, App
Sequence 109, App
Sequence 300, App
Sequence 300, App
Sequence 14239, A
Sequence 14239, A
Sequence 8098, Appli
Sequence 212, App
Sequence 212, App
Sequence 212, App
Sequence 212, Appli
Sequence 16, Appli
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US-09-915-242-12713
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Sequence 272, App Sequence 284, App Sequence 296, App Sequence 314, App Sequence 314, App Sequence 22, Appl Sequence 45, Appl Sequence 45, Appl Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 34086, A Sequence 36184, A Sequence 36184, A		Sequence 11, Appl Sequence 12, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 10, Appl Sequence 10, Appl Sequence 116, Appl Sequence 17, Appl Sequence 27, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 19, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 21, Appl Sequence 25, Appl Sequence 27, Appl Sequence 28, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 18, Appl	
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APPLICANT: NACAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MADO, SEIKO
APPLICANT: HAYASHI, MIKKRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NACKO
APPLICANT: TATEISHI, NACKO
APPLICANT: SENCH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR TILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3830
LENGTH: 223
TYPE: PRT
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Sequence 3830, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
Query Match 2.5%; Score 8; DB 9; Best Local Similarity 100.0%; Pred. No. 23; Matches 8; Conservative 0; Mismatches
                                                                                                                                                ORGANISM: Corynebacterium glutamicum -09-738-626-3830
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COMPUTER READABLE FORM: MEDIOM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MCCOMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: BALENILIA Release #1.0, Version #1.2 CURRENT APPLICATION NUMBER: US/09/944,411 FILING DATE: A1-SEP-2001

PRIOR APPLICATION NUMBER: US/09/944,411 FILING DATE: US/08/05/944,411 FILING DATE: US/08/05/944,411 FILING DATE: US/08/05/944,411 FILING DATE: US/08/05/944,411 FILING DATE: US/08/05/944,893 FILING DATE: US/08/05/944,893 FILING DATE: US/08/05/94/93 APPLICATION NUMBER: US/08/05/299 FILING DATE: 10-UN-1994 APPLICATION NUMBER: US/08/076,299 FILING DATE: 11-UN-1993 ATTORNEY/AGENT INFORMATION: NUMBER: 34,647 REFERENCE/DOCKET NUMBER: CELL 13.3 TELECOMMUNICATION INFORMATION: TREATH TREATH A15-358-9600 X131 TELEFAX: 415-349-7392 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: SELECT TYPE: amino acids TYPE: pamino acids TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-09-944-411-9 DESCRIPTION: SEQ ID NO: 9: US-09-944-411-9

US-09-944-411-9

LENGTH: 13 amino acids TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-09-944-411-9
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    RESULT 3
US-09-759-352-44
; Sequence 44, Application US/09759352
; Patent No. US20020111474A1
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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CORRESPONDENCE ADDRESS
ADDRESSEE: CELL GI
STREET: 322 LAKES
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                                                                                                                                                                                                                                                                                    41 STSGSGS 47
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                                                                                                                                                                                                                                                                                                                                                                              2.2%; Score 7; DB 10; ilarity 100.0%; Pred. No. 15; Conservative 0; Mismatches
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INVENTION: METHOD FOR PRODUCTION OF HIGH TITER

VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION

OF MAMMALIAN CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZSEBO, KRISZTINA M.
COOKE, KEEGAN
FARSON, DEBORAH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 13; .
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US-09-533-029-70
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; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-759-352-44
                                                                                                                                                                                                                                                                                                                      Query Match 2.:
Best Local Similarity 100
Matches 7; Conservative
                                                                                      GENERAL INFORMATION:
                                                                                                        Sequence 70, Application US/09533029 Publication No. US20030046723A1
APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: CAPON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/567,393
FILLING DATE: 01-DEC-1995
APPLICATION NUMBER: US 08/475,442
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/238,405
FILING DATE: 05-MAY-1994
APPLICATION NUMBER: US 07/988,194
FILING DATE: 09-DEC-1992
APPLICATION.NUMBER: US 07/627,643
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: WO PCT/US91/09431
FILING DATE: 12-DEC-1991
                                                                                                                                                                                                                                      2 STSGSGS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/759,352 FILING DATE: 16-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415)349-7392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVENTION: CHIMERIC CHAINS FOR RECEPTOR-ASSOCIATED SIGNAL TRANDUCTION PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROBERTS, MARGO R
ZSEBO, KRISZTINA
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100.0%; Pred. No. 15,
tive 0; Mismatches
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;, BRYAN A
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5. 15;
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Query Match
Best Local Similarity
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                                                                                          ORGANISM: Arabidopsis thaliana; FEATURE:
OTHER INFORMATION: G620
US-10-286-264-72
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; OTHER INFORMATION: G620
US-09-533-029-70
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                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 72
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Best Local :
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LENGTH: 208
                                                                                                                                                                                                                                                                     FILE REFERENCE: MBI-008
CURRENT APPLICATION NUMBER: US/10/286,264
CURRENT FILING DATE: 2002-11-01
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CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
                                                                                                                                                        LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/125,814 PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                  APPLICANT: Reuber, Lynne
APPLICANT: Pilgrim, Marsha
APPLICANT: Samaha, Raymond
TITLE OF INVENTION: POLYNUCLECTIDES FOR SEED TRAIT ALTERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
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314 YVDPLTV 320
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Ratcliffe, Oliver
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Zhang, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pineda, Omaira
Heard, Jacqueline
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Ratcliffe, Oliver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang, James
                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    James
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100.0%;
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                                        Score 7; u
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                              Mismatches
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                                         DB 9; Lei
5. 1.7e+02;
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o. 1.7e+02;
                                                          Length 208
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                            Indels
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105 YVDPLTV 111

RESULT 6 US-10-180-375-195 ; Sequence 195, A

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GENERAL INFORMATION:

APPLICANT: LEVINE, 'et al.

FILLE OF INVENTION: VARIANTS Of PROTEIN KINASES

FILLE REFERENCE: 802620-2005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 09/724,676

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 136776

PRIOR APPLICATION NUMBER: 136776

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12
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US-09-771-161A-109
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; NAME/KBY: misc_feature
; LOCATION:
; OTHER INFORMATION: gi 6552738
US-10-180-375-195
                                                                                                                                            ; TYPE: PRT; ORGANISM: Homo sapiens US-09-771-161A-109
                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TATCZYNEK!, Mitchell C.
APPLICANT: TATCZYNEK!, Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BB1458 US NA1
CURRENT APPLICATION NUMBER: US/10/180,375
CURRENT FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 222
SOFTWARE: Microsoft Office 97
SEQ ID NO 195
LENGTH: 208
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE.
                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0
SEQ ID NO 109
LENCTH: 213
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Patent No. US20020110811A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.2%; Score 7; DB 9; L
Best Local Similarity 100.0%; Pred. No. 1.7e+02
Matches 7; Conservative 0; Mismatches 0
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                                              h 2.2%; Score 7; DB 10; Le Similarity 100.0%; Pred. No. 1.7e+02; 7; Conservative 0; Mismatches 0;
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Cahoon, Rebecca E.
Famodu, Omolayo O.
Harvell, Leslie T.
Helentjaris, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oliveira, Igor Cunha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10180375
b. US20030126638A1
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e, Keith
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                                                                                             Length 213;
                                                    Indels
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTZ14C1

CURRENT APPLICATION NUMBER: US/10/125,540

CURRENT APPLICATION NUMBER: US/10/125,540

CURRENT EDILON NUMBER: See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 646

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 300

LENGTH: 251

TYPE: PRT

CORGANISM: Homo sapiens

US-10-125-540-300
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US-10-125-540-300
US-10-125-540-300
; Sequence 300, App
; Publication No. 1
; Publication No. 1
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US-10-156-761-14239
Sequence 14239, Application US/10156761
Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Homo sapiens US-09-764-870-300
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US-09-764-870-300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 300, Application US/09764870
Patent NO. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: FTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 300
LENGTH: 251
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                          167 KPTPTPP 173
                                                                                                                                                                                                                                                                                                       211 KPTPTPP 217
F: SHIBA, TADAYOSHI
F: SAKAKI, YOSHIYUKI
F: HATTORI, MASAHIRA
INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10125540 to. US20030059875A1
                                                                            ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                          , SATOSHI
                                                                                                                      HARUO
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; Pred. No. 2e
0; Mismatches
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SEQ ID NO 14239
LENGTH: 343
TYPE: PRT
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Best Local Similarity
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Best Local Similarity
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Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09943671
Patent No. US20020106733A1
                            APPLICANT: IKEDÀ, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHTBA, TADAYOSHI
APPLICANT: SHTBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/943,671
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/232,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
CURRENT APPLICATION NUMBER: US/10/156,761
                                                                                                                                                              APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-10-14
APPLICATION NUMBER: 60/093,491
FILING DATE: 1998-07-20
APPLICATION NUMBER: 60/110,941
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                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                              186 TEAPFAT 192
                                                                                                                                                                                                                                                                                                            145 TEAPFAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 GTATVAG 221
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                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
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No. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptomyces avermitilis US-10-156-761-8098
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Best Local Similarity luv.
Thes 7; Conservative
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Best Local Similarity lou.
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8098
LENGTH: 375
                                                                                                                                                                                                                Sequence 212, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 13366
LENGTH: 490
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Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                               GENERAL
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEC_ID NOS: 15109
     APPLICANT: Frey, Gerhard
APPLICANT: Short, Jay M.
APPLICANT: Mathur, Eric J.
APPLICANT: Gray, Kevin A.
APPLICANT: Kerovuo, Janne S.
APPLICANT: Slupska, Malgorzata
TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
TITLE OF INVENTION: AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                          ENERAL INFORMATION:
APPLICANT: Callen, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
'ILE REFERENCE: 09010-108001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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PPLICANT: HATTORI, MASAHIRA
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                              179 APVAPPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 GTATVAG 182
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                                                                                                                                                       Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                 Application US/10081872
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100.0%; Pred. No. 2.8
rative 0; Mismatches
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100.0%; Pred. No. 3.
1ve 0; Mismatches
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No. 3.6e+02;
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APPLICANT: LEVINE, et al.
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS Of PROTEIN KINASES
FILE REFERENCE: 802620-2005 1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 13676
PRIOR APPLICATION NUMBER: 13679
PRIOR APPLICATION NUMBER: 13679
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
SEQ ID NO 200
LENGTH: 505
TYPE: PRT
COCCANISM: Homo sapiens
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CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,495
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,496
PRIOR FILING DATE: 2001-02-21
PRIOR PRIOR APPLICATION NUMBER: US 60/291,122
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 321
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 212
LENGTH: 496
TYPER: DET
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US-09-771-161A-200
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Matches 7; Conserva
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                                                                                                                                                                                                                                                                                                    RESULT 16
US-09-903-068-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-771-161A-200
                                                                                                                                                                                                                              Sequence 8, Application US/09903068
Patent No. US20020123139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Query Match
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0;
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Patent No. US20020110811A1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                    APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
Having Serine Threonine Kinase Domains And Their Use
                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 NNLNSSY 173
                                                                                                                                                                                                                                                                                                                                                                                                   187 STSGSGS 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                         41 STSGSGS 47
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US-09-903-068-16
; Sequence 16, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 7; Conservative (
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHA:: (212) 688-9200
TELEPHA:: (212) 688-9201
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEX: LIPY
CORRATING SYSTEM: PC-DOS
SOFTWARE: WOrdperfect
CURRENT APPLICATION NUMBER: US/99/903,068
FILING DATE: 11-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/679,187
FILING DATE: 11-NO. US20020123139A1ember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 11-NO. US20020123139A1ember-1993
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 931047.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 3-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 15-OCCOBET-1993
APPLICATION NUMBER: 9313763.7
FILING DATE: 15-OCCOBET-1993
APPLICATION NUMBER: 9313763.7
APPLICATION NUMBER: 9313763.7
FILING DATE: 15-OCCOBET-1993
APPLICATION NUMBER: 9313763.7
APPLICATION NUMBER: 9313763.7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin,
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteir
Having Serine Threonine Kinase Domair
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS
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; Pred. No. 3.'
0; Mismatches
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                                                                 360 kb storage
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US-09-874-628-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-May-1933
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOhlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%; Pred. No. 3. nes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                               ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                        APPLICANT: WOZNEY, John
CELESTE, Anthony J.
THIES, R. Scott
YAMAJI, No. USZ0020137133Aloru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                      CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 ŚTŚĠŚĠŚ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 STSGSGS 47
                                                                                                                                                                             CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/903,068 FILING DATE: 11-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/679,187
FILING DATE: «Unknown»
APPLICATION NUMBER: PCT/GB93/02367
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. US20020123139Alember-1993
APPLICATION NUMBER: US/09/874,628
                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                ADDRESSEE: Genetics Institute Inc.- Legal Affairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)
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FILING DATE: 17-No. US2002012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICATION NUMBER: 9304680.3 ILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLICATION NUMBER: 9304677.9

CLING DATE: 8-March-1007
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RESULT 20
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                                                                                                                                                         Query Match
Best Local :
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US-09-738-626-5890
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                                                                                                                                                                                                            SOFTWARE: PatentIn ver. SEQ ID NO 5890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5890, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                    LENGTH: 806
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
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APPLICATION NUMBER: 08/123,934
FILING DATE: 17-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617 876 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                 230 WFSGRDG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 STSGSGS 193
631 WFSGRDG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 505 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617 876 5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIZOGUCHI, HIROSHI
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Conservative
                                                                    Conservative
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                                                                  Score 7; DB 9
;; Pred. No. 5.5
0; Mismatches
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Pred. No.
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b. 3.7e+02;
                                                                                     DB 9; Le
                                                                                                  Length 806;
                                                                    0; Indels
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US-09-978-303-25

quence 25, Application US/09978303 blication No. US20030049728A1

INFORMATION:

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GENERAL INFORMATION: David J.

APPLICANT: Ullius, David J.

APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthony J.

TILE OF INVENTION: Nucleic acid sequences encoding TITLE OF INVENTION: capsaicin receptor and capsaicin ? TITLE OF INVENTION: capsaicin receptor and capsaicin ? TITLE OF INVENTION: polypeptides and uses thereof FILE REFERENCE: UCALO84CON

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/235,451

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 60/072,161

PRIOR APPLICATION NUMBER: 60/072,161

PRIOR APPLICATION NUMBER: 60/072,161

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 60/072,151

PRIOR APPLICATION NUMBER: 60/072,161

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PRIOR APPLICATION NUMBER: 60/072,161

PRIOR APPLICATION
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/278,173
; CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1090-03-23
PRIOR FILING DATE: 1099-03-23
PRIOR FILING DATE: 1099-03-23
NUMBER OF SEQ ID NOS: 177
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 128
LENGTH: 1336
                                                                       ; FEATURE:
; OTHER INFORMATION: G987
US-10-278-173-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
Query Match
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TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jiang, Cai-Zhong
APPLICANT: Broun, Pierre
                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICANT: Samaha, Raymond
B OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
REFERENCE: MBI-009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692 TVSKIAO 698
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Pineda, Omaira
Zhang, James
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b. US20030061637A1
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lgrim, Marsha
ddie, James
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larity 100.0%;
Conservative
    2.2%;
Score 7;
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No. 5.7e+02;
smatches 0;
DB 9;
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Length 1336;
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RESULT 22
US-09-934-455-22
Sequence 22, Application US/09934455
Sequence No. US20030121070A1
                                                                                                                                                                                                                                                                                                                                            RESULT 23
US-09-815-242-12713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arabidopsis thaliana US-09-934-455-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR PPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 1336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                  APPLICANT: Yamamoto, Robert T.
APPLICANT: Yau, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
TILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                              BENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith /
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QVITDSQ 67
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INVENTION: Genes for Modifying Plant Traits IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%; 7; Conservative
                                                                                                                                                                                             Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
CATION NUMBER: 60/206,848
                                                                                                                                                         Carr, Grant J.
Vamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heard, Jacqueline
Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                         Application US/09815242
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iffe, Oliver
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mann, Jose Luis
                                                                                                                                                                                                                                                                                                          061569A1
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   Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; L. No. 8.5e+02;
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FILING DATE:

2000-05-23

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; ORGANISM: Mycobacterium bovis
US-09-870-759-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-712-363-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
RUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 114
LENGTH: 2796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12713
LENGTH: 2344
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 246, Application US/09712363
Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-870-759-114
                               APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
APPLICANT: MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCOTTEN MARCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 870759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 IHIKDAQ 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09870759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; --
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60/179,531
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Pred. No.
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No. 1.4e+03;
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o. 1.6e+03;
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Query Match
Best Local Similarity
Matches 7; Conserva
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US-09-956-086-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09956086 Patent No. US20020155498A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 246
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIOR APPLICATION NUMBER: 60/134,093
RIOR FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/165,124
FILING DATE: 1999-11-12
APPLICATION NUMBER: 60/165,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-02-01
APPLICATION NUMBER: 60/117,844
FILING DATE: 1999-01-29
                                  APPLICATION NUMBER: US 60/044,449 FILING DATE: 30-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
APPLICATION NUMBER: US 60/063,074
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-0CT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/134,092 FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/126,593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FILPULA, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 IHIKDAQ 278
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                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/956,086 FILING DATE: 20-Sep-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WASHINGTON
REGISTRATION NUMBER: 40,679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WANG, MAOLIANG SHORR, ROBERT
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lo. 1.8e+03;
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STRANDEDNESS: single
; TOPOLOGY: No. US20020155498A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-956-086-7
PATECH TO. USZŐÖZ0157120A1

PATECHT NO. USZŐÖZ0157120A1

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Tsien, Roger Y.

APPLICANT: Baird, Geoffrey

TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS

FILE REFERENCE: REGEN1470-1

CURRENT APPLICATION UNMBER: US/09/99,745

CURRENT FILING DATE: 2001-10-23

PRIOR APPLICATION NUMBER: 09/316,920

PRIOR APPLICATION NUMBER: 09/316,920

PRIOR FILING DATE: 1999-05-21

NUMBER OF SEO ID NOS: 67

SOFTWARE: PatentIn version 3.0
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US-09-999-745-60
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US-09-999-745-58
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Best Local S
Matches 6
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Best Local Similarity 100.0%; Pred. No. 1.3e+02
Matches 6; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                 Sequence 60, Application US/09999745
Patent No. US20020157120A1
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ENERAL INFORMATION:
ENERAL INFORMATION:
ENERAL INFORMATION:
ENERAL INFORMATION:
OF THE UNIVERSITY OF CALIFORNIA
APPLICANT:
TSien, Roger Y.
APPLICANT:
Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR FILING DATE: 1999-05-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 14
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58, ADP1110A1
0. US20020157120A1
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (20
TELEFAX: (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09999745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.9%; Score 6; DB 9; Le llarity 100.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09956087 Patent No. US20020161201A1 GENERAL INFORMATION:
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Best Local
Query Match
Best Local Similarity
                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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APPLICATION NOMBER: 09/069,821

FILING DATE: 1998-04-30

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-0CT-1997

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U.

REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9%;
Local Similarity 100.0%;
es 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: CUNKNOWN>
                                                                             STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
.
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHORR, ROBERT WHITLOW, MARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILPULA, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WANG, MAOLIANG SHORR, ROBERT
  1.9%; Score 6; DB 9; Le 100.0%; Pred. No. 1.3e+02;
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Pred. No.
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                  Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 44, Application U Patent No. US20020165364A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/09/554,000
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
NUMBER: 0F SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 42
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Patent No. US20020165364A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OP INVENTION: PLUORESCENT PROTEIN SENSORS FOR
TITLE OP INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/554,000 CURRENT FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION:
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TYPE: PRT
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                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                            Local Similarity
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                                                                                                           1.9%; Score 6; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                            Length 14;
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                                                                                                                                                                 RESULT 34
US-10-158-238-9
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US-09-792-793A-4
                                                                                                     Sequence 9, Application US/10158238
Publication No. US20030040604A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
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Matches 6; Conser
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                 APPLICANT: Immunex Corporation
APPLICANT: Dirk, Anderson M.
APPLICANT: Marken, John S.
TITLE OF INVENTION: SIGLEC-12 POLYPEPTIDES,
FILE REFERENCE: 3290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER
TITLE OF INVENTION: OTHER
TITLE OF INVENTION: OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
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APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
CURRENT APPLICATION NUMBER: US/10/158,238
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: peptide linker for use in conjugates
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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US20020168370A1
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100.0%; Pred. No. 1.3e+02;
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100.0%; Pred. No.
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                                    POLYNUCLEOTIDES,
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                                    AND METHODS OF USE THERE
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Sequence 3, Application US/10247279

Publication No. US20030086928A1

GENERAL INFORMATION:
APPLICANT: WONTHINY, MARC
APPLICANT: WONTHINY, MARC
ITILE OF INVENTION: COMPOSITIONS ASSOCIATED WITH COMPLEX
TITLE OF INVENTION: FORMATION AND METHODS OF USE THEREOF
FILE REFERENCE: SALKINS.036CP1
CURRENT APPLICATION NUMBER: US/10/247,279
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/190,705
PRIOR APPLICATION NUMBER: 60/190,705
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
LENGTH: 14
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US-10-247-279-3
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US-10-052-942-6
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; OTHER INFORMATION: Linker
US-10-247-279-3
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/294,199
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 14
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Best Local S
Matches 6
                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Zaudezer, Maurice
APPLICANT: Smith, Ernest
APPLICANT: Wei, Chungwen
TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in
FILE REFERENCE: 1821.0090004
CURRENT APPLICATION NUMBER: US/10/052,942
CURRENT FILING DATE: 2002-01-23
RRIOR APPLICATION NUMBER: 60/298,095
PRIOR APPLICATION NUMBER: 60/291,422
PRIOR APPLICATION NUMBER: 60/271,422
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ORGANISM: Artificial Sequence
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CURRENT APPLICATION UNMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: US 60/203,347
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/742,454
PRIOR APPLICATION NUMBER: US 09/742,454
PRIOR APPLICATION NUMBER: US 09/742,454
PRIOR APPLICATION NUMBER: US 09/742,454
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 13
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PRIOR FILING DATE: 2001-01-24
; PRIOR FILING DATE: 2001-01-23
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 6
; SEQ ID NO 6
; LENGTH: 14
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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Linker Moiety
US-09-883-777-13
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US-09-987-456-11
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Best Local Similarity
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GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: University of Rochester
APPLICANT: Zauderer, Maurice
APPLICANT: Ernest S. Smith
TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
FILE REFERENCE: 1821.0070004
CURRENT APPLICATION UNMEER: US/09/987,456
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                   Sequence 11, Application US/09987456 Patent No. US20020123057A1
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TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
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APPLICATION NUMBER: 60/271,424 FILING DATE: 2001-02-27

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RESULT 40
US-09-883-777-15
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US-09-883-777-14
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; TYPE: PRT
; CRGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker peptide
US-09-987-456-11
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PRIOR FILING DATE: 1999-12-20
PRIOR PPLICATION NUMBER: US 60/203,347
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: PCT/US00/34755
PRIOR APPLICATION NUMBER: PCT/US00/34755
PRIOR PILING DATE: 2000-12-19
PRIOR PPLICATION NUMBER: US 09/742,454
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
                   Sequence 15, Application US/09883777
Patent No. US20020110853A1
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
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Best Local Similarity 100.0%; P
Matches 6; Conservative 0;
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0;
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SEQ ID NO 11
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CURRENT FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
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PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/249,268
PRIOR FILING DATE: 2000-11-17
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URRENT APPLICATION NUMBER: US/09/883,777
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16
TYPE: PRT
ORGANISM: Artificial sequence
PEATURE:
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US20020110853A1
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CURRENT FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: US 60/172,878

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR APPLICATION NUMBER: US 60/203,347

PRIOR APPLICATION NUMBER: US 99/742,454

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGTH: 16

TYPE: PRI
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Linker Moiety

US-09-883-777-15

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels

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RESULT 1
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Conserved hypothetical protein ykuD - Bacillus subtilis
C.Species: Bacillus subtilis
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R.; Kunst, F.; Ogassawara, N.; Moszer, Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A.; Brunch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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hypothetical protein BH3888 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (c;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: H84135
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H84135
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A;Residues: 1-164 <KUN>
A;Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13277.1; PID:e1184994;
A;Experimental source: strain 168
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%; Pred. No. 5.5
0; Mismatches
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F7161701
AE01701
AE01701
F70559
D95247
A98112
A96955
AC11644
S301164
S301164
S301164
C63349
D713349
D713308
D81236
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5 2
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threonine ammonia-
L1 protein (altern
hypothetical prote
NADH2 dehydrogenas
flagellar M.ring p
hypothetical prote
hypothetical protein
excinuclease ABC c
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hypothetical prote
probable transport
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RESULT 4
T52340
Cell wall-plasma membrane linker protein homolog [imported] - Arabidopsis thaliana (c)Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C;Accession: T52340
R;Goo, J.H.; Park, A.R.; Park, W.J.; Park, O.K.
Plant Mol. Biol. 41, 415-423, 199
A;Title: Selection of Arabidopsis genes encoding secreted and plasma membrane protein Seference number: Z25437; MUID:2064977; PMID:10598107
A;Accession: T52340
A;Accession: T52340
A;Accession: T52340
A;Accession: T52340
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A;Accession: T52340
                                                                                                                                               A;Cross-references:
C;Genetics:
A;Note: CWLP
                                                                                                                                                                                                                                           A; Molecule type: r
A; Residues: 1-306
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submitted to the EMBL Data Library, November 1994
A;Description: The sequence of S. cerevisiae cosmid 8003
A;Reference number: S50366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: MIPS:YLR301W
A;Gene: MIPS:YLR301W
A;Cross-references: SGD:S0004292
A;Map position: 12R
C;Superfamily: Saccharomyces cerv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: The sequence of S. Cerevisiae cosmid 8003.
A;Reference number: S50366
A;Accession: S50385
A;Molecule type: DNA
A;Residues: 1-244 <PAU>
A;Cross-references: EMBL:U17243; NID:g596030; PIDN:AAB67346.1;
C;Genetics:
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S50385

Sypothetical protein YLR301w - yeast (Saccharomyces cerevisiae)
hypothetical protein L8003.2

C/Species: Saccharomyces cerevisiae
C/Species: Saccharomyces cerevisiae
C/Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and caracterium and caracterium sequence of the alkaliphilic bacterium bacillus halodurans and caracterium sequence of the alkaliphilic bacterium bacillus halodurans and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium sequence and caracterium 
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Query Match 2.5%; S
Best Local Similarity 100.0%;
Matches 8; Conservative 0;
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Best Local S
Matches 8
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Best Local S
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8; Conserv
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8; Conservative
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ilarity 100.0%;
Conservative
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   Score 8; DB 2;
Pred. No. 9.4;
0; Mismatches
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0; Mismatches
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Indels

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Gaps

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A;Residues: 820-960 (20.271519)
A;Cross-references: EMBL:Z71519
A;Cross-references: EMBL:Z71519
A;Experimental source: strain S288C
R;Holtzman, D.A.; Yang, S.; Drubin, D.G.
J. Cell Biol. 122, 635-644, 1993
J. Cell Biol. 122, 635-644, 1993
A;Title: Synthetic-lethal interactions identify two novel
A;Title: Synthetic-lethal interactions identify two novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Saccharomyces cerevisiae C;Date: 27-Apr-1996 #sequence revision 03-Way-1996 #text_change 29-Oct-1999 C;Accession: S63211; S63209; B40673; S61932; S64652; S67355; S72073; S36354; S42278 R;Saiz, J.E.; Baladron, V.; Del Rey, F. submitted to the Protein Sequence Database, April 1996
                                                                                A;Cross-references: GB.222811; NID:g311412; PIDN:CAA80464.1; R;Yoon, H.; Donahue, T.F. submitted to the EMBL Data Library, March 1994 A;Description: DNA sequence of ufg1 gene in yeast. A;Reference number: S61932 A;Accession: S61932
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                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-343, 'A', 345-968 < HOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 820-968 < PAN>
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R;Experimental source: strain S288C
R;Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G.
submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytoskeleton assembly control protein SLA2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: MOP2 protein; protein N1102; protein YNL243w; UFG1 protein
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F;1-27/Domain: signal sequence #status predicted <SIG>F;1-27/Domain: signal sequence #status predicted <SIG>F;28-376/Product: probable cell wall-plasma membrane linker protein
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A; Residues: 1-968 <SAI>
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type: DNA
: 327-343,'A',345-559,'R',561-886,'NTVP',891,'MLPMHAEVWVTTSW',904 <YOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%;
8; Conservative (
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Pred. N
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                                                                                      Matches
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86885
                                                                                                                                                                                                                                                                                                                                                                                                                     50S ribosomal protein L24 [imported] - Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: H86885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yeast 12, 1071-1076, 1996
A;Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals
A;Reference number: $72073; MUID:97051596; PMID:8896273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: the nucleotide sequence was submitted to the EMB: R;Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G. submitted to the EMBL Data Library, February 1996 A;Description: DNA sequence of cosmid 14-5 from chromoso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Nolecule type: DNA
A; Nolecule type: DNA
A; Residues: 1-51,'A',53-343,'A',345-968 <NAS>
A; Residues: 1-51,'A',53-343,'A',345-968 <NAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: transmembrane protein F;771-787/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Pandolfo, D.; de Antoni, A.;
Yeast 12, 1071-1076, 1996
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A; Residues: 820-968 < PAW>
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J. Biol. Chem. 270, 6815-6823, 1995
A;Tille: MCD2 (SLA2) affects the abundance of the plasma membrane
A;Reference number: S64652; MUID:95204480; PMID:7896828
                                                                                                C; Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                           A; Experimental source: strain
                                                                                                                                                                                                                            A;Residues:
                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 11,
                                                                                                                                                                                                                                                                                                                                                                                              R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CAA93355.1; PID:e221951; PID:g1183971
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CAA93355.1; PID:e221951; PID:g1183971
R;Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: DNA sequence A; Reference number: S67355
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A;Experimental source: strain 117-8A
                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                           ;Cross-references: GB:AE005176; PID:g12725141; PIDN:AAK06186.1; 
;Experimental source: strain IL1403
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                                              Query Match
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Residues: 820-968 <PAF>
                         Local
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Similarity 7; Conserv
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8; Conserv
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                       2.2%;
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                       Score 7;
; Pred. No
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5. 26;
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279 VKTGDTV 285

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A; Map position: 1L
C; Genetics: <RP2>
A; Gene: SPCC1322.11
A; Map position: 3
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N;Alternate names: 60s ribosomal protein
C;Species: Schizosaccharomyces pombe
C;Date: 16.Jul-1999 #seguence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T11639; T40942
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submitted to the EMBL Data Library, August 1994
A;Reference number: $47445
A;Accession: $69849
A;Molecule type: DNA
A;Residues: 1-115 <BAR>
A;Residues: 1-115 <BAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL021046
R;Lucas, M.; Gaillardin, C.; Lyne, M.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, January 1999
A;Reference number: Z21959
A;Recession: T40942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: 217304
A;Accession: T11639
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-139 <WOO>
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C; Superfamily: Sacci
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R;Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
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A;Residues: 1-139 <LUC>
A;Residues: 1-139 <LUC>
A;Cross-references: EMBL:AL035259; PIDN:CAA22864.1; GSPDB:GN00068; SPDB:SPCC1322.
A;Experimental source: strain 972h-; cosmid c1322
                                                                                                                                                                        ;Superfamily: Escherichia coli ribosomal protein
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Best Local :
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                                                                                     Matches
                                                                                                     Query Match
Best Local
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132 ASNAGTV 138
                                         241 ASNAGTV 247
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                                                                                   Similarity 7; Conserv
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                                                                             2.2%; Score 7; DB 2; ilarity 100.0%; Pred. No. 46; Conservative 0; Mismatches
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Pred. No.
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RESULT

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-141 <DUZ>
A;Cross-references: EMBL:U80445; PIDN:AAB37800.1; GSPDB:GN00019; CESP:C50F2.7
A;Experimental source: strain Bristol N2; Clone C50F2
C;Genetics:
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A;Map position: 1
A;Introns: 19/3; 106/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C50F2.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Datc: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T25781 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 R;Du, Z:; Le, T:T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBI/DDBJ
A;Molecule type: DNA
A;Residues: 1-161 <WIL>
A;Cross-references: EMBL:AL117202; PIDN:CAB55080.1; CESP:Y47D3A.20
A;Experimental source: clone Y47D3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: CESP:Y47D3A.20
A;Introns: 42/1; 55/1; 83/2; 122/1
C;Superfamily: Caenorhabditis elegans hypothetical
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Ribmitted to the EMBL Data Library, October 1999
A;Reference number: Z21043
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Aug-2000
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                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z20319
A; Accession: T27153
                                                                                                                                                                                        hypothetical protein Y5482A.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T27153
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A;Cross-references: EMBL:AL032646; PIDN:CAA21686.1; GSPDB:GN00019; CESP:Y54E2A.4
A;Experimental source: clone Y54E2A
                                          A; Molecule type: DNA
A; Residues: 1-177 <WIL>
                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 46;
0; Mismatches
                                                                                                                                                  October 1998
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46;
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A; Cross references: GB: U23797; NID:g1143815; PIDN:AAC44000.1; PID:g1143817
A; Cross references: GB: U23797; NID:g1143815; PIDN:AAC44000.1; PID:g1143817
C: Bron, S: Brouillet, S: Bruschi, C.V; Caldwell, B.; Capuano, V; Carter, N.M.; Chd A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Mature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueely, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteteller Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sakowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein YPO1754 [imported] - vers C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: YPO1754
C; Superfamily:
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A; Introns: 13/1; 86/3
                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Identification of a membrane protein involved in A;Reference number: JC6024; MUID:96165276; PMID:8576055 A;Accession: JC6024
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A; Residues: 1-189 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-198 < DAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinB sporulation signaling pathway activator kbaA - N;Alternate names: integral membrane protein kbaA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413, 523-527, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Bacillus subtilis;
Date: 31-Dec-1996 #sequence_revision 31-Dec-1996;
Accession: JC6024; F69647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: YP01754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AL590842; PIDN:CAC90573.1; PID:g15979781; GSPDB:GN00175
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Bacteriol. 178, 1178-1186,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.; Rutherford, K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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Simmonds, M.; Skelton, J.;
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Stevens, K.; Whitehead, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change 09-Nov-2001
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                                                                              Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65003
                                                                                                                                                                                  R;Blattner, F.R.; Plunkett III, A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                        RESULT
XMECDD
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                                  A;Status: preliminary; nucleic acid sequence not A;Molecule type: DNA
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type: DNA : 1-211 <BLAT>

shown; translation

not

shown

K-12

Escherichia coli (strain K-12)

Plunkett III,

G.; Bloch, C.A.; Perna, N.T.; Y.

Burland, V.; Riley,

3

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; ansen, N.F.; Hughes, B.; Huizar, L.

Rature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.C.; Li, J.H.; Li, Y.; Lin, X. D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of Chmosoome 1 of the plant Arab A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G86352
protein T26F17.20 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C:Nate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; A;Experimental source: strain 168 C;Comment: This protein is an intrinsic membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: kbaA
C;Keywords: membrane protein
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                                                                                                                                                       A;Map
                                                                                                                                                                                                                  A;Cross-references:
                                                                                                                                                                                                                                       A;Residues:
                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
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105
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                                      314 YVDPLTV 320
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ALTAGAX
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111
                                                                                              2.2%;
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Pred. No.
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Pred. No.
                                                                             Mismatches
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5. 65;
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Conway, A.R.; C
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8
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.S.; Maiti, R.;
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conserved hypothetical protein AF0441 - Archaeoglobus fulgidus
(;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: A69305
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Reference number: A69305
A;Recession: A69305
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A;Experimental source: strain K-12, substrain MG1655
R;Nomet, M.L.; Marvel, C.C.; Tolan, D.R.
J. Biol. Chem. 262, 12209-12217, 1987
A;Title: The hisT purf region of the Escherichia coli K-12 chromosome.
A;Reference number: A29803; MUID:87308226; PMID:3040734
A;Accession: E29803
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C; Superfamily: dedD pr
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A;Residues: 'V',2-211 <NON>
C;Comment: This protein is encoded
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A;Experimental source: strain A3(2)
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Best Local S
Matches 7
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;Residues: 1-225 <K
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;Residues: 1-211 <SEE>
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                                                                                                                                                                                     preliminary; nucleic acid sequence not shown; translation
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       Similarity
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                                                                                              GB:AE001074;
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       2.2%;
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                                                                                          GB:AE000782; NID:g2689397; PIDN:AAB90793.1; PID:g26501
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       Score 7;
Pred. No.
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5. 66;
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RESULT 21
C84340
ABC transport protein [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-3001 #text_change 02-Feb-3001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-3001 #text_change 02-Feb-3001
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C;Date: 02-Feb-3001 #sequence_revision 02-Feb-3001 #text_change 02-Feb-3001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-3001 #text_change 02-Feb-3001
C;Date: 02-Feb-3001 #sequence_revision 02-Feb-3001 #text_change 02-Feb-3001
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RESULT 19
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C;Decies: Methanobacterium thermoformicicum plasmid pFV1
C;Species: Methanobacterium thermoformicicum plasmid pFV1
C;Species: Methanobacterium thermoformicicum
C;Date: 17-Apr-193 #sequence_revision 17-Apr-193 #text_change 22-Oct-1999
C;Accession: $30305; $26440
R.Nocelling, J.; van Beden, F.J.M.; Eggen, R.I.L.; de Vos, W.M.
Nucleic Acids Res. 20, 6501-6507, 1992
Nucleic Acids Res. 20, 6501-6507, 1992
A;Title: Modular organization of related Archaeal plasmids encoding different restriction
A;Reference number: $30302; MUID: 93126090; PMID: 1336177
A;Accession: $30305
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Recession: H82435
                                                                                                                                                       A;Gene: VCAU634
A;Map position: 2
                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-241 <HEI>
A;Cross-references: GB:AE004393;
A;Experimental source: serogroup
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein VCA0634 [imported] - Vibrio cholerae (strain N16961 serogate; Vibrio cholerae (c;Species: Vibrio cholerae (c;Species: Vibrio cholerae (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 c;Accession: H82435
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A;Molecule type: DNA
A;Residues: 1-227 <NOE>
A;Residues: 1-227 <NOE>
A;Residues: 1-227 <NOE>
A;Residues: 1-227 <NOE>
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                                                                                                   Score 7;
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Pred. No. 70
0; Mismatches
                                                                                  ore 7; DB 2; red. No. 74; Mismatches
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I.; Sellers, P
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D.; Lasky, S D.G.; Jablor

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R;anonymous, The C. elegans Sequencily Collection.

R;anonymous, The C. elegans Sequencily Collection.

R;anonymous, The C. elegans Sequence 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Rote: mebsites genome.wistl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and www
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Recession: C70151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 10-Ma
C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein F55A4.4 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein BB0412 -
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A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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ACCESSION: C70151

Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, Fraser, C.M.; Casjens, S.; Hanson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, D.; Horst, K.; Roberts, K.; Hat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ypothetical protein BB0412 - Lyme disease spirochete
;Species: Borrelia burgdorferi (Lyme disease spirochete)
;Jate: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
                                                                                         Gene: F55A4.4
                                                                                                                                                Cross-references:
                                                                                                                                                                                                     Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-259 <KLE>
Cross-references: GB:AE001146; GB:AE000783; NID:g2688312; PIDN:AAC66791.1; PID:g26883:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
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   Query Match
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                                                                                                                                    1-269 <STO>
erences: GB:chr_X;
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   . 28 ;
                                                                                                                                          PIDN:AAB07562.1; PID:g1519659; GSPDB:GN00028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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   Score
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   7;
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o. 79;
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   269;
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C;Species: Methanobacterium C;Date: 05-Dec-1997 #sequenc C;Accession: D69184
                                                                                  RESULT 26
D69184
UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) MTH634 [similarity]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; y, P.; Sun, P.M.; Winkler, M.E.
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J. Bacteriol. 183, 5
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C;Superfamily: maltose transport protein malG
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C;Genetics:
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A;Status: prelimina
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: H98073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ABC-MSP [imported] - C;Species: Streptococcus pneumoniae
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N;Alternate names: hypothetical prot
C;Species: Saccharomyces cerevisiae
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A; Residues: 1-283 < ROS>
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C;Accession: S57134
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Best Local S
Matches 7
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Matches
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                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 VDPLTVL 321
                                                                                                                                                                                                                                                                                                               254 MDGASIV 260
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                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                    MDGASIV 187
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                       #sequence_revision 05-Dec-1997 #text_change
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           DB . 86;
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ki, S.; Church, G.N J. Bacteriol. 179, A; Title: Complete (

R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, urch, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. ol. 179, 7135-7155, 1997

Б. И.,

D.R.;

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C;Accession: 528264
R;Raz, R.; Jose, M.; Moya, A.; Martinez-Izquierdo, J.A.; Puigdomenech, P.
Mol. Gen. Genet. 233, 252-259, 1992
A;Title: Different mechanisms generating sequence variability are revealed in distinct A;Recession: 528264
A;Accession: 528264
A;Molecule type: DNA
A;Residues: 1-303 <RAZ>
A;Cross-references: EMBL:x63134; NID:g22332; PIDN:CAA44844.1; PID:g22333
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                       hydroxyproline-rich glycoprotein - maize
C;Species: Zea mays (maize)
C;Date: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 24-Sep-1999
C;Accession: S28264
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JH0204
hypothetical 30.5K protein precursor - Enterococcus faecalis plasmid pAM-beta-1
C;Species: Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Species: Interococcus faecalis
C;Accession: JH0204
R;Swinfield, T.J.; Oultram, J.D.; Thompson, D.E.; Brehm, J.K.; Minton, N.P.
A;Title: Physical characterisation of the replication region of the Streptococcus {
A;Reference number: PH0201, MUID:90236302; PMID:2110101
A;Accession: JH0204
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C;Superfamily: probable pheromone-responsive protein
C;Keywords: plasmid replication
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-288/Product: hypothetical 30.5K protein #status pr
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Best Local Similarity 100.0%; Pred. No.

Matches 7; Conservative 0; Mismatc.
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C;Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
C;Keywords: nucleotidyltransferase
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A;Experimental source: strain Delta H
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A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatc
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Residues: 1-285 <MTH>
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5.86;
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hypothetical protein Y44A6B.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                   RESULT
T26886
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Best Local
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A;Map position: I
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AE3325
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                                                                                                                                                                                                                                                                                               256 GASIVIQ 262
                                                                                                                                                                                                                                                               290 GASIVIQ 296
                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
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RESULT 30

GR4936

Kinase [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: G84936
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: G8493
                                                                                                                   ;Status: preliminary
;Molecule type: DNA
;Residues: 1-315 <STO>
;Cross-references: GB:AP000398; GSPDB:GN00144
;Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Nolecule type: DNA
A;Residuse: 1-309 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51768.1; PID:g17982509;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commi, competence lipoprotein [imported] - Brucella melitensis (strain 16M)
C;Bpcies: Brucella melitensis
C;Accession: AE3325
R,DelVecchio, V.G; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melite;
A;Accession: AB3325
A;Screen. AB3252; PMID:1175688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 KPTPTPP 173
         2.2%; Score 7; DB ; ilarity 100.0%; Pred. No. 94; Conservative 0; Mismatches
                              DB 2;
o. 94;
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o. 91;
                                               Length 315;
    0; Indels
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    0;
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Gaps
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0;
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R;Stiefel, V.; Ruiz-Avila, L.; Raz, R.; Valles, M.P.; Gomez, Plant Cell 2, 785-793, 1990
A;Tille: Expression of a maize cell wall hydroxyproline-rich A;Reference number: JQ0985; MUID:93005673; PMID:2152127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ś
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A;Reference number: Z20280
A;Accession: T26886
                                A;Cross-references: EMBL:AL031966; PIDN:CAA21450.1; GSPDB:GN00068; SPDB:SPCC1442.16c
                                                                                                                                                                                 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, submitted to the EMBL Data Library, October 1998
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A; Residues: 1-326 <WIL>
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R;Ainscough, R.
                                                                              A; Residues: 1-329 <LYN>
                                                                                                  A; Molecule type: DNA
                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                      A; Accession: T40981
                                                                                                                                                         A; Reference number: Z21961
                                                                                                                                                                                                                                                                                   probable quinone oxidoreductase - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                             T40981
                                                                                                                                                                                                                                                                                                                              RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:S45164; NID:g257040; PIDN:AAB23539.1; PID:g257041
A;Accession: PS0215
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Matches
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Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
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Residues: 1-328 <STI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Zea mays (maize)
Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Sep-1999
Accession: JQ0985; PS0215
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les 7; Conserv
SPCC285.01c; SPDB:SPCC1442.16c
                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
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                                                                                                                                                                               Library,
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Mismatches
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5. 97;
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3. 97;
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RESULT 35
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A;Cross-references: EMBL:D26185; NID:g467326; PIDN:BAA05224.1; PID:d1005766; PID:g467378
A;Cross-references: EMBL:D26185; NID:g467326; DIDN:BAA05224.1; PID:d1005766; PID:g467378
A;Cores the nucleotide sequence was submitted to the EMBL Data Library, December 1993
R;Kunst, F; Ogasawara, N; Moszer; I; Albertini, A.M.; Alloni, G; Azevedo, V; Berterc
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chool
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.,
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Stabber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
R; Geger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Vamamoto, H.; Vamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
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C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I40448; S66018; C70084; S18084
                                                                                                                                                                                                                                                                A;Gene: yyaD
A;Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrome A;Reference number: S65967; MUID:96051385; PMID:7584024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X62539; NID:g40020; PIDN:CAA44412.1; PID:g580907 R;Ogasawara, N.; Nakai, S.; Yoshikawa, H. DNA Res. 1, 1-14, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol. 6, 629-634, 1992
A;Title: Genes and their organization in the replication
A;Reference number: I40435; MUID:92204018; PMID:1552862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: I40448; S66018; (R; Ogasawara, N.; Yoshikawa, H
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-338 <KUN>
A;Cross-references: GB:299124; GB:AL009126; NID:g2636442; PIDN:CAB16131.1; PID:g2636641
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                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: C70084
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                                                                                                                                                              Query Match
Best Local
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213 GLIFGVI 219
                                                               19 GLIFGVI 25
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                                                                                                                                                                                                                                                                    GIG
                                                                                                                                  Conservative
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Pred. No.
                                                                                                                                                                 Score 7; DB 2;
Pred. No. 1e+02;
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o. 97;
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proline rich protein TPRP-F1 - tomato
(;Species: Lycopersicon esculentum (tomato)
c;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 2
c;Accession: S19129; S16589; S16751
C;Accession: S19129; S16589; S16751
R;Salts, Y.; Kenigsbuch, D.; Wachs, R.; Gruissem, W.; Barg, R.
Plant Mol. Biol. 18, 407-409, 1992
A;Title: DNA sequence of the tomato fruit expressed proline-rich |
A;Reference number: S19129; MUID:92119262; PMID:1731999
A;Accession: S19129
A;Molecule type: DNA
A;Residues: 1-346 <SAL>
A;Residues: 1-346 <SAL>
A;Reference number: SMAL>
A;Residues: 1-346 <SAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Du, Z.; Le, T.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C42D4.
A;Reference number: Z21483
A;Accession: T34158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C42D4.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
RESULT 37
522456
Species: Zea diploperennis (perennial teosinte c;Species: Zea diploperennis (perennial teosinte)
C;Species: Zea diploperennis (perennial teosinte)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Sep-1999
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Sep-1999
C;Accession: S22456; S18964
C;Accession: S22456; S18964
C;Accession: S22456; S18964
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A;Gene: CESP:C42D4.6
A;Introns: 135/1; 158/3
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A;Molecule type: DNA
A;Residues: 1-339 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X61395; NID:g1669697; PIDN:CAA43666.1;
A;Experimental source: cv. VPNT cherry
R;Salts, Y; Wachs, R; Gruissen, W; Barg, R.
Plant Mol. Biol. 17, 149-150, 1991
A;Title: Sequence coding for a novel proline-rich protein prefer A;Reference number: S16589; MUID:91329722; PMID:1868217
A;Accession: S16589
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S19129
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A;Residues: 34-346 <SAW>
A;Cross-references: EMBL:X57076; NID:g19520; PIDN:CAA40361.1;
A;Experimental source: cv. Arava; haplotype 2n
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Best Local S
Matches 7
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Best Local S
Matches 7
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;Accession: T34158
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;Superfamily: hydroxyproline-rich glycoprotein
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;Gene: TPRP-F1
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                                                                                                                                                                                                                                                                                                          Local Similarity nes 7; Conserv
                                                                                                                                                                                                                      190
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/ 100.0%; Pr
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Pred. No. 1e
0; Mismatches
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o. 1e+02;
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Mol. Gen. Genet. 233, 252-259, 1992
A;Title: Different mechanisms generating sequence variability
A;Reference number: S22456; MUID:92293123; PMID:1603067
A;Reference: S22456
A;Molecule: type: DNA
A;Residues: 1-350 <RAZ>
A;Residues: 1-350 <RAZ>
A;Cross-references: EMBL:X64173; NID:g22091; PIDN:CAA45514.1;
C;Keywords: glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein YPO2474 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis C;Pate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 C;Accession: AC0302 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Pr
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AC0302
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C; Genetics:
A; Gene: YPO2474
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A; Residues: 1-351 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: Genome sequence of Yersinia pestis, the causative agent of plague A,Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                  A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathous A,Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                    C;Accession: G71958

R;Alacession: RA; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;

Rives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V

Nature 397, 176-180, 1999

Nature 397, 176-180, 1999
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                                                                                                                                                                                                                                                                                                                                           A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein jhp0220 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
                                                                              A; Gene:
                                                                                                                  A;Molecule type: DNA
A;Residues: 1-355 <ARN>
A;Cross-references: GB:AE001460; GB:AE001439; NID:g4154733; PIDN:AAD05807.1;
A;Experimental source: strain J99
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Best Local S
Matches 7
    Query Match
Best Local S
Matches 7
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                              jhp0220
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l Similarity
7; Conserv
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2.2%; but
100.0%; Pr
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0; Mismatches
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      Score 7; DB;
; Pred. No. 1e
0; Mismatches
DB 2; L.
Mo. 1e+02; 0;
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n. 1e+02;
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lo. 1e+02;
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Conservative

Indels

0

Gaps

0;

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poly(beta-d-mannuronate) lyase precursor AlgL PA3547 [imported] - Pseudomonas aeruginosa (;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H83202 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, it cory, S.; Olson, M.V. ature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathola, Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: H83202 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-367 <STO> A;Cross-references: GB:AE004775; GB:AE004091; NID:g9949692; PIDN:AAG06935.1; GSPDB:GN001 A;Experimental source: strain PA01
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H83202
Search completed: July 8, 2003, 11:21:37 Job time: 65 secs
                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: algL; PA3547
C;Superfamily: Pseudomonas aeruginosa poly(beta-D-mannuronate) lyase
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                                                                                                                                                                                                                                  Query Match 2.2%; Score 7; DB 2; Length 367; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.

A MARCHALS V., COULDING SIDURITY ANTIOLIDARY WHICH CONSTITUTES

SUBmitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

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I SUBMITTED (MAY-1999) to the EMBL/GenBank/DDBJ databases.

C AN ENZYMATIC DEFENSE AGAINST SULFUR-CONTAINING WHICH CONSTITUTES

AN ENZYMATIC DEFENSE AGAINST SULFUR-CONTAINING OXIDATION SYSTEM BUT

C NOT AGAINST AN OXIDATION SYSTEM WITHOUT THIOL.

C I-! SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION.

C -!- SUBCELIULAR LOCATION: CYCOPLASMIC.

C -!- SUBCELIULAR LOCATION: CYCOPLASMIC.

C -!- SUBCELIULAR LOCATION: CYCOPLASMIC.

C -!- SUBCELIULAR LOCATION: CYCOPLASMIC.

C -!- SUBCELIULAR LOCATION: TO THE PRIMARY SITE OF OXIDATION.

BY THORESOXIN.

C -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
        Query Match 2.5%; Score 8; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 8; Conservative 0; Mismatches
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InterPro; IPR000866; AhpC-T
Pfam; PF00578; AhpC-TSA; 1.
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P01586
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lophura leu
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DY 14-OCC7-2001 (Rel. 40, Last annotation update)

DY 16-OCC7-2001 (Rel. 40, Last annotation update)

DY 16-OCC7-2001 (Rel. 40, Last annotation updated)

DY 16-OCC7-2001 (Rel. 40, Last annotation updated)

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RESULT 16-OCC7-2002 (Rel. 40, Last annotation updated)

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RESULT 16-OCC7-2004 (Rel. 40, Last annotation updated)

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RESULT 16-OCC7-2004 (Rel. 40, Last annotation up
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                YEAST 12:1071-1076(1996)

1: FUNCTION: REQUIRED FOR CELLULAR MORPHOGENESIS AND POLARIZATION OF -IP-FUNCTION: REQUIRED FOR CELLULAR MORPHOGENESIS AND POLARIZATION OF FUNCTIONS CONTICAL CYTOSKELETON. IT MIGHT ACT IN CONCERT WITH PROTEINS SUCH AS CIDC42 AND CIDC43 TO LIMIT THE REGION OF CORTICAL PATCH FORMATION TO THE CORTEX OF THE BUD. REQUIRED FOR THE ACCUMULATION AND/OR MAINTENANCE OF PLASMA MEMBRANE H(+)-ATPASE ON THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
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||||||||
| PVVQQPAP 10
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ACT_SITE
SEQUENCE 19

TSAL CANAL (977F0; Q9Y7F0; 16-OCT-2001 (Re. 16-OCT-2001 (Re. Thiol-specific TSAL)

S36354; S36354 B40673; B40673

Z69381; CAA93355.1;

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RA Sgource, J. Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cromin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Volckaett G., Aert R., Robben J., Grymonpres B.,
RA Godel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Morseno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR FTT FTT ST
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Best Local (
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042867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
608 ribosomal protein L23
(RPL23A OR RPL23 OR SPAC3G9.03) AND (RPL23B OR SPCC1322.11).
Schizosaccharomyces pombe (Fission yeast).
Sukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomycetales; Schizosaccharomycetaceae;
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Pfam; PF01608; I_LWEQ; 1.
ProDom; PD011820; ILWEQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00273; ENTH; 1.
SMART; SM00307; ILWEQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
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InterPro; IPR001026; ENTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002558; ILWEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rajandream M.A.,
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0; Mismatches
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P -> A (IN REF. 2).

A -> R (IN REF. 4).

A -> R (IN REF. 3).
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TLKTAEMEQQVEILKLEQSLSNARKRLGEIRRHAYYNQDDD
-> NTVPKMLPMHAEVNVTTSWV (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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). 7.4;
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P48337;
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EMBL; X70810; CAASO117.1; -

InterPro; IPR001700; RNA pol A bac; 1.

Chloroplast; Hypothetical protein.
SEQUENCE 161 AA; 18606 MW; 3779
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort Orsat B., Spielmann A., Stutz E.; "Complete sequence of Euglena gracilis chloroplast DNA."; Nucleic Acids Res. 21:3537-3544(1993).
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ProDom; PD001093; Ribosomal_L14; 1.
PROSITE; PS00049; RIBOSOMAL_L14; 1.
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-1- SIMILARITY: BELONGS TO THE L14P FAMILY OF RIBOSOMAL PROTEINS.
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    -!- SIMILARITY: BELONGS TO THE YCF67 FAMILY.

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RC MEDLINE=9804/303; PubMed=9384377;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
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RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Broiss R., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
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RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,
RA Kurita K., Lapidus A., Lardinois S., Kullo M.F., Itaya M., Jones L.,
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RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sator T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sator J., Sekowska A., Seror S.J., Seroror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Wedler E., Wedler E., Vasamoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane K., Yasamoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane K., Yasamoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane K., Yasamoto K., Yata K.,
RA Winters P., Wipat A., Yanamoto H., Yamane K., Yasamoto K., Yata K.,
RA Winters P., Wipat A., Park M., P., Zumstein E., Yoshikawa H.
       KBAA BACSU
P16449;
01-AUG-1990
01-OCT-1996
15-JUN-2002
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STRAIN=168 / JH642;
MEDLINE=96.165276, PubMed=8576055;
MEDLINE=96.165276, PubMed=8576055;
MEDLINE=96.165276, PubMed=10.55;
"Identification of a membrane protein involved in activation wind pathway to sporulation in Bacillus subtilis.";
J. Bacteriol. 178:1178-1186(1996).
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Yasumoto K., Liu H., Jeong S.M., Ohashi Y., Kakinuma S.
Tanaka K., Kawamura F., Yoshikawa H., Takahashi H.;
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Bacillus subtilis.
Bacteria; Firmicutes;
MEDLINE=90257591; PubMed=2517635;
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EMBL; Z99104; CAB11932.1; -.
EMBL; Z99104; CAB11932.1; -.
EMBL; M27259; AAAC22469.2; ALT_INIT.
Subtilist; BG10643; kbaA.
Sporilation; Transmembranc; Complete; POTENVIA, TRANSMEM 42 62 POTENVIA, TRANSMEM 42 62 POTENVIA, TRANSMEM 117 137 POTENVIA, TRANSMEM 117 137 POTENVIA, TRANSMEM 117 137 POTENVIA, TRANSMEM 117 137 POTENVIA, TRANSMEM 117 137 POTENVIA, TRANSMEM 118 166 POTENVIA, TRANSMEM 119 193 POTENVIA, TRANSMEM 119 194 AA; 22775 MW; 24917B
                                                                                                     MEDLINE=97426617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
"The complete genome sequence of Escheric
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P09549;
01-MAR-1989
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRALN=K12;
STRALN=K12;
MEDLINE=87308226; PubMed=3040734;
MODEL M.L., Marvel C.C., Tolan D.R.;
"The hisT-purF region of the Escherichia contentification of additional genes of the J. Biol. Chem. 262:12209-12217(1987).
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"Cloning and sequencing of the gerb gene of Bacillus
J. Gen. Microbiol. 135:3431-3445(1989).
IF FUNCTION: INVOLVED IN THE ACTIVATION OF THE KINB
OF SPORTUATION.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
SEQUENCE FROM N.A.
STRAIN=K12;
MEDLINE=97349980; PubMed=9205837;
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Bacteria; Proteobacteria;
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STRAIN=K12 / MG1655;
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DEDD OR B2314.
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Similarity 100.0%;
7; Conservative
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198 AA; 22775 MW; 24917B51
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(Rel. 40, Last sequence update)
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Pred. No. 19;
0; Mismatches
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.D., Rode C.K., Mayhew
A., Goeden M.A., Rose I
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STRAIN-DSM 3848 / THF;
MEDLINE-93126090; PubMed-1336177;
Medling J., van Beden F.J.M., Eggen R.I.L., de Vos W.M.;
Noelling J., van Beden F.J.M., Eggen R.I.L., de Vos W.M.;
Noelling J., van Beden F.J.M., Eggen R.I.L., de Vos W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation updat
Hypothetical 24.7 kDa protein (ORF5A).
Methanobacterium thermoformicicum.
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EMBL; AE000320; AAC75374.1; ALT_INIT.
EMBL; D90862; BAA16162.1; ALT_INIT.
EMBL; D90863; BAA16170.1; ALT_INIT.
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                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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"Construction of a contiguous 874-kb sequence of the Escherichia coli-
"Construction of a contiguous 874-kb sequence of the Escherichia coli-
-K12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
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                                                                                EMBL; X68366; CAA48429.1;
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220 AA; 22938 MW;
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Best Local (
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01-FEB-1996 (
01-FEB-1996 (
01-NOV-1997 (
                                                                                                                                                                                                                                                                        P50177;

D1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Type II restriction enzyme LlaDCHI (EC 3.1.21.4)
LlaDCHI) (R.LlaDCHI) (LlaII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 32.2 kDa protein in CPA2-NNF1 intergenic region
YJR111C OR J2009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstating the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 2
MEDLINE=95314272; PubMed=7793939; Moineau S., Walker S.A., Vedamuthu "Cloning and sequencing of LlaDCHI
                                                                                                                                                                         Plasmid pSRQ700.
Bacteria; Firmicutes;
                                                                                                                                                                                              Lactococcus lactis (subsp. cremoris)
Plasmid pSRQ700.
                                                                                                                                                                                                                                                   LÌADCHI) (R.LlADCHI) (LÌAII).
LLADCHIR OR LLAIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rose M., Koetter P., Entian K.D.; submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                           STRAIN=DCH-4;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=1359;
                                                                                                                                                                                                                                                                                                                                                                                                                               T2L2_LACLC
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hetical protein; Plasmid.
NCE 227 AA; 24681 MW;
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100.0%; Pred. No.
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100.0%; Pred. No
                                                                                                                                                                         Lactobacillales; Streptococcaceae; Lactococcus.
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  E.R., Vandenbergh P.A.; restriction/modification
                                                                                                                                                                                                                           (Streptococcus cremoris)
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o. 21;
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o. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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Matches 7
                                                                                                                                  EMBL; Arun
InterPro;
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P57168;
15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                           EMBL; AP001118; BAB12783.1; -.
Interpro; IPR002173; PfkB.
Pfam; PF002294; pfkB; 1
PROSITE; PS00583; PFKB KINASES_1; 1.
PROSITE; PS00584; PFKB KINASES_2; FALSE_NEG.
PROSITE; PS00584; PFKB TAINSFETASE; Kinase; Compl
Hypothetical protein; Transferase; Kinase; Compl
SEQUENCE 315 AA; 35023 MW; 69B3707C601EFD25
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a center the Swiss Institute of Bioinformatics and the RWBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Lactococcus lactis and relatedness of this system to the Streptococcus pneumoniae DpnII system.";

Appl. Environ. Microbiol. 61:2193-2202 (1995).

-!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED UNMETHYLATED SEQUENCE GATC AND CLEAVES BEFORE G-1.

-!- CATALYTIC ACTIVITY: Endomucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5'-phosphates.

-!- SIMILARITY: TO R.DPNII AND R.MBOI.
                                                                                                                                                                                                                                                                                                          Nature
                                                                                                                                                                                                                                                                                                            "Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H., "Ganome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
Nature 407.81-86 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
BU060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U16027; AAB06313.1; -. REBASE; 2772; LlaDCHI.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera aphidicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                   ure 407:81-86(2000).
SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES
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     Similarity 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterium).
Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 41, Created)
(Rel. 41, Last seque
(Rel. 41, Last annot
sugar kinase BU060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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2.2%; Pr
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
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   Score 7; DB;
; Pred. No. 28
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 AA
                 DB 1;
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b. 27;
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                                                                             Complete
     0,
                               Length 315;
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                                                             cRC64;
     Indels
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RESULT 11
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                                                                                                                                                                             RA KINST F. OGSAWATA N. MOSERI I. Albertini A.M., Alloni G.,
RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A.M. Borchert S.,
RA Borriss R., Boursier L., Brans A., Brann M., Brignell S.C.,
Bron S.,
RA Borriss R., Boursier L., Brans A., Brann M., Brignell S.C.,
Bron S.,
RA Borriss R., Boursier L., Brans A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Chim S.Y., Glaser P., Goffeau A., Golighty E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Kolsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Menne D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sechleich S., Schroeter R., Scoffone F.,
Sato T., Scanlan E., Takagi T., Takahashi H., Takenaru K.,
RA Yashida K., Yoshikawa H.S., Zumsten E., Yoshikawa H.F., Zumsten E., Yoshikawa H.F., Zumsten E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E
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01-OCT-1994
01-OCT-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
MEDLINE=96051385; PubMed=7584024;
Ogasawara N., Nakai S., Yoshikawa H.;
Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the Bacillus subtills chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
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                                                                                                                            Nature 390:249-256(1997).
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"Genes and their organization in bacterial chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98044033; PubMed=9384377;
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MEDLINE=92204018; Pub
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                                                                                          DB 1;
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CONFLICT

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POTENTIAL.
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STRAIN-ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrer Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., La Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              006749; Q57292; O1-FEB-1995 (Rel. 31, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alginate lyase precursor (EC 4.2.2.3) (Poly(beta-D-mannuronate)
                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93328683; PubMed=8335634; Schiller N.L., Monday S.R., Boyd C.M., Keen N.T., Ohman D.E.; Schiller N.L., Monday S.R., Boyd C.M., Keen N.T., Ohman D.E.; "Characterization of the Pseudomonas aeruginosa alginate lyase gene (algL): cloning, sequencing, and expression in Escherichia coli."; J. Bacteriol. 175:4780-4789(1993).
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                                                                                                                                                   EMBL; AE004775; AAG06935.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Depolymerizes alginate by cleaving the beta-1,4
glycosidic bond. May enhance the production of alginate by
controlling the length of the polymer chain during export.
-!- CATALYTIC ACTIVITY: Eliminative cleavage of polysaccharides
containing beta-D-mannuronate residues to give oligosaccharides
with 4-deoxy-alpha-L-erythro-hex-4-enopyranuronosyl groups at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
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[2]
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Boyd A., Ghosh M., May T.B., Shinabarger D.,
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ALGL OR PA3547.
                                                                                                                 PIR; JN0777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
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SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 5.
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                                                                                                                                                                            L14597; AAA71990.1; -. U27829; AAA91127.1; -.
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                                                                                                                    JN0777
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K., Lim R.M.,
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.J., Lagrou M.,
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Yuan Y.
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CONFLICT

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Best Local S
Matches 7
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P14126; 008459;
01-JAN-1990 (Rel. 13, C
01-NOV-1997 (Rel. 35, I
15-DEC-1998 (Rel. 37, I
60S ribosomal protein I
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=97279235; PubMed=9133743;

Valens M., Bohn C., Daignan-Fornier B., Dang V.,

"The sequence of a 54.7 kb fragment of yeast chro
the presence of two tRNAs and 24 new open reading
Yeast 13:379-390(1997).
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                          GETEVISIAE.";
J. BIOL. Chem. 267:5442-5445 (1992).
J. BIOL. Chem. 267:5442-5445 (1992).
J. FUNCTION: THE L3 PROTEIN IS A COMPONENT OF CYTOPLASMIC RIBOSOMES.
CYTOPLASMIC RIBOSOMES.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MISCELLANEOUS: A MUTANT ALLELE OF TCM1 CONFIRENCE CONFIRENCE TOXIN PRODUCEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schultz L.D., Friesen J.D.;
"Nucleotide sequence of the tcm1 gene
Saccharomyces cerevisiae.";
J. Bacteriol. 155:8-14(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPL3 OR TCM1 OR MAKE OR YOR063W OR YOR29-14.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Sacch
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                               Otaka E., Higo K.I., Itoh T.;
"Yeast ribosomal proteins: VII. Cytoplasmic
Schizosaccharomyces pombe.";
Mol. Gen. Genet. 191:519-524(1983).
                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-9.
MEDLINE=92184799; PubMed=1544921;
Takakura H., Tsunasawa S., Miyagi M., V
"NH2-terminal acetylation of ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-19.
MEDLINE=84038947; PubMed=6355773;
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                                                                                                                                                             SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
 J01351; AAA88732.1; -. Z74971; CAA99256.1; -.
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Mismatches
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(Trichodermin
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                                                                                                                                                                                        TCM1 CONFERS RESISTANCE TO PRODUCED BY PLANT-PATHOGENIC
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l proteins of Saccharomyces
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ading frames.";
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Q03420;
01-OCT-1993
01-OCT-1993
15-JUN-2002
                                                                                                                                                                                                                                                                                                       Geremia R.A., Goldman G.H., Jacobs D., Ardiles W., Vila S.B.,
Van Montagu M., Herrera-Estrella A.;

"Molecular characterization of the proteinase-encoding gene, prb
related to mycoparasitism by Trichoderma harzianum.";

Mol. Microbiol. 8:603-613 (1993).

"Ol. Microbiol. 8:6103-613 (1993).

-i- FUNCTION: SERINE PROTERASE, SECRETED SPECIFICALLY DURING THE
MYCOPARASITIC PROCESS, WHICH IS INVOLVED IN THE DEGRADATION
PHYTOPATHOGEN CELL WALLS, MEMBRANES AND OF THE PROTEINS RELE
AFFER LYSIS OF THE HOST.

-i- SUBCELLULAR LOCATION: Secreted.
-i- INDUCTION: BY MYCELIA, FUNGAL CELL WALLS, AND CHITIN, BUT ON
IN THE ABSENCE OF GLUCOSE.
-IN THE ABSENCE OF GENERALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000209; Peptidase_S8.

Pfam; PF00082; Peptidase_S8; 1.

PRINTS; PR00723; SUBTILASE ASP; 1.

PROSITE; PS00136; SUBTILASE_HIS; 1.

PROSITE; PS00138; SUBTILASE_SER; 1.

PROSITE; PS00138; SUBTILASE_SER; 1.

PROSITE; PS00138; SUBTILASE_SER; 1.

PROSITE; PS00138; SUBTILASE_SER; 1.

PROSITE; PS00138; SUBTILASE_SER; 1.

POTENTIAL.

PROPEP 21 120 POTENTIAL.
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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INIT MET 0
CONFLICT 254
                                                                                                                                 EMBL; M87518; AAA34211.1; -.
EMBL; M87516; AAA34209.1; -.
EMBL; S32905; S32905.
HSSP; Q99405; 1MPT.
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STRAIN=IMI 206040;
MEDLINE=93316857; Po
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Eukaryota; Fungi; Ascomycota; Pezizo
Hypocreales; mitosporic Hypocreales;
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NCBI_TaxID=5544;
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ilarity 100.0%;
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(Rel. 27, Last sequence update)
(Rel. 41, Last annotation update)
steinase precursor (EC 3.4.21.-) (
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Pred. N
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reales; Trichoderma.
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HSSP; P17679; IGNF.
ZFIN; ZDB-GENE-990415-82; gata3.
InterPro; IPR000679; Znf GATA.
InterPro; IPR001164; hRIP_like.
Pfam; PF00320; GATA; 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91428;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last amotation update)
Transcription factor GATA-3 (GATA binding f.
GATA3 OR GTA3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neave B., Rodaway A., Wilson S.W., Patient R., Holder N.; "Expression of zebrafish GATA 3 (gta3) during gastrulation and neurulation suggests a role in the specification of cell fate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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GAT3_BRARE
                                                                   SEQUENCE
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PROSITE; PS00344; GATA_ZN FINGER_1; 2.

PROSITE; PS50114; GATA_ZN FINGER_2; 2.

Transcription regulation; Activator; DNA-binding;
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or send an email to license@isb-sib.ch).
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Neave B., Rodaway A., Wilson S.W.,
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Mech. Dev. 51:169-182(1995)
                                                                                                                                    DOMAIN
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SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.
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GATA-TYPE 2.
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POLY-SER.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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                    Length 438;
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RESULT 18
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InterPro; IPR000120; Amidase.
InterPro; IPR004120; GatA.
Pfam; PF01425; Amidase; I.
TIGRPAMB; TIGR00132; gatA; 1.
TIGRPAMB; TIGR00132; gatA; 1.
PROSITE; PS00571; AMIDASES; 1.
PROCEIN biosynthesis; Ligase; Co
SEQUENCE 478 AA; 53229 MW; F
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P36896; Q15479;
01-JUN-1994 (Rel
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P75534;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase receptor R2 p
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                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae.";
Nucleic Acids Res. 24:4420-4449
-!- FUNCTION: FURNISHES A MEANS
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01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Glutamyl-tRNA(Gln) amidotransferase subunit A
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MEDLINE=97105885; PubMed=8948633;
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himmelreich R., Hilbert H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2104;
                                                                                                                            187
                                                                                                                                                   308 ISRNGVY 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                               STANDARD; PRT; 50; Q15480; Q15481; Q15482;
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ISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
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precursor

(EC 2.7.1.37)

receptor-like

kinase

4

(ALK-4)

(ACTR-IB)

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                                                                                                                                                    EMBL; 222536; CAA80258.1; -.
EMBL; U14722; AAA50246.1; -.
EMBL; L10125; AAA60555.1; -.
EMBL; L10126; AAA60555.1; -.
EMBL; L31848; AAA53350.1; -.
EMBL; L31848; AAA53350.1; -.
EMBL; L31848; AAA53351.1; -.
EMBL; BC000254; AAA60254.1; -.
PIR; S37184, S37184.
HSSP; P36897; ITBI.
Genew; HGNC:172; ACVR1B.
MIM; 601300; -.
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ACVR1B OR ACV
Homo sapiens
Eukaryota; Me
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Carcamo J., Weis F.M., Ventura F., Wieser R., Wra
Attisano L., Massague J.;
"Type I receptors specify growth-inhibitory and tresponses to transforming growth factor beta and mol. Cell. Biol. 14:3810-3821(1994).
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MEDLINE=93390967; PubMed=8397373;
ten Dijke P., Ichijo H., Franzen P., Schulz P., Saras J.,
Toyoshima H., Heldin C.-H., Miyazono K.;
"Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity.";
Oncogene 8:2879-2887(1993).
                                             InterPro; iPR000472; Activin_rec.
InterPro; iPR000719; Euk pkinase:
InterPro; iPR002290; Ser thr pkinase.
InterPro; iPR003605; TGFbeta_GS.
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entities requires a license agreement (See http://www.
or send an email to license@isb-sib.ch).
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Xu J., Matsuzaki K., McKeehan K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITTED (NOV-2000) to the EMBL/GenBank/DDBJ databases.

CAPALIYIIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1/SKR2-1 (SHOWN HERE), 2/SKR2-1

AND 3/SKR2-3, ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES, MOST STRONGLY IN HUMAN KIDNEY, PANCREAS, BRAIN, LUNG, AND LIVER.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

TGFB RECEPTOR SUBFAMILY.
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pkinase; 1.
Activin_recp; 1.
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Primates;
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P80202;
01-OCT-1993
01-OCT-1993
16-OCT-2001
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TRANSMEM
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01-OCT-1993 (Rel. 27, Last sequence up
16-OCT-20901 (Rel. 40, Last annotation
Serine/threonine-protein kinase recept
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SMART; SM00467; GS; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

Receptor; Transferase; Serine/threonine protein kinase; AT

Transmembrane; Glycoprotein; Signal; Alternative splicing;
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DOMAIN
SEQUENCE FROM N.A.
TISSUE=Pituitary;
PubMed=7813622;
MEDLINE=95113007; PubMed=7813622;
Takuni T., Moustakas A., Lin H.Y., Lodish H.F.;
Takuni T., Moustakas A., Lin H.Y., Lodish H.F.;
Tokuni T., Moustakas A., Lin H.Y., Lodish H.F.;
Takuni T., Moustakas A., Lin H.Y., Lodish H.F.;
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Takuni T., Lodish H.F.;
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Takuni T., Lodish H.F.;
Takuni T., Lodish H.F.;
Takuni T., Lodi
                                                                                                                                                                                                                                              STRAIN-Sprague Dawley; TISSUE-Urogenital ridge; MEDLINE-93372378; PubMed-8395914; He W.-W., Gustafson M., Hirobe S., Donahoe P.; "Developmental expression of four novel serine/threonine receptors homologous to the activin/transforming growth f type II receptor family."; Dev. Dyn. 196:133-142(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACVRIB OR ACVRIK4.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
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Pred. No
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VHEEYQLPYYDLVPS)PSIEEMRKVVCDQKLRPNIPNWWQS
YBALRVMGKMMRECMYANGAARLTALRKKTLSQLSVQEDV
KI -> TELFCLCSYLPFQDAGSPKAVLLPPFFLQPVGCLL
PBEDESSFKVAIKGVEVAVLRVKLFFRDQFVE (IN
1SOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALRYMGKMMRECWYANGAARLTALRIKKTLSQLSVQEDVKI
-> VRSWPPAAFPSA (IN ISOFORM 2).
L -> V (IN DBSNP 928906).
/FTId=VAR_011716.
I -> F (IN REF. 3).
WR -> MA (IN REF. 3).
WR -> MA (IN REF. 3).
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ATP (BY SIMILARITY).
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CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cation update)
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o. 43;
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; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                          e kinase
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BINDING
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CARBOHYD
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SMART; S
"Marcey D., Watkins W.S., Hazelrigg T.;
"The temporal and spatial distribution pattern of maternal exuperantia protein: evidence for a role in establishment maintenance of bicoid mRNA localization.";
EMBO J. 10:4259-4266(1991).
                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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HSSP; P36897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restrate by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                    Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Ephydroidea; Drosophilidae; Dros
                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                     EXU OR CG8994.
                                                                                                                                                                 Maternal
                                                                                                                                                                                                            EXU_DROME
P28750; Q9V967;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                        SEQUENCE FROM N.A.
MEDLINE=92097546; PubMed=1756733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cransmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
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PF01064; Activin recp; 1.

m; PD000001; Euk pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PD000001; Et SM00467; GS;
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00107; PROTEIN KINASE ATP; 1.
PS00108; PROTEIN KINASE ST; 1.
PS50011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                               exuperantia protein.
                                                                                                                                                                                                                                                                                   STSGSGS 193
                                                                                                                                                                                                                                                                                                          STSGSGS 47
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IPRO00719; Euk_pkinase.
IPRO02290; Ser thr pkinase.
IPRO03605; TGFbeta_GS.
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24 505
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                                                                                                                                                                                                                         STANDARD;
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PROTEIN KINASE.
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ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                            DB 1;
o. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                 Pancrustacea; Hexapoda;
Diptera; Brachycera;
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EMBL; PIR; S PIR; 1

S18643; S18643. A41639; A41639.

FlyBase; FBgn Developmental

FBgn0000615; exu

VARIANT VARIANT

DOMAIN

al protein; RNA-binding. 207 246 SER-RI 223 223 M -> I 339 339 R -> S

SER-RICH. M -> I. R -> S (IN PJ42 MUTANT,

LOSS OF EXU

EMBL;

\$72757; AAB20673.1; -. \$72363; AAB20670.1; -.

(See http://www.isb-sib.ch/announce/

and

for

commercia.

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RA Brandon R.C., ROGERS Y.-H.C., Malazej R.C., Champe W., Chell L.A.,
RA Wan K.H., Doyle C., Baxcer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C. Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.
RA Durbin K.J. Evangelista C.C., Perris C., Ferrisca S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris M.I., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris M., Kalush F., Sarpen G.H., Ke Z., Kennison J.A.,
RA Harris M., Kalush F., Sarpen G.T., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., My M., Murphy L., Muzny D.M., Nelsen D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Calus F., Ke S., Chang G., Zhao Q., Zhang S., Yao Q.A.,
Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissenbach J.,
RA Shue S. M., Woy M., Murphy L., Smith H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; Pubmed=10/31131, Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Pfeiffer B.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macdonald P.M., Luk S.K.-S., Kilpatrick M.; "Protein encoded by the exuperantia gene is concentrated at sites of bicoid mRNA accumulation in Drosophila nurse cells but not in oocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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CUEO_YI
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RA PARKHILL J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Ctronin A., Davies R.M., Davis P., Dougan G.,
RA Chillingworth T., Ctronin A., Davies R.M., Davis P., Dougan G.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Leather S., Woule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RA Leather S., Woule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT Nature 413:523-527(2001)
CC (copper by oxidizing Cu(I) to Cu(II) and thus preventing its uptake
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Q8ZBK0;
15-JUN-2002
15-JUN-2002
15-JUN-2002
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Blue copper oxidase cueO precursor (Copper efflux oxidase)
CUEO OR YPO3409.
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EMBL; AJ414117; CAC92639.1; -.
InterPro; IPRO01117; Cu-oxidase.
InterPro; IPRO02355; MultiCu_oxidse2.
Pfam; PP00394; Cu-oxidase; 1.
PROSITB; PS00080; MULTICOPPER OXIDASE2; 1.
Oxidoreductase; Copper; Metal-binding; Periplasmic;
                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a copyright of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conten
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MEDLINE=21470413; Publ
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: The methionine-rich domain could provide binding sites exogenous copper ions. This methionine-rich region is probably important for copper tolerance in bacteria. SINILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES. SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
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532 AA;
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; Pred. No. 45
0; Mismatches
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50BD15B712A62C4E CRC64;
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Best Local S
Matches 7
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P70459;
P70459;
15-JUL-1998
15-JUL-1998
15-JUN-2002
                                                                                                                                                                                                                                                                                                                       STRAIN=129/Sv0;
STRAIN=129/Sv0;
STRAIN=129/Sv0;
MEDLINE=9728708; PubMed=9136988;
Liu D., Pavlopoulos E., Modi W., Moschonas N., Mavrothalassitis G.
PERF: genomic organization, chromosomal localization and promoter analysis of the human and mouse genes.";
Oncogene 14:1445-1451(1997).

-i. FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVE IN CELLULAR PROLIFERATION (BY SIMILARITY).

-i. SUBCELLULAR INCATION: Nuclear.
-i. SUBCELLULAR LOCATION: Nuclear.
-i. PTM. PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).
-i. SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Bh the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                         EMBL; U58533; AAC09474.1;
EMBL; U58534; AAC09474.1;
HSSP; Q01543; 1FLI.
MGD; MGI:109637; Erf.
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Mammalia; Eutheria;
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(Rel. 36, Last sequence up
(Rel. 41, Last annotation
transcription factor ERF.
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PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
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IPR000418; ECS.
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01-FEB-1996
01-FEB-1996
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"Role of the fixGHI region of Azorhizobium caulinodans in free-living and symbiotic nitrogen fixation.";

FEMS Microbiol. Lett. 114:185-189(1993).

-i- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C OR A QUINOL ARE TRANSFERRED TO THE BIMETALLIC CENTER FORMED BY A HIGH-SPIN HEME AND COPPER B.

-i- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
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Azorhizobium caulinodans.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Hvohomicrobium group; Azorhizobium.
                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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                                                                     EMBL; X74410; CAA52429.1; -. InterPro; IPR000883; COX1.
                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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PROSITE; PS00346; ETS_DOMAIN 2; 1.
PROSITE; PS50061; ETS_DOMAIN 3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Respiratory chain; terminal step. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. POTENTIAL TRANSMEMBRANE DOMAINS.
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                             PF00115;
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01-MAR-1989
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McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: VIRION PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Bithe European Bioinformatics Institute. There are no restue by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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PIR; G30084; WMBEW5.
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SEQUENCE 580 AA; 62669 MW;
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Alphaherpesvirinae; Simj
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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SPPA_ECOLI STANDARD; PRT; 618 AA. P08395; P77752; Q46723; Q46724; Q46725; Q46726; 01-AUG-1988 (Rel. 08, Created).

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EMBL; M13359; AAA24648.1; --
EMBL; AE000271; AAC74836.1; --
EMBL; D90820; BAA15570.1; --
EMBL; U13772; AAA57008.1; --
EMBL; U13773; AAA57009.1; --
EMBL; U13774; AAA57010.1; --
EMBL; U13775; AAA57011.1; --
EMBL; U13776; AAA57012.1; --
EMBL; U13777; AAA57013.1; --
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MEDLINE-97251357; PubMed=9097039;

Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Ito Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Kasai H., Mashimoto K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Makaino K., Miki T., Mashimoto H., Nishio Y., Oshima T., Sait Nakade S., Nakamura Y., Nashimoto H., Tishio Y., Oshima T., Sait Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Mada C., Yamamoto Y., Horiuchi T.;

"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";

[14]
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16-OCT-2001
Protease IV
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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J. Biol. Chem. 261:9405-9411(1986)
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Ichihara S., Suzuki T., Suzuki M., Mizushima S.;
"Molecular cloning and sequencing of the sppA gene and
characterization of the encoded protease IV, a signal peptidase, of Escherichia coli.";
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FUNCTION: DIGESTION OF THE CLEAVED SIGNAL PEPTIDE
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EMBL; U13790; AAA57015.1; -.
EMBL; U13780; AAA57015.1; -.
EMBL; U13780; AAA57017.1; -.
EMBL; U1382; AAA57030.1; -.
EMBL; U1383; AAA57030.1; -.
EMBL; U1383; AAA57031.1; -.
EMBL; U1383; AAA57031.1; -.
EMBL; U1383; AAA57031.1; -.
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EMBL; U1383; EAAS7031.1; -.
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EMBL; EAAAA57031.1; -.
EMBL; EAAAA57031.1; -.
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P38225;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable long-chain fatty acid transport protein.
PATI OR YBR041W OR YBR0411.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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SEQUENCE
MEDLINE 97236810; PubMed=9079682;

Faergeman N.J., Dirusso C.C., Elberger A., Knudsen J., Black P.N.;

Faergeman N.J., Dirusso C.C., Elberger A., Knudsen J., Black P.N.;

Faergeman N.J., Dirusso C.C., Elberger A., Knudsen J., Black P.N.;

Fatty acid transport protein impairs uptake homologue to the murine fatty acid transport protein impairs uptake and growth on long-chain J. Biol. Chem. 272:8531-8538(1997)

J. Biol. Chem. 272:8531-8538(1997)

-! FUNCTION: MAY BE INVOLVED IN LONG-CHAIN FATTY ACIDS UPTAKE, AND PRIOR TO METABOLIC UTILIZATION. MAY PLAY AN IMPORTANT ROLE IN PRIOR TO METABOLIC UTILIZATION. MAY PLAY AN IMPORTANT ROLE IN UPTAKE OF THESE HYDROPHOBIC COMPOUNDS UNDER CONDITIONS WHERE FAI ACID SYNTHESIS IS COMPROMISED.
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VARIANT
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CHARACTERIZATION.
STRAIN=W303A;
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Submitted (AUG-1994)
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STRAIN=S288c;
Andre B., Cziepluch
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Best Local
                                                                                                                                               MEDILING., Runquist U.G.,
Morton T.A., Runquist U.G.,
Wood H.G., Ljungdahl L.G.,
Wood H.G., Ljungdahl L.G.,
"The primary structure of the subunits of carbon monoxid
dehydrogenase/acetyl-CoA synthase from Clostridium therm
J. Biol. Chem. 266:23824-23828(1991).
-i- FUNCTION: CATALYZES THE INTERCONVERSION OF CO AND CO
SYNTHESIS OF ACETYL-COENZYME A FROM THE METHYLATED
SULPUR PROTEIN, CO, AND COENZYME A.

SULPUR PROTEIN, CO, AND COENZYME A.
between the Swiss Institute or Bivinive are no rest the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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CARBOHYD
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TRANSMEM
CARBOHYD
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbon monoxide dehydrogenase alpha subunit (EC 1.2.99.2)
Moorella thermoacetica (Clostridium thermoaceticum).
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae; Moorella group; Moorella.
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PIR; S
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Lipid tra
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Morton T.A., Runquist J.A., Ragsdale S.W.,
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P27988;
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                                                                                                                              SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
                                                                                                                                         COFACTOR: NICKEL.
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                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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PS00455; AMP_BINDING; 1.
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RESULT 29 CPN_DROME

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Best Local S
Matches 7
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Matches
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01-NOV-1995
                                                                                                                                                 CARBOHYD
SEQUENCE
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TIGRFAMs; TIGR00316; cdhC; 1.
Oxidoreductame; Nickel.
SEQUENCE 729 AA; 81725 MW;
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DOMAIN
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
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B0285.7.
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SIGNAL
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Pfam; PF01433; Peptidase_M1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z34533; CAA84298.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                   SISSGVN 132
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70
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                                                                        Conservative
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(Rel. 36.0 kDa protein B0285.7 in ch
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ilarity 100.0%;
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Caenorhabditis.
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Ballinger D.G., Xue N., Harshman K.D.;
"A Drosophila photoreceptor cedll-specific protein, calphotin, binds calcium and contains a leucine zipper.";
Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
-i- FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPONGE" TO REGULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BINDS 0.3 MOLOF CA+2 PER MOLOF PROTEIN.
-i- SUBURNIT: HOMODIMER (PROBABLE).
-i- TISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CELLS OF COMPOUND EYES AND OCELLI.
-I- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L02111; AAA28405.1; -.
EMBL; L05080; AAA28420.1; -.
EIR; A47282; A47782;
ElyBase; FBgn0010218; Cpn.
Calcium-binding.
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Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
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APVAPPV 118
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I -> V (IN REF. 2).

T -> A (IN REF. 2).

P -> PP (IN REF. 2).

VQ -> AP (IN REF. 2).

I -> V (IN REF. 2).

S -> T (IN REF. 2).

A -> E (IN REF. 2).

A -> E (IN REF. 2).

I -> T (IN REF. 2).

I -> T (IN REF. 2).

I -> L (IN REF. 2).

I -> L (IN REF. 2).

V -> E (IN REF. 2).

V -> E (IN REF. 2).
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RC STRAIB-Berkeley;
RX MEDLINE-20196006; pubMed=10731132;
RA Adams M.D., Celniker S.E., Lit P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Atchards S., Ashburner M., Henderson S.N.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Barendal M.D., Enandari D., Pédiffer B.D.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boother P.V.,
RA Berkova D., Botchan M.R., Bouck J., Borkstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier R.,
RA Cherry J.M., Cawlley S., Dahlke C., Davenport L.B., Davies P.
RA Dodson K.O., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Bornel B., Daves M.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N., Malushn F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
RA Harris N., Moland T.J., Hernandez J.R., Houck J.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Merkilov G., Stepleton M., Skupski M.P., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M.,
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HIRA_DROME
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brack
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Kirov N., Shtilbans A., Rushlow C.;
"Isolation and characterization of a new
HIRA family of proteins from Drosophila m
Gene 212:323-332(1998).
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Lievadot R., Marques G., Pritchard M., Estivill X.,
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ProDom; PD000018; WH40; 3.
SMART; SM00320; WD40; 6.
PROSITE; PS00678; WD_REPEATS 1; 1.
PROSITE; PS50082; WD_REPEATS_2; 3.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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EMBL; AF071281; CAA10954.1; -.
EMBL; AF071281; AAC64041.1; -.
EMBL; AE003441; AAF46267.1; -.
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.

BEVELOPMENTAL STAGE: EXPRESSED MATERNALLY, AND ZYGOTICALLY THROUGHOUT DEVELOPMENT TO ADULTS (MALE AND FEMALE).

SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
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                                                                                                                                       Similarity 7; Conserv
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264 31
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bifunctional autolysin precursor [Includes: N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28); Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase (EC 3.2.1.96)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. I entities requires a license agreement (See ht)
                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                       SIGNAL
                                                                                                                                                       InterPro; IPR002502; Amidase 2.
InterPro; IPR002501; Amidase 4.
Pfam; PF01510; Amidase 2; 1.
Pfam; PF01832; Amidase 4; 1.
                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95116542;
Oshida T., Sugai M
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                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                             unit in high-mannose glycopeptides and glycoproteins contains the [Man(GlcNac)2]Asn-structure. One N-acetyl-D-glucosamine residue remains attached to the protein; the rest of the oligosaccharide is released intact.

SUBCELLULAR LOCATION: Secreted.

PIM: UNDERGOES PROTEOLYTIC PROCESSING TO GENERATE THE TWO EXTRACELLULAR LYTIC ENZYMES.

SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE N-
                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY 2.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 73
                                                                                                                                                                                                                                                                                                                                             GLYCOSYL HYDROLASES.
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CATALYTIC ACTIVITY: Endohydrolysis of the di-N-acetylchitobiosyl
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Sci. U.S.A. 92:285-289(1995).
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2.2%;
                                    137384
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                                                                                                                                 Signal; Multifunctional enzyme;
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                                    ¥.
Score 7;
Pred. No.
                                                                                 BIFUNCTIONAL AUTOLYSIN.
N-ACETYLMURAMOYL-L-ALANINE AMIDASE.
ENDO-BETA-N-ACETYLGLUCOSAMIDASE.
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                                    2BB76CAA292FDD20 CRC64;
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AC P39059;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; L25286; AAA58429.1; -.
EMBL; L01697; -; NOT ANNOTATED_CDS.
EMBL; D10507; COL15A1.

EMBL; 101697; -; NOT COL15A1.
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TISSUS-Placenta;
TISSUS-Placenta;
MEDLINE=94140817; PubMed=8307960;
Muragaki Y., Abe N., Ninomiya Y., Olsen B.R., Ooshima A.;
"The human alpha 1(XV) collagen chain contains a large amino-terminal non-triple helical domain with a tandem repeat structure and homology to alpha 1(XVIII) collagen.";
J. Biol. Chem. 269:4042-4046(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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), PubMed=8106446;
ainamaki P., Rehn M.V., Honkanen N., Myers J.C.,
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STRAIN-MOBEN / Nigg;
MEDLINE-20150255; PubMed=10684935;
MEDLINE-20150255; PubMed=10684935;
Meddine C., Brunham R.C., Shen C., Gill S.R., F.
White O., Hickey E.K., Peterson J., Utterback
Linher K., Weidman J., Khouri H., Craven B., F.
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Bacteria; Chlamydiales;
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PMPB OR TC0694
                                                                                                                                                                                                                                                                                                                                                         Probable
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SMART; SM00210; TSDN; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            780
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(Rel. 40, Last sequence update)
(Rel. 40, Last snnotation update)
cer membrane protein pmpB precursor (Polymorphic
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COLLAGEN ALPHA 1(XV) CHAIN.

NONHELICAL REGION 1 (CC)

TRIPLE-HELICAL REGION 2 (NC2).

TRIPLE-HELICAL REGION 3 (NC3).

TRIPLE-HELICAL REGION 3 (NC3).

TRIPLE-HELICAL REGION 4 (NC4).

TRIPLE-HELICAL REGION 4 (NC4).

TRIPLE-HELICAL REGION 5 (NC5).

TRIPLE-HELICAL REGION 5 (NC5).

TRIPLE-HELICAL REGION 6 (NC5).

TRIPLE-HELICAL REGION 7 (NC7).

TRIPLE-HELICAL REGION 7 (NC7).

TRIPLE-HELICAL REGION 9 (NC6).

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TRIPLE-HELICAL REGION 10 (NC10).
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      Heidelberg J.F.,
k T., Berry K., Bass
Bowman C., Dodson R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1388;
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SEQUENCE OF 544-1252 FROM N.A.
MEDLINE=93066196; PubMed=1279671;
Myers J.C., Kivirikko S., Gordon M.K., Dion A.S., Pihla
"Identification of a previously unknown human collagen
1(XV), characterized by extensive interruptions in the

Pro; IPR000087; Collagen. Pro; IPR001791; Laminin_G. Pro; IPR003129; TSPN. PF01391; Collagen; 5. PF02210; TSPN; 1.

gene

Biol. Chem. 269:4773-4779(1994).

"Primary structure of the alpha exon-intron organization in the

wμ

TISSUE=Umbilical of MEDLINE=94148920; Kivirikko S., Heinamaki Pihlajaniemi T.;

SEQUENCE FROM N.A.

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RESULT 34
YS89_CAEEL
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                               Durbin R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Pot-
-!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
                                                                                                                                                                                                 STRAIN-Bristol N2; Wilkinson-Sproat J.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      Q09624; Q09625; Q969D4;
01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein ZK945.9 in chromosome II.
ZK945.9/ZK945.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane; Signal; Multigene family; Complete proteome SIGNAL 1 14 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02385; OMP; 1.
Pfam; PF02415; DUF145; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
EMBL; Z48544; CAB70192.1; -.
EMBL; Z48582; CAB70192.1; JOINED.
EMBL; Z48582; CAB70201.1; -.
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                               REVISIONS.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; TC0694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000)
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                                                                                                                                                                                                                                                                                                                                                                         S89_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequences of Chlamydia trachomatis MoPn and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  404
                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 PTPTPPV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1672 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s Score 7; DB 1
b; Pred. No. 1.3;
0; Mismatches
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                                                                                                                                            membrane protein (Potential).
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o. 1.3e+02;
                                                     (See http://www.isb-sib.ch/announce/
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DBH1_BIFLO
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Matches 7
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01-AUG-1990
01-AUG-1990
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Query Match
Best Local Similarity
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-!- FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS.
                                                                                                                                                                                                                                                                                                 STRAIN-ATCC 15703;
MEDLINE=90344917; PubMed=2116910;
Goshima N., Kano Y., Imamoto F.;
"Characterization of HJ-like protein from Bifidobacterium longum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Last annotation DNA-binding protein HB1 (Fragment).
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InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR000036; M+channel_nlg.
InterPro; IPR000203; PXD_cys_rich.
Pfam; PF00520; ion_trans; 1.
Pfam; PF00577; PLAT; 1.
                                                                                 DNA-binding; DNA condensation.
NON TER 27 27
                                                                                                           Pfam; PF00216; Bac DNA binding; 1.
PROSITE; PS00045; HISTONE LIKE; PARTIAL
                                                                                                                                                 PIR; A43768; A43768.
InterPro; IPR000119; Bac_DNAbind.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00303; GPS; 1
SMART; SM00308; LH2; 1
                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY
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                                                              27 AA; 2863 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 36, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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           100.0%;
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                           1.9%;
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         Score 6; I Pred. No.
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                                                              6A201A5965A1BD64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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DB
33;
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                         1;
                           Length 27;
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RESULT 37
YSXC_SULAC
ID YSXC_S
AC P39477
DT 01-FEB
DT 16-OCT
DE Hypoth
OS Sulfol
OC Archae
OC Sulfol
OX NCBI_T
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RA Luebbe
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Matches 6
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                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 4.5 kDa protein in SOXC 3'region.
Sulfolobus acidocaldarius.
Archaea, Crenarchaeota; Thermoprotei; Sulfolobales;
                                                                                                                                                                                                                             YSXC SULAC
P39477;
01-FEB-1995
01-FEB-1995
16-OCT-2001
  SEQUENCE FROM N.A.
STRAIN-ATCC 33909 / NCIB 11770 /
MEDIINE-92192013; PubMed-1372250;
Luebben M., Kolmerer B., Saraste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=83272939; PubMed=6308564;

Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;

Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;

"Sequence homologies in the protamine gene family of rainbow trout.",

"Sequence homologies in the protamine gene family of rainbow trout.",

"Sequence homologies in the protamine gene family of rainbow trout.",

"ISEQUENCE HOMOLOGIES OF SPERMATOGENESIS. THEY COMPACT

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

"I SUBCELLULAR LOCATION: Nuclear.

"I SUBCELLULAR LOCATION: Nuclear.

"I SUBCELLULAR SPECIFICITY: TESTIS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomal protein; Nucleosome core; Spermatogenesis; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                              NCBI_TaxID=2285;
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6; Conserv
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                                                                                                                                                                                                                                                                                                                     STANDARD;
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Last annotation updat
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          Saraste M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6; DB Pred. No. 38
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                                                                                                                                                             Sulfolobaceae;
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Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                       01.FEB-1991 (Rel. 17, Created)
01.FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Venom chymotrypsin inhibitor.
Naja naja (Indian cobra)
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae; Naja.
NCBI TaxID=35670;
                                                                                                                                                                                                    SMART; SM00131; KU; 1.
PROSITE; PS00280; BPTI KUNITZ 1; 1.
PROSITE; PS50279; BPTI KUNITZ 2; 1.
Venom; Serine protease inhibitor.
Venom; Serine protease inhibitor.
DISULFID 5 55
DISULFID 14 38
DISULFID 14 38
DISULFID 30 51
BY SIMILARITY.
ACT_SITE 15 16 REACTIVE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X62643; CAA44512.1;
PIR; S21044; S21044.
Hypothetical protein.
SEQUENCE 40 AA; 4502 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVBC_NAJNA
P19859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitochondrial respiratory EMBO J. 11:805-812(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "An archaebacterial terminal oxidase combines core structures mitochondrial respiratory complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
                                                   266 GFVSSY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 LGLIFG
       16 GFVSSY 21
                                                                                       . Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGLIFG
                                                                                                                                                                                  57 AA;
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                                                                                       Larity 100
Conservative
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                                                                                                                                                                                  6508 MW;
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                                                                                            Score 6; DB 1
Pred. No. 64;
D; Mismatches
                                                                                                                                                                                  REACTIVE BOND (BY 4BFB26A010C1737A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; DB:
Pred. No. 47
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5EEA6A276C0E8A1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a chymotrypsin Kunitz inhibitor cobra (Naja naja naja).";
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                                                                                                                                   Length 57;
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Gaps

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RESULT 40
EC_MAIZE
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P43401;
01-NOV-1995 (Rel. 32, Created)
15-UNV-1995 (Rel. 32, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
2 EC protein homolog (Zinc-metallothionein class II).
3 Zea mays (Maize).
5 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Madgnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                     SEQUENCE FROM N.A.

White C.N., Rivin C.J.;

White C.N., Rivin C.J.;

Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: BINDS 5 MOLECULES OF ZINC. MAY HAVE A ROLE IN ZN(2+)

HOMEOSTASIS DURING EMBRYOGENESIS (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
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Hypothetical protein.
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01-NOV-1991 (Rel. 20, Last sequence update)
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Hypothetical 6.9 kDa protein in 100 kDa protein region.
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Metal-binding; Metal-thiolate cluster; Zinc.
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RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Apbayani A., An H.-J., Bayraktaroglu L., Beasley E.M.,

RA Baltew R.M., Basundale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA George R.S., Downes M., Dugan-Rocha S., Dunn P.,

RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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Q9VCB2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG5669 protein (LD04007p).
CG5669.
CG5669.
ED040700 (Fruit fly).
Drosophila melanogaster (Fruit fly).
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O22842 arabidopsis
O828k7 yersinia pe
O91g92 oryza sativ
O9a4hi anulobacter
Q47809 enterococcu
Q91g94 arabidopsis
O8zdj0 yersinia pe
O8yzt8 ralstonia se
O97zx1 sulfolobus
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gulbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McParson D.
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskarn D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskarn D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woolaye T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
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RI Science 287:2185-2195(2000).
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RP STRAIN-BERKELEY;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

RA George R., Gonzalez M., Bundoo J., Parcleb J., Paragas V.,

RA Champe M., Nungall C.J., Nundoo J., Parcleb J., Paragas V.,

RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RE MEL, ANO89533; AAL90271.1; -.

REMEL; ANO89533; AAL90271.1; -.

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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
p0506A10.26 protein.
p0506A10.26 protein.
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embr
Spermatophyta; Magnoliophyta; Liliopsida; Po
Ehrhartoideae; Oryzeae; Oryza.
NCBI TaxID=39947;
SEQUENCE FR
STRAIN=CV.
Sasaki T.,
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    Matsumoto
         Yamamoto
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0; Mismatches
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annotation update)
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01-NOV-1996
01-JUN-2002
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Bacteria; Firmicutes;
Bacillaceae; Bacillus
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InterPro; IPR001768; Try/amyl_inbtr.
Pfam; PF00224; tryp_alpha_amyl; 1.
PRINTS; PR01217; PRICHEXTENSN.
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Submitted (AUG-1993) to
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Arabidopsis thaliana (Mouse-ear cress).
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                                                          Scanlan E., Devine K.M.;
Submitted (NOV-1997) to
                                                                                              STRAIN=168;
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HSSP; P24337; 1HYP.
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A Hildert H., Hildert H., Klaerr Hlancharu H., Klaerr Hlancharu H., Klaerr Hlancharu H., Karamata D., Kasahara Y., Klaerr Hlancharu H., Kumano M., RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., RA Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., RA Sekiguchi J., Sekowska A., Tanaka T., Terpstra P., Tognoni A., RA Sekiguchi J., Sekowska A., Tanaka T., Terpstra P., Tognoni A., RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., RA Winters P., Wapata A., Yamamoto H., Yamane K., Yasumoto K., Yata K., RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the gram-positive bacterium Bacillus
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           SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=C9512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y.,
Fuji F., Hirama C., Nakamura Y., Og
                                                                                                                  Bacteria; Firmicutes;
Bacillaceae; Bacillus,
NCBI_TaxID=86665;
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EMBL; Z99111; CAB13777.1; -.
InterPro; IPR002487; LysM.
Pfam; PF01476; LysM; 1.
SMART; SM00257; LysM; 1.
                                                                                                                                                                                                             Hypothetical
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                                                                                                                                                                           Bacillus halodurans.
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
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             Ogasawara
                               Maeno
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Marter N.M.,
Daniel R.A.,
                             Masui
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Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APO01520; BAB07607.1; -

HYDO1520; BAB07607.1; -

HYDO1520; BAB07607.1; EBBC5FACDDC3D6F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-97313267; PubMed-9169971;

MEDLINE-97313267; PubMed-9169971;

Johnston M., Hillier L., Riles L., Dubois E., Dusterhoft A.,

Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,

Entian K.D., Floeth M., Goffeeu A., Hebling U., Heumann K.,

Entian K.D., Floeth M., Goffeeu A., Kleine K., Kotter P.,

Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D.,

Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

Wierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";

Nature 387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                              Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
EMBL; U17243; AAB67346.1; -
SGD; S0004292; YLR301W,
SEQUENCE 244 AA; 27501 MW; 80D813586A1930E
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Submitted
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(NOV-1994)
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InterPro; IPR003862; Pistil_extensin.
InterPro; IPR003882; Pistil_extensn.
InterPro; IPR002965; Pistin_extensn.
InterPro; IPR001768; Try/amyl inhbtr.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR01211; PRICHEXTENSN.
PRINTS; PR01211; PRICHEXTENSN.
SMART; SM00499; AAI; 1.
SMART; SM00499; AAI; 1.
SMOO499; AAI; 31609 MW; F3E6385C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=COLUMBIA;
Kaneko T., Kato T., S;
Submitted (MAR-2000) t
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Q9SET1;
01-MAY-2000
01-MAY-2000
01-JUN-2002
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Plant Mol. Biol. 41
EMBL; AF104328; AAD
HSSP; P24337; 1HYP.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 21, Last annoctation update)
01-JUN-2002 (TrEMBLrel. 21, Last annoctation update)
Similarity to cell wall-plasma membrane linker protein.
Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheof Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheof Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=20064977; PubMed=10598107;
GOO J.H., Park A.R., Park W.J., Park
"Selection of Arabidopsis genes encod
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-VAY-2000 (TrEMBLrel. 21, Last annotation update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Cell wall-plasma membrane linker protein homolog.
                                                                                                                                                  EMBL; AP001306;
HSSP; P24337; 1
                                                                                                                                                                                                                   "Structural analysis of
Sequence features of the
TAC and BAC clones.";
DNA Res. 7:217-221(2000)
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            InterPro; IPR003612;
InterPro; IPR003882;
InterPro; IPR002965;
InterPro; IPR001768;
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; AAI.
; Pistil_extensin.
; P_rich_extensn.
; Try/amyl_inhbtr.
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) to the EMBL/GenBank/DDBJ databases.
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Q9UGQ5;
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Q1-MAY-2000 (TrEMBLrel. 13, Cr
Q1-MAY-2000 (TrEMBLrel. 13, Lr
Q1-DEC-2001 (TrEMBLrel. 19, L
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Best Local
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Bukaryota; Metazoa;
Mammalia; Eutheria;
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Q39353;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the compani
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Brassica.
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SMART; SM00499; AAI; 1.
SEQUENCE 376 AA; 38667 MW; 7E1
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PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
SMART; SM00499; AAI; 1.
                                       EMBL; Z83851;
NON_TER
                                                                                               Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                          Ramsay H.;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                BK989H11.1.
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       88
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                                                               CAB62962.1;
   9699 MW;
                                                                                                                                                                                                                                                                      Chordata;
Primates;
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Last annotation update)
(Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Last annotation update)
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C2ED8FE7AB67CFA1 CRC64;
                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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o. 14;
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Best Local S
Matches 7
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Best Local S
Matches 7
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"The complete genome sequence of the lactic ac lactis ssp. lactis II1403.";
Genome Res. 11.731-753 (2001).
EMBL; AE006437; AAK06186.1; -.
InterPro; IPR00302; KOW motif.
InterPro; IPR003026; Ribosomal_L24.
Pfam; PF00467; KOW; 1.
ProDom; PD001677; Ribosomal_L24; 1.
TIGRAMS; TIGR01079; rplX bact; 1.
PROSITE; PS01108; RIBOSOMAL_L24; UNKNOWN_1.
Ribosomal protein; Complete proteome.
SEQUENCE 101 AA; 10877 MW; B4CAF87BE72C902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8S142
Q8S142;
clone:P0042A10.";
Submitted (FEB-2001) to the
EMBL; AP003343; BAB90081.1;
                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                          SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
"Oryza sativa (japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17
01-JUN-2001 (TrEMBLrel. 17
01-JUN-2002 (TrEMBLrel. 21
01-JUN-2002 (TrEMBLrel. 21
50S ribosomal protein L24
RPLX OR LL2088.
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Weissenbach J., Ehrlich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21235186; PubMed=11337471;
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"Oryza sativa (japonica cultivar-group) genomic LNA, L.,

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SEQUENCE FROM N.A.
TISSUE=LEAF SHEATH;
MEDLINE=99408265; PubMed=10480388;
MEDLINE=99408267. PubMed=10480388;
Ogawa M., Kusano T., Koizumi N., Katsumi M., Sano H.;
"Gibberellin-responsive genes: high level of transcript
in leaf sheath meristematic tissue from Zea mays L.";
                                                                                                                                                                                                                                                                                                           Zea mays (Maize).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

Panicoideae; Andropogoneae; Zea.

NCBI TaxID=4577;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0703B11.17 protein (P0485B12.9 protein)
P0703B11.17 OR P0465B12.9
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:P0703B11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZMGR1A.
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STRAIN=CV. NIPPONBARE;
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Last sequence update)
Last annotation update)
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Pred. No.
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Pred. No. 53;
0; Mismatches
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RESULT 16
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Best Local
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Ogawa M., Kusano T., Koizumi N., Katsumi M., Sa:
"Gibber=allin_responsive genes: high level of tr.
in leaf sheath meristematic tissue from Zea may.
In leaf sheath meristematic tissue from Zea may.
Plant Mol. Biol. 40:645-657(1999).
EMBL; AB018588; BAA74804.1; -
PLANTE PRO1373; 1HYP.
INTERPRO; IPR001768; Try/amyl inhbtr.
Pfam; PF00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI.
SMART; SM00499; AAI.
SMART; SM00499; AAI.
SMART; SM00499; AAI.
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Best Local
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01-MAY-2000
01-JUN-2002
                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative lipid transfer protein.
OSJNBA001515.11
ORYZA SATIVA (Rice)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                              Q9FWP4;
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EMBL; AB018587; BAA74803.1; -.
HSSE; P24337; 1HYP.
InterPro; IPR003612; AAI.
InterPro; IPR0037618; Try/amyl_inhb!
Pfam; Pf00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
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 SEQUENCE
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FROM N.A.
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ilarity 100.0%;
Conservative
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Pred. No.
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RESULT 18
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ID Q9FWP0
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InterPro; IPRO01768; Try/amyl inhbtr.
Pfam; PP00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
SEQUENCE 136 AA; 13982 MW; 9F785E
                                                                                                                                                         "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U80445; AAB37800.1; -.
Hypothetical protein.
SEQUENCE 141 AA; 15050 MW; 1F655AC7BAE14E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P91181,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C., Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E., Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; "Oryza sativa chromosome 10 BAC OSJNBa0015J15 genomic sequence."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                  Du Z., Le T.T.;
"The sequence of C. (
Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC026758; AAG13475.1; HSSP; P24337; 1HYP.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001
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Buell C.R., Yuan Q., M
Hsiao J., Zismann V.,
                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 
nes 7; Conserv
                                                                                   222
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                                                                                                           Similarity 7; Conser
                                                                                    STVTSNG 228
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al 15.0 kDa protein.
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 PRELIMINARY;
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7) to the
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EMBL/GenBank/DDBJ databases.
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 PRT;
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Best Local S
Matches 7
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Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
Allen N., Maylor J., Stange-Thomann N., DeArellano K., Johnson R.,
Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
Linton L., McEwan P., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Metcalf W.W., Birren B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Multiple resistance/pH regulation related protein E (Na+/H+'
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                                                                            "The genome of Methanosarcina acetivorans and physiological diversity."; Genome Res. 12:532-542(2002).
EMBL; AE011178; AAM07907.1; -.
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Oryza sativa (Rice).
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C2A / ATCC 35395 / DSM 2834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
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InterPro; IPR001768; Try/amyl_inhbtr.
InterPro; IPR001768; Try/amyl_inhbtr.
InterPro; IPR00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanosarcinaceae;
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Hsiao J., Z
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        proteome.
165 AA;
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        18327 MW;
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        DCAB72532F74E05E CRC64;
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ujii C.Y., VanAken S.E.,
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18 LGLIFGV 24

Query Match Best Local S Matches 7

Similarity 7; Conserv

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Mismatches

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Score 7; Pred. No.

DB 17; o. 76;

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Q926C3;
Q1-DEC-2001 (TEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TEMBLRel. 20, Last annotation update)
Probable peptidoglycan-associated lipoprotein precursor.
PAL OR R02738 OR SMC02942.
PAL OR R02738 OR SMC02942.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-2336507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Gloux Gapela D., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Boistard P., Becker A., Boutry M., Cadieu E., Lelaure V., Masuy D., Pohl T., Forcetille D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont sinorhizobium mellloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL, AL591791, CAc47317.1;
InterPro. IFR001145; Bac_OmpA.
Pfam, PF00691, OmpA; 1.
ProDom; PD000930; Bac_OmpA; 1.
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Lloyd C.R.;
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SEQUENCE 176 AA; 18735 MW; A6F162CB35042268 CRC64;
                                                                                                                   SEQUENCE FROM N.A. MEDLINE=99069613;
investigating biology."
                                    Genome sequence of the nematode
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KX MEDLINE=21192684; PubMed=11296296;

KA PETRETTI J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,

AP Primeaux C., Jeszate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

AA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

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"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

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REMBL; AE006596; AAK34332.1;

REMBL; AE006596; AAK34332.1;

REMBL; AE006596; AAK34332.1;

REMBL; AE006596; Cons hypoth95.

REMBL; AE00690498; Cons hypoth95.

REMBL; PS00025; NG MTase

PIGRFAMS; TIGRO0095; Cons hypoth95; 1.

REMONITE; PS00092; NG MTASE; UNKNUN.

REMONITE; PS00092; NG MTASE; UNKNUN.

REMONITE; PS00092; NG MTASE; UNKNUN.

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Eukaryota; Metazoa; (Mammalia; Eutheria; CNCBI_TaxID=9823;
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Q95KR4;
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01-DEC-2001
01-JUN-2002
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EMBL; AL032646; CARA21686.1; -
SEQUENCE 177 AA; 20062 MW; E3BA47B50CCFA329 CRC64;
                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Kuehl M., Glowacki G.,
"Molecular cloning and
ecto-mono (ADP-ribosyl)
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NCBI_TaxID=1314;
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Bacteria; Firmicutes; Bacillus/Clostridium
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7; Conservative (
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( protein SPy1538.
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., Haag F., Koch-Nolte F.;
nd characterization of human ART5,
yl) transferase from testis.";
to the EMBL/GenBank/DDBJ databases
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MEDLINE=21470413; PubMed=11586360;

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Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                  SC35 protein (LD32469p)
SC35 OR CG5442.
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Hypothetical protein; Complete
SEQUENCE 189 AA; 20660 MW;
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EMBL; AJ414150; CAC90573.1; -.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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100.0%; Pred. No.
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Last sequence update)
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598D4DF73D5E48C5 CRC64;
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5. 86;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Amanatides P.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaze's R.G., Champe M., Pfeiffer B.D.,
RA Bril J.F., Agbayani A., An H.-J., Andrews-Fennhoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendail J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Cherraz C., Ferriera S., Fleischmann W.,
RA Gebabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Harris N.L., Harvey D., Heiman T.J., Gelbart W.M., Glasser K.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Diegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Diegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Diegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Diegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krantison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krantison J.A., Weshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Melson D.R., Nalley M., Murphy B., Murphy L., Munny D.M., Nalson D.L.,
RA Harris R., Marke
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                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                       EMBL; AY069584; AAI
HSSP; P11940; 1CVJ
                                                                                                                                                                                                                                                                                                                                                       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. EMBL; AFC332775; AAFC3415.1; -. EMBL; AE003636; AAFC53192.1; -. EMBL; AE003636; AAFC53193.1; -. EMBL; AE003636; AAFC53193.1; -. EMBL; AY069584; AAL39729.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/CenBank/DDBU darabases.
                                                                                                                                                                                    FlyBase; FBgn0040286; SC35.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006;
                                                                                                 PS50102; RRM; 1.
PS00030; RRM_RNP_1; UNKNOWN_1.
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                                                  MISSING (IN SHORT ISOFORM)
                  65E922F8C34C7536
                  CRC64;
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RESULT 27

O881130 PRELIMINARY; PRT; 208 AA.

AC 081120;
DT 01-NOV-1998 (TYEMBLrel. 08, Created)
DT 01-NOV-1998 (TYEMBLrel. 09, Last sequence update)
DT 01-NAR-2002 (TYEMBLrel. 20, Last annotation update)
DT 01-MAR-2002 (TYEMBLrel. 20, Last annotation update)
DE CCAAT-box binding factor HAP3 homolog.
CC Arabidopsis thaliana (Mouse-ear cress)
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Core eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosi
CC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosi
CC SPERMATOPHYTA; Magnoliophyta; Eudicotyledons; core eudicots; Rosi
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WEDLINE=21681879; PubMed=11823852;

WEDLINE=21681879; PubMed=11823852;

REDLINE=21681879; PubMed=11823852;

A Arlat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

A Arlat M., Billault A., Brottier P., Camas J.C., Cattolico L.,

A Arlat M., Billault A., Brottier P., Cunnac S., Demange N.,

Chandler M., Choisen N., Claudel-Renard C., Cunnac S., Demange N.,

A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

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A Gaspin C., Tavie M., Moisan A., Robert C., Saurin W., Schiex T.,

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A Gaspin C., Lavie M., Moisan A., Robert C., Saurin B., Moisan A., Robert C., Saurin B., Moisan A., Robert M., Moisan A., Robert M., Moisan A., Robert M., Moisan A., Robert M., Moisan A., Robert M., Moisan A., Robert 
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ProDom; PD004109; IPP isomerase; 1.

Hypothetical protein; Complete proteome
SEQUENCE 205 AA; 22905 MW; 011998A4555B1B10 CRC64;
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0; Mismatches
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Q9SFD8,
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
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InterPro; IPR003958; CBFA_NEYB_domain.
InterPro; IPR003957; CBFA_NEYB_COpis.
InterPro; IPR004822; Histone_core.
Pfam; PF00808; CBFD_NEYB_HMF; 1.
PRINTS; PR00615; CCGATSUBUNTA.
SEQUENCE 208 AA; 22693 MW; 4E2D249AE2525DDB CRC64;
                                                                                                                                                                                AF036684; AAC39488.1;
P19267; 1A7W.
h 2.2%; Score 7; DB 1
Similarity 100.0%; Pred. No. 94;
7; Conservative 0; Mismatches
        DB .
94;
                                       10;
    0,
                                     Length 208;
    Indels
    0,
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Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;

Eurosids II; Brassicales; Brassicaceae; Arabidopsis. Created)
Last sequence update)
Last annotation update) AA.

SEQUENCE FROM N.A.

Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Conn L., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J Conway A., Jiu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.; sequence for Arabidopsis thaliana BAC T26F17 from EMBL/GenBank/DDBJ databases. chromosome Lee J., S

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

В Š

SEQUENCE FROM N.A.

Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.

Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,

Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.

Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M.,

Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,

Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis J.

Ecker J.,

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. Lee J., ₽

REQUENCE FROM N.A.

Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson W. Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Chon L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam W., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., W., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., W., Lee J., Lenz C., Li J., Liu A., Liu J., Schwartz J., Southwick A., W., W., Manney C., Sakano H., Schwartz J., Southwick A., W., Thaveri A., Toriuni M., Vaysberg M., Yu G., Davis R., Federspiel N. Theologis A., Ecker J., W., W. G., Davis R., Federspiel N. W., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

RMBL, AC013482; AAF16537.1; 
RMSDF, E19267; 1A7W.

RINTETPRO; IPR003958; CBFA_NFYB_topis.

InterPro; IPR003958; CBFA_NFYB_topis.

InterPro; IPR003957; CBFA_NFYB_topis.

InterPro; IPR003957; CBFA_NFYB_topis. Johnson-Hopson Lam z. ₩. c.,

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Q9S2U3;
01-MAY-2000
      "Oryza sativa nipponbare(GA3) genomic clone:p0433F09.";
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Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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                                                                                        Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
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01-DEC-2001
                                                                                                                                                                                     Q9FYQ4;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of "Coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL096884; CAB51434.1;
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STRAIN=A3(2) / M14
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Sasaki T.,
                                                                                                                             Oryza sativa (Rice).
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01-JUN-2002
                                                         SEQUENCE FROM N.A.
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                                            NIPPONBARE;
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uprotein (P0011G08.31 protein).
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                               RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Boxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daviss P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devis P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E. Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nowland T.J., Li Z., Liang Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Nelson S.M., Woodage T., Worls S., Chang K., Tunner R., Wang A.H., Wang X.,
RA Ye J., Yeh R., -F. Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng I...
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AP002539; BAB08181.1; -
EMBL; AP003225; BAB64659.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE 21
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STRAIN=CV. NIPPO
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RA Kichardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

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Hong L., Hallick R.B.;
"Gene structure and expression of
operon encoding cytochrome b6 and
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Curr. Genet. 25:270-281(1994).
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; X70810; CAC69148.1; -.
Chloroplast
Chloroplast
SEQUENCE 216 AA; 25364 MW; BFBF1385921BC18
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STRAIN=Z;
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"Alternative splicing
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100.0%; Pr
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of the Euglena gracilis chloroplast
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Pred. No. 97;
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the beta and epsilon subunits of the
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Best Local S
Matches 7
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Best Local :
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Q9H5P8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence
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Kawakami T., Noguchi S., Itoh T., Shigeta K., Kawakami T., Noguchi S., Itoh T., Shigeta K., Makajima Y., Mizuno T., Morinaga M., Taniagami Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmoi Obayashi M., Nishi T., Shibahara T., Tanaka T. Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ EMBL; AK026842; BAB15572.1; -.
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R00142 OR SMC04110.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q92KU4
Q92KU4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE 2:
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                                                                                                                                                                                                                                                                                                               TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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226 AA; 24278 MW; CF2611BE91D7B48E CRC64;
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b. le+02;
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b. le+02;
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M. A., Fujiwara T., Ono T
Mori Y., Ota T., Suzuki Y
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Q8TUT2;
01-JUN-2002
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                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed-11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin Slesarev A.I., Mezhevaya K.V., Belova G.I., Aravind Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind Shcherbinina O.V., Shakhova V.V., Belova G.I., Wolf Y.I., Ste
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01-OCT-2000
01-MAR-2002
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O. Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C
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Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., St
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus
                                                                                                                                                               Archaea; Euryarchaeota;
Methanopyrus.
                                                                                                                                                                                         Methanopyrus kandleri.
                                                                                                                                                                                                           COBS OR MK1671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes cholerae.";
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STRAIN=EL TOR N16961 / SEROTYPE
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Bacteria; Proteobacteria;
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                                                                                                                                            NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000)
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(TrEMBLrel. 20, Last annotation update)
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WASDLINE-20504483; PubMed=11016950;

WASDLINE-20504483; PubMed=11016950;

ANG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

ANG Swartzell S., Weir D., Hall J., Danson M.J., Hough D.W.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Randocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

ANG Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

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ANG Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Jablonski P.P., Omer A.D.,

Ball T.A., Maddocks D.G., Jablonski P.E., Maddocks D.G., Ball T.A.,

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O9HNY3;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence)
O1-JUN-2002 (TrEMBLrel. 21, Last annotat)
ABC transport protein.
TRP2 OR VNG1893G.
Halobacterium sp. (strain NRC-1).
Halobacteriaceae; Halobacteria; Ha
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O51373;
O1-JUN-1998 (
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Hypothetical
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Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002)
EMBL; AE010456; AAM02884.1; -.
Complete proteome.
SEQUENCE 241 AA; 25264 MW; E1C25302FBF7F6B6
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SEQUENCE
                                                                                           Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                 NCBI_TaxID=139;
   SEQUENCE
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MEDLINE=89065943; PubMede9403685;

A Fraser C.M. (Easjens S., Huang W.M., Sutton G.G., Clayton R.A.

A Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K.,

A Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

A Dougherty B., Kerlavage A.R., Quackenbush J., Salzberg S., Han

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Han

A Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

A Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatc

A Garlind S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatc

T "Genomic sequence of a Lyme disease spirochaete, Borrelia

T burgdorferi.";

L Nature 390:580-586(1997).

R EMBL; AB001146; AAC66791.1; -

TIGR; BB0412; -

G SEQUENCE 259 AA; 30809 MW; 2137010F9140D0FF CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 30.2 kDa protein.
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01-FEB-1997
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI — TaxID=6239;
                                                                                            Waterston R.;
"Direct Submission.";
submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U67949; AAB07562.1;
HSSP, Q91836; D112.
InterPro; IPR001159; DS_RBD.
Pfam; PF00035; dsrm; 2.
SMART; SM00358; DSRM; 2.
SMART; SM00358; DSRM; 2.
PROSITE; PS50137; DS_RBD; 2.
Hypothetical Protein.
Hypothetical Protein.
SEQUENCE 269 AA; 30169 MW; 2028FE3245563191 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of C. Submitted (SEP-1996)
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STRAIN=BRISTOL N2;
Bradshaw H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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STRAIN-BRISTOL N2;
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EMBL/GenBank/DDBJ
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Roberts K., Hatch
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                                                   Length 269;
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## SUMMARIES

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ALIGNMENTS

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41 SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySer 60 	21 IlePheGlyVallleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40 	1 MetThrValThrIleAlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeu 20 	B-706-2 (1-322) x AX067452 (1-48328)	it Scores: 8.02e-89	14211 a	1 /org /db	Patent: WO 0078968-A 27 28-DEC-2000; Incyte Genomics, Inc. (US) Incation/onalifiers	Lagace, R.E., Nucleotide se	Moraxella catarrhalis. SM Moraxella catarrhalis Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;	AX067452 AX067452 N Sequence 27 from Patent WO0078968. N AX067452 AX067452.1 GI:12545072	961 CTTAAA 966	321 Leulys 322	01 GCGCACTATTTGAATTTAGAATTTCTAGAAATGGCGTGTATGTTGATCCATTGACAGTA 96	01 AlaalaLeupheGlupheArdIleSerArdAsnGlvValTvrValAsnDroLeuThrVal 32	281 TATGIYABDTHYVALARGTHRGIYGLHARGILEALBSEMECLYSASHGIHPTOSERGIY 300	81 ATTCAGCATACCAATGGATTTGTTTCAAGCTATATCCATATTAAGGACGCTCAAGTTAAA 8	261 IleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLys 280	TCATTCAAGCTGATCACAATATGGACGGGGCGAGTA	aSerAsnAlaGlyThrVallleGlnAlaAspHisAsnMetAspGlyAl	ATGGCATG		

AXO63565 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL		B 8 B	& & &	Db Qy	dg Qy	dg Qy	g Q	g Q	B & B & B & B & .
AX063565  AX063565  ON AX063565  AX063565.1 GI:12541292  S  Moraxella catarrhalis Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.  (CB 1 (bases 1 to 966) RS Thonnard, J.S.  Cloning of basb110 antigen from moraxella (branhamella) catarrhalis SMITHKLINB BEECHAM BIOLOGICALS (S.A.)	301 AlaAlaLeuPheGluPheArg1leSerArgAsnGlyValTyrValAspProLeuThrVal 320	<u> </u>	241 AlaSerAsnAlaGlyThrVallleGlnAlaAspHisAsnMetAspGlyAlaSerIleVal 260	221 GlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsn 240 	201 ArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAla 220	181 ValAlaProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPhe 200 	161 ProvalvalvalvaliysLysEroThrProThrProProValValGlnGlnProAlaPro 180 	141 AlaValGinSerSerArgProProValGinGinHisProAlaValGinLysProThrPro 160	61 GlnvalileThrAspSerGlnGlyValProAsnArgTyrGlnvalLysGlnGlyAspThr 80
50 D	S B S B S	Db Db	8 B 8	dg VQ	\$ &	g 9y	\$ &	B 6	S P P P P P P P P P P P P P P P P P P P
b 601 CGCTATCCTGTTGGTGCGACCAATCCAGTGGTTCGACGCTTTGGTACGCCGACGTGGCC 660  221 GlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuileAsn 240  241 GCTCAACTGTTACCAGTTGGCACCATTTGTTTCTGGTACGCGACAGTGGCC 660  25 GGCTCAACTGTTACCAGTAATGGCATGTGGTTTTCTGGACGAGATGGCGATTTAATTAA	161 481 181 541	b 361 AAGGTGCGTGAGCGTAGTATCAGCTCTGGGTGAATACAGCTCACACACCTTCGCCTGTG 420  141 AlavalGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThrPro 160	· 101 301 121	y 81 ValSerLysIleAlaGinArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsn 100 	97 61 GlnVallleThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThr 80	41 SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySer 60	y 21	y 1 MetThrValThrIleAlaIleAenSerGlnAsnGlnLysProIleLysArgLeuGlyLeu 20	### PRATURES    Source

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rpoS; RNA polymerase principal sigma factor; protein L-aspartyl carboxy methyltransferase.
Pseudomonas aeruginosa (strain:PAOI) DNA, clone:pDB18R, pDB19R,
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Takahashi,H.
Direct Submission
Submitted (11-DEC-1993) Hideo Takahashi, The University of Tokyo,
Submitted (11-DEC-1993) Hideo Takahashi, The University of Tokyo,
Inst. of Mol. & Cell. Biosci, Yayoi 1-1-1, Bunkyo-ku, Tokyo 113,
Japan (Tel:03-3812-2111(ex.7825), Fax:03-3813-0539)
Location/Qualifiers
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision;
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Tanaka, K. and Takahashi, H.
Tanaka, K. and Takahashi, H.
Cloning, analysis and expression of
Pseudomonas aeruginosa PAO1
Gene 150 (1), 81-85 (1994)
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Best Local Similarity:
Query Match:
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  ---PheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThr
                                       TCGACCACGACCCAGCAGCAGCGGCGCGACTCCCGTCGTCGCGGGGCCTGCGGTGGGG
                                                                          ValThrGluAlaProPheAlaThrGlySerSerGlyValMetGln-------
                                                                                                                                           ProThrProProValValGln------GlnProAlaProValAlaProPro
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                                                                                                            CCGGTTCCACCCGCAGTTAGTACGTCGGTACCTGCCAAGCCCGCACCG---
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EVVIRRFGLRGHESSTLEEVGQEIGLTRERVRQIQVEALKRLREILEKNGLSSDALFQ
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Stover,C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J.,
Hagrou,M., Garber,R.L., Goltry,L., Tolentino,E.,
Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N.,
Polger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H.,
Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
Hancock,R.E.W., Lory,S. and Olson,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M. Garber, R.L., Goltty, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y. Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R., Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T. Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Pseudomonas aeruginosa
                                                                                                                                                                                                                              University of Washington Genome
Box 352145, Seattle, WA 98195,
                                                                                                                                                                                                                                                                        Submitted (16-MAY-2000) Department of Medicine
                                                                                                                                                                                                                                                                                              Direct Submission
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AE004782.1 GI:9949772
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                                                                                                                                                                                                                                   USA
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University Of Washington,
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	Nagashima, K.V., Igarashi, N., Harada, J., Nagashima, S., Matsuura, K. and Shimada, K.	AUTHORS
	6 (bases 1 to 58996)	REFERENCE
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	PI., Nagasiiilla, N. v., Mac	A O I I ONO
	hida M. Jamiland M. Nacachima V.V.	REFERENCE
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	g. 36, 185-191 (1993)	JOURNAL REFERENCE
,	gelacinosus: rossibility of norizontal gene transfer in purple bacteria	
	V., Shimada, K. and Matsuura, K. analysis of photosynthetic genes of Rhodocy	AUTHORS TITLE
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                                                                                                                                                                         HCPRGIAFNEILFRTFRLELWFAALLSAGALLGSMIAR"
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Methylobacterium extorquens AM1"
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SGC

gene

Sg

gene

SgS

complement (4158. .4991)

gene

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ATCGCCGAGATGGGCGCCAGCGACGCCGACAGGGTGCAGCTGCACTTCGAGATCCGGCGT: 54257
                                        IleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArg
                                                                                         TACGCGCACAACCAGACCCTGCTGGTCAAGGAGGACCAGGCGGTCCGCCGCCGGCCAGAAG
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2. (bases 1 to 3122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Products Research Institute, Bio-Resource Development;
Matsunosato-1, Kukizaki-machi, Ibaraki 305-8687, Japan
(E-mail:murmur@ffpri.affrc.go.jp, Tel:0298-73-3211(ex.458),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (26-JUL-1997) Hitoshi Murata, Forestry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (E-mail:murmur@ffpri.affrc.go.jp, Fax:0298-73-3795)
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Pseudomonas tolaasii
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Pseudomonas tolaasii DNA for
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KNSTALKQHKYIDYTRALDATQLYLNEIGFSPLLTPEEEVHFARLSQKGDPAGRKRMI
ESNLRLVVKIARRYVNRGLSLIDLIEEGNLGLIRAVEKFDPERGFRFSTYATWWIRQT
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5876 bp DNA linear BCT 07-MAY-2002
Azotobacter vinelandii L.isoaspartate o-methyltransferase (pcm)
gene, partial cds; murein endopeptidase (mep), stationary phase
sigma factor (rpoS), aerotaxis sensor (aerP), aerotaxis transducer
(aerH), and ferredoxin A (fdxA) genes, complete cds; and DNA
mismatch repair protein (mutS) gene, partial cds.
                                             Azotobacter vinelandii.
Azotobacter vinelandii
               Azotobacter
                             Bacteria; Proteobacteria;
                                                                                               AF421351.2
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                                                                                                                                                                                                                                                                                                                                                    GTCGGACAGACAATTGCCGAAATGGGGTCAACGGGTACAGACCGGGTGAAACTGCACTTT
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                             gamma subdivision; Pseudomonadaceae;
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COMMENT
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Location/Qualifiers
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Submitted (19-SEP-2001) Biological Sciences, University of Alberta, CW405 Biological Sciences Bldg., Edmonton, Alta T6G 2E9, Canada 4 (bases 1 to 5876)
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Tindale, A.E., Meakin
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Direct Submission
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codon_start=1
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  63 IleThrAspSerGlnGlyValPro------AsnArgTyrGlnValLysGlnGly ::: ::: ||| |||||||
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                                                                                                                                                                                                                      23 GlyVallleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThr 42
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                                                                                                                                {\tt SerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnVal}
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MRGEIGRLMDMLIIKRTSLGNIVTDVYQCLGBVQPAA"
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Simpson, A.J., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvas, T.M., Araya, J.E., Baia, G.S., Bapista, C.S., Barvarenga, R., Alves, T.M., Araya, J.E., Baia, G.S., Bapista, C.S., Barvaros, M.H., Bonaccorei, E.D., Bordin, S., Bove, J.M., Briones, M.R., Bueno, M.R., Camargo, A.A., Camargo, L.E., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costa, F.F., Costa, M.C., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-Dorry, H., Faccincani, A.P., Ferreira, A.J., Ferreira, V.C., Ferro, J.A.,
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Xylella fastidiosa 9a5c,
AE003925 AE003849
                                                                                                                                                                                       Bacteria;
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Xylella fastidiosa 9a5c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCGGGGCTACGGCGAACTGATCATCATCAAGCATAGCGATGTTTACGTCAGCGCCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAATTGGGCCAGCCTGTCCTGGCTGCGTCTGATGGGTCGGTTGTGTACGCCCGGAGGTGGT 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAAACCTGTGGACCCTCTGCAATATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGAAATGGGGTCGACGGGTACCGATCGGGTGAAGCTCCATTTCGAGATTCGCCGCCAG 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCATAACCGCAGGCTGCTGGTCCGGGAAGGACAACAGGTGAAGGCGGGGCAGGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-2000) Organization for N Analysis, Bioinformatics Lab - IC/Unicamp,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10910347
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                                                                                                    RYGCTVQRLSVDGPRVTGAWINGALERADCCVVALGSYSPLLLAPLGLRLPVYPLKGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP|P29011 (percent identity: 54 %/query alignment coverage: 95.6 %/subject alignment coverage: 96.3 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder/Start codon shift: -6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
/gene="XF0852"
1363. .2460
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(6792), 151-157
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ocated using

gene

CDS

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GGYVGATSPGIGAMETTVSLLRXVCAIDVADTVICDRRIGSAGDQGEX"
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/gene="XF0854"
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                                                                                                                                                                                                                    AsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGly 118
                                                                                                                                                                                                                                                                                                         AspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIle
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                                                                                                                 AspLeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSer 138
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complement (6964...7641)
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located using Glimmer/RBSfinder"
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complement (6327. .6944)
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                                                                                                                                                                                                          Submitted (24-OCT-2000) Department of Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome
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Pasteurella multocida PM70 section
                                                                                                                                                                                          University of Minnesota, 55108, USA
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Zhang, Q. and Kapur, V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                             Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                         May, B.J., Zhang, Q., Li, L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
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204 of the
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:::|||:::
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261 AAAGAATTGGCATCATTAAACAATATGTCTGAACCTTATCGTCTAAGTGTTGGGCAAACC 10320
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                                  CAAGCGGTGAATGCCGCCGCCGCCAGGCAGAGTGGTTTATGCGGGTAATGCATTACGTGGT 10749
                                                                                                                                                                                                                                                                                                 ATGTAACTTGGCAATGGCCAAACCAAAGGCAAT-----ATTGTACAAGGCTTTTCAACC
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gene CDS

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236

10644

10689

216

10590

198

10530

162

10470

152

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fdxA gene; ferrodoxin; lipoprotein; mismatch binding protein; mutS gene; nlpD gene; RNA polymerase sigma factor; rpoS gene. Pseudomonas putida. Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic Engineering & Biotechnology, 99, 34012 Trieste, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-JUN-1999) V. Venturi, International Centre for Genetic Engineering & Biotechnology, Bacteriology Group, Pad
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139 ProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysPro
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                                                                                                                                                                                                                                                                                                                             codon_start=2
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303	-TCCACGGCAGCACCACGGTGGTGCCAGCCCGTCG	TCCACG			268	밁
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210	GAGTTGGCTGCCCGTAAC	TTCCGTTACGGC	CTCCATCGCC	ACGCTGTTC	151	뮍
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48	CTGGTGCTTGCACTGGCCATGGGCACCTTGCTGGCGGTTGC	ATGGGCACCTTG	rgcacTggccs	CTGGTGCT	7	<b>D</b>
39	LeullePheGlyVallleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyr 39	[hrThrCysIle]	eGlyValIle		20	Ş
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	;ches: 119	Mismatches:	30.45%	milarity:	Best Local Similarity:	Beg
	tive:	Conse:	43.59%	arity:	Percent Similarity	Pe
		Matches:	245.00		Score:	SC
	1: 3539	Length:	9.74e-06		d. No.:	Pred.

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                        Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                  Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T. Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., N. Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Mau, B. and Shao, Y.
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Escherichia coli K12
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Escherichia coli K12 MG1655
                                                                                                 Direct Submission
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Blattner, F.R.
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AE000369.1 GI:2367168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a, N.T., Burland, V., K., Mayhew, G.F.,
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AL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

On Sep 9, 1997 this sequence version replaced gi:1789214.

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director).

Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NGHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 (e-mail: markeamber.gatech.edu). Open reading frames that have been correlated with genetic loci are being annotated with CG site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (GSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://ogsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide web site

(http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated of RNA. encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
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ICIDKSLQLEPRRRKAVVIKECVDMYVPNPLKNNIKLYYKETESESHRVIIDNILKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="putative factor; Not classified" note="0458; This 458 ad ORF is 28 pct identical (6 gaps) to 407 residues of an approx. 560 aa protein IAGA_SALTI sw: P43016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mstetieifnnsdemanqlkhalskgenlallhgltpdildriy
ayafdyhekgnitdaeiyykflciyafenheylkdfasvcqpkkkkyqqaydlyklsyn
yffyddysviyrmgqcqigaknidnamqcfyhiinnceddsvkskaqayiellndnse
                                                                   to 128 resi
SW: P43018"
                                                                                                                                                     /gene="b2854"
3561. .3977
                                                                                                                                                                                                                                  /transT_table=11
/product="orf, hypothetical protein"
/protein_id="AAC75892.1"
/protein_id="AAC75892.1"
/db_xref="c1:1789217"
/translation="MTNPIGINNLSQSSNIANATGDEVVSLDKHINTSATDTDQIQAF
IVSTWMAPFQNDMYSEDNPISPYYKIEW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3039. .3061
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/protein_id="AAC75891.1"
/db_xref="GI:1789216"
                                                                                  /gene="b2854"
/function="orf; Unknown"
/note="0138; This 138 aa
to 128 residues of an app
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="central position to predicted /bound_moiety="PhoB predicted site"
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/db_xref="GI:1789215"
/product="orf, hypothetical protein"
/protein_id="AAC75893.1"
                                                                                                                                                                                                      'note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="central position to predicted
/bound_moiety="Fur predicted site"
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                                 transl_table=
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                                                                                                                                                                                                         factor Sigma70;
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                                   table=11
                                                                                  aa ORF is 39 pct identical (7 approx. 168 aa protein IAGB_S
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Best Local Similarity:
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US-10-018-706-2 (1-322) x AE000369 (1-9720)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 LysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIle 95
ValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrp 230
                                                                                                                                                                                                                                                                                                                                                                         AAAACCGCATCGGTTACACCGTCATCAGCGGTACCGAAATCATCCTGGCCGCCAGTAGGG 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGCGACTGAACGGCATTTCCCCCCCCTTACACCATTGAAGTTGGTCAGAAACTAAAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATCTCTGGGTATCGTGATGTTGTTATCGGTTGGACTGCTTTTGGCCGGGCTGT-----
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                                                                                                     AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210
                                                                                                                                                                                                             ThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPhe 190
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nnniksldywlmqinomhipllkkrgiikderdlldnpclnikigteilynhfsrcgv
Twoclgtynagfaminokkrooyapkyilyipglmn"
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NKEIANFLQLSRKTVETHRLNIMKKLDVHSGIELIKTALRMGVCTI"
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'protein_id="AAC75894.1"
'db_xref="GI:1789219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4022.
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/transl_table=11
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REFERENCE
AUTHORS
TITLE
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ECU28375/c
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Escherichia coli K-12 genome;
U28375
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Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics,
Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequence was determined as part of the E. coll Genome Project
(Frederick R. Blattner, director) at the University of
Wisconsin. Madison. Supported by award H900301 from the NIH Human
Genome Project. The entire sequence was independently determined
from E. coll MG1655; overlaps with other sequence determinations
are annotated. This entry should be considered somewhat
provisional; it will be updated and merged with others at a later
date.
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Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAACCAGCTGGCTACGGTAATCTCATCATTAAACACAGTGAAGATTACATT 8887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases
                                                                                                                                                                                                                                                                                                                       /map="approximately 64 to 65 minutes"
/note="this sequence comprises the following lambda
/note="this sequence comprises the following lambda
clones: DD644 [EC30K464-1), DD645 (EC27-1154),
DD649 (EC22-159), and DD653 (EC18-341); M13Janus vector was
used for subcloning"
                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 to 55175)
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                                                                                                                      /1abel=ORF o148
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KIENNVDLNKFTTICTDVLSPRVTRHNKEKNKRHSTLLKNPLFNPH"
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| strain="K-12"
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/protein_id="AAA83033.1"
                                                                                  note="ORF_0163"
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transl_table=
                                                                                                                                                                                                                                                                                  lote="ORF_o148"
                                                                                                                                                                                                                                                                                                                                                                                                                                  xref="taxon:562"
                                                                                                                                                                                                                                              table=11
                                          table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp DNA linear BCT 08-DEC-1995
; approximately 64 to 65 minutes.
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complement (4754. .4909)
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FKDKSLEVESYFVDKSIWNVHITFHDDKRFVFFTDQFIAEFSPQEFVDNCEQYLINNH
CFSPDKVNEICEQARHYLVEKWFETHSLDMNNSVLASPEDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAA83036.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Codon Start=1
(codon Start=1
(trans] table=1
(rans] table=1
(labl=2 or 072
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(VSTWMAPFQNDMYSEDNPISPYYKIEW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1816. .4232
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                                                                                                                                                                                                                         complement (5131. .5562)
note="ORF_f143"
                                                                                                                                                                                                                                                                                                                    /label=ORF_f51
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                                                                                                                                                                                                codon_start=1
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                                                                                                                                                              label=ORF
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                                                                                                                                                                                       misc_feature
/note="codon recognized: GGG;
672; alternate gene names suA3
complement(8953. .9732)
                                                                                                                                                                                                                                          t tabia lelon="mytyafnkrlmyymkgksaltillagifscgtcqatgabytse
svenilnstgaatdksylslnpdkypnyrllihsaklobikkshytkdbiqglitite
ntrkltitekemgtfilastfeddktaaethydavmladslkeymalvsdqgnsyaak
kvlltimdynstpdqikemodvisnpkrldgipvomavhirpdsnspymadvqeegk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKNTAVRSPESNGIAESFVKTIKRDYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSAL
GYRSPREYLRORACNGLSDNRCLEI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon start=1
/transI_table=11
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                                                                                                                                                   /note="corresponds to X52798 differences outside tRNA"
                                                                                                                                                                                       complement (8664. .8962)
                                                                                                                                                                                                             DS"
                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7851. .8687)
/note="was f268 and f157p before splice"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mivlilvfrlvigeomidvlgpekrrrtioekiaivoosfepg
mivslvarohgvaasolflwrkoyoegsltavaageovvpaselaaamkoikelorll
gkkimenellkeaveygrakkwiahapllpgdgb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mdsarallargwgvslvsrclrvsraqlhvilrrtddwmdgrrs
RHTDDTDVLLRIHHVIGELPTYGYRRVWALLRRQAELDGMPAINAKRVYRIMRQNALL
LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFCCDNGERLRVTFALDCCDREALHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (6189.
/note="ORF_f301"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="msgniganpinnmnllplicllsgchfyrerfaergffykvpdv
Lrdylsaipleinekarykpgianyhniitcgfstllpyirqqplamqqrfnllfpdf
VDHIQsplplastlleritfyakknrdeldkisckmccd"
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complement (5779. .6204)
/note="ORF_£141"
                                                                                            complement (8801.
                                                                                                                                  complement (8801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (7506. .7805)
/note="ORF_f99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (7052. .7462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=ORF_f90
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                                                                            /gene="glyU"
                                                                                                              gene="glyU"
                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1/
transl_table=
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/db_xref="GI:887812"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAA83041.1"
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db_xref="GI:887813"
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transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein_id="AAA83040.1"
db_xref="GI:887809"
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                 3GG; aa: Glycine; CG Site No. suA36, sufD, sumA, sumB, sup
                                                                                                                                                                   (ECTRNAG); 4 sequence
                   sumB, supT"
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                                                                                                                                                                     9261
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                     9141
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                                                                                                                                                                                                         231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnThrAlaHis---ThrProSerProValAlaValGlnSerSerArgProProValGln 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGly
                   ACGGCTTACGCCCATAATGACACGATGCTGGTAAATAATGGGCAAAGCGTGAAGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGCGACTGAACGGCATTTCCCCCCCCTTACACCATTGAAGTTGGTCAGAAACTAAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIle
                                                   SerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGly
                                                                                            GGCAACCAGCTGCGTGGCTACGGTAATCTCATCATGATTAAACACAGTGAAGATTACATT
                                                                                                                                AspHisAsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheVal
                                                                                                                                                                     ATCTCAGCTCCACGGGGTACACCTATTTACGCCGCGGGTGCAGGAAAGGTGGTGTATGTG
                                                                                                                                                                                                         PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla
                                                                                                                                                                                                                                                                                ValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrp
                                                                                                                                                                                                                                                                                                                           TCGACAGCAGATGGCGGC
                                                                                                                                                                                                                                                                                                                                                             AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACGTTGTTGGTTATGGCCAACGACAGGGAAAGTTATCATG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANACGGGGGGATACGCTATATCGTATTTCGCGCACCACGGGAACCAGCGTAAAAGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGGGGCGAAAAGTAGCAGTATTACACGTAAATCAACCGCCAAATCAACGACC
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Becherichia coli 0157:H7 DNA,
AP002563 BA000007
AP002563.1 GI:13363121
                                                                                                                                Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (B-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
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Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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20198780
2 (sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Bacherichia coli 0157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Kurokawa, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T., Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and Shinagawa, H. Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                             5 (bases 1 to 266658)
Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T.,
Hayashi,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Yokoyama,K., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Tanaka,M., Tobe,T., Iida,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
Turunahi m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli O157:H7
Bacteria, Proteobacteria,
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                        /organism="Escherichia
/strain="O157:H7"
                                                                                          location/Qualifiers
                                                                     .266658
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                                                                                                                                                                                                                                                                                                                                        /note="inhibitor of CsrA"
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complement (2444. .2989)
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complement(1493..1822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (711. .1493)
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complement (711. .1493)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1865. .2233)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to YQCB_ECOLI
99 in 260 aa (Conserved in E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_strain="RIMD 0509952"
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complement(244. .693)
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100 in 149 aa (Conserved in E.coli K-12)"
/codon_start=1
                                                                                                                                                                                                                                                                                                note="similar to SYD_ECOLI gi|1789157 percent identity in 181 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1/
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                          'gene="ECs3654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="CsrB RNA"
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.coli K-12)"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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IVKAMSILVFPFVGVLMLLALYLI PQMMADALETLSLDTASATGINGLMMTLWLAIPVM
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SLRGKGKSIEINKLNRITALFMLVTTWIVATLNPSILGMIETLGGPIIAMILFLMPMY
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LVSFRHHNEFHEQCVERIFNDLLRFCQPEKLSVYARYTRRGGLDINPWRSNSDFVPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENEYLYARRVGNQLGLRELNICTGCGPGAMEAPMKGAAVGHAQQRYKDSRFIGMTEPS
IIAAEPPNPLVNELIIMPDIEKRLEAFVRIAHGIIIFPGGVGTAEELLYLLGILMNPA
NKDQVLPLILTGPKESADYFRVLDEFVVHTLGENARRHYRIIIDDAAEVARQMKKSMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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DILFYYGQIHMTVRFPNLNLDNSVHIINLVFSILRNARALHYGEADMVVCWGGHSIN
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4017. .5381
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5938. .7227
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                                                                                                                                                           /note="similar to SDAA_ECOLI gi|1788116 percent identity 77 in 455 aa, similar to SDAB_ECOLI gi|1789161 percent identity 99 in 455 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="BAB37077.1"
/db_xref="GI:13363126"
                                                                                                                                                                                                                                                                                        AIQKVPAMRKYSGHISNVFVVVMGLIAISAIFYSLFS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVKENRRDTGDAYSFNWSMRIAPDLQMPFEPSHENMANLKLYPDQPVEVLAADLRRAF
SGIVAGNVKEVGIRAIEEFGPYKINGDKEIMRRMDDLLQGFVAQHRMKLPGSAYIPCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/evidence=not_experimental
                                                                                                                                                                                                                   /gene="ECs3657"
                                                                                                                                                                                                                                    /gene="EC83657"
7285. .8652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/transl_table=11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to SDAC_ECOLI gi|1789160
100 in 429 aa (Conserved in E.coli K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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99 in 454 aa (Conserved in E.coli K-12)"
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of 460 of the complete genome. AE012272 AE008922 AE012272.1 GI:21112795
                                                    AE012272
Xanthomonas
                                                10773 bp DNJ campestris
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93506 AAAICTCTGGGTATCGTGATGTTGTTATCGGTTGGACTGCTTTTGGCGGGCTGT-----
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                                                                                                                                                                                        CGTTACCGTGCAACGGCAATTGATCCGCTACGTTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                 GlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIle 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGGCTTACGCCCATAATGACACGATGCTGGTAAATAATGGGCAAAGCGTGAAGGCTTGGG 92904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAACCAGCTGCGTGGCTACGGTAATCTCATCATGATTAAACACAGTGAAGATTACATT 92964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTCAGCTCCACGGGTACACCTATTTACGCCGCGGGGCAGGAAAGGTGGTGTATGTG 93024
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                                    DNA
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linear BCT 23-MAY-2002
ATCC 33913, section 180
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS
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CE 1 (bases 1 to 10773)

RS da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camartotte,G., Cannavan,F., Cardozo,J., Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L., Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L., Cursino-Santos,J.R., Bl-Dorry,H., Paria,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.T.T., Formighieri,E.F., Franco,M.C., Ferreira,R.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,E.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A., Madeira,A.M., Martins,E.C., Meidanis,J., Madeira,A.M.B.N., Martinez,Rossi,N.M., Martins,E.C., Meidanis,J., Menok,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K., Oliveira,V.R., Pereira Jr.,H.A., Novo,M.T.M., Oliveira,V.R., Pereira Jr.,H.A., Tamura,R.E., Teixeira,E.C., Tezza,R.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Spinola,L.A.F., Takita,J.P., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P. Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Comparison of the genomes of two Xanthomonas pathogens with differing host specificities

B. 10204217

D. 2022145

D. 2022145

D. 2032145

D. 2032145
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Submitted (28.NOV-2001) Departmento
Sao Paulo, Av. Prof. Lineu Prestes '
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Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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748, Sao Paulo,
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SP 05508-900,
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ocated using Blastx/Glimmer/Genemark"
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Query Match:
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Best Local Similarity:
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                                                   4338
                                                                                                                                                                                                           4224 CTGACGGCCTGCAGCAGCGCGACAGTGGTGCGTTCGCCC-----AACTCGGGCAGTGGT
            82
                                                                                        62
                                                                                                                                                                  45 SerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIle------GlySerGln
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Nature 406 (6799), 959-
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                                                             Stover,C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadnan,S., Yuan,Y., Brody,L.L., Coulter,S.N., Polger,K.R., Kas,A., Larbig,K., Lim,R., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T. Complete genome sequence of Pseudomonas aeruginosa PA01, an
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Stover, C.K., Pham, X. -Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.
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strain="PAO1"
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGGAACTACAAGGACCTGGCGCGCGCCCAACGGCATCCGCCCCGCCCTACGCGGTCAAG 5734
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                                                                                                                                                                                                                                                                                                                                                                                                                      ValGlnGlnHisProAlaValGlnLysProThrProProValValValValLysLysPro 168
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                                                                                                                                                     ProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsn 208
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LNALLADLYGDQRLLAEGLLPSELVFGHPNFLWPALGIRPFGGIFLHSYAVDLARDAD
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LLVAAAALMEKIFREFAFDAQATQVATPLDEVLERRRGVCQDFAHLMLACLRARGLAA
RYVSGYLLTREPPGQARLIGADASHARVSLYCPENGWVDFDPTNDLLFDLEHITLAWG
RDFSDVSPLRGVILGGGSHDPEVRVTVLPLQETAG"
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/transl_table=11
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AE008839/c
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Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,
Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,
Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,
Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-MAR-2001) Genome Sequencing Center, Department Genetics, Washington University School of Medicine, 4444 Fore Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
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Salmonella typhimurium LT2
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                             EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the progiging finder, http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark, http://opal.biology.gatech.edu/GeneMark/
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The Salmonella typhimurium Genome Sequencing Project.
Direct Submission
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complement(241.
/gene="yqeF"
/EC_numbe=
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/gene="yqeF"
/note="putative RBS for yqeF; RegulonDB:STMS1H003067"
complement(1542. .2410)
/gene="STM3020"
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Complement (1542. .2405)

Gene="STW3020"

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AENLAREYGISRELQDAYALSSQOKARAAIDTGRFKDEIVPIVTQRNGGTAIUTDEQ
RENLAREYGISRELQDAYALSSQOKARAAIDTGRFKDEIVPIVTQRNGGTAIUTDEQ
RENLAREYGISRELQDAYALSSQOKARAAIDTGRFKDEIVPIVAIR
RENADASAEGLALLHPAFDSLGSVTAGNASSINDGAAAVMMSEAKAQALGVGKMLEWDE
RASVGVDPALMGIAPVYATRRCLERAGWQLTBVDLIBANEAFAAQALSVGKMLEWDE
RRVNVNGGAIALGHPIGASGCRILVSLVHEMVKRDARKGLATLCIGGGQGVALTIERD
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/gene="yqeF"
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ANAIDEVILGQVLTAGAGQNPARQSAIKGGLPTTVSAITINDVCGSGLKALHLATQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="putative RBS for STM3020; RegulonDB:STMS1H003068"
2476. .2964
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/note="similar to E. coli putative acyltransferase
/note="similar to E. coli putative acyltransferase
/AAC75883.1 (394 aa), 91%
identity in aa 2 - 393"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Salmonella typhimurium LT2"
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/db_xref="ATCC:700720"
3106. .4335
/gene="STM3022"
/note="similar to E. coli putative transporter protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="STM3021"
2476. .2481
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|protein_id="AALI21895.1"
/db_xref="GI:16421570"
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note="LT2"
                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="G1:16421572"
| Vranslation="MIKSKVFSMOHDAIQRRSLPERIFHAVCFEGIATAILAPTTAW
| Vranslation="MIKSKVFSMOHDAIQRRSLPERIFHAVCFEGIATAILAPTEAW
| MQRSIVAWVLNVSLLQAFTLEIGFFLFFLPYTMLYNWAYDVLRQRIVTRQQRVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="putative inner membrane protein"
protein_id="AAL21897.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
transl_table=11
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PRILMCYMNOLMHREILAGUSGLAQUELLQETYRGRGRLSALCGRLNTQEKQIWQDKY
RLLYKLGMRNRIRELLEGTRFCKSLQRTPFIAPQ"
complement (6596. .6601)
/gene="STM3025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"similar to E. coli orf, hypothetical protein (AAC75166.1); Blastp hit to AAC75166.1 (90 aa), 93% identity in aa 1 - 90" (codon statt=1 (rans_table=1) (rans_table=1) (product="putative cytoplasmic protein" (protein_id="AAL21899.1" (protein_id="AAL21899.1" (protein_id="AAL21899.1" (db_xref="GI-16421574" (ranslation="MSHTIRDKOKLKARTSKIQGQVIALKKULDEPHECAAVLOQIAA IRGAVNOLMREVIKGHLTEHITHGOKLEARTSKIQGQVIALKVLDSYIK" (complement (4644...4649)
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LVAWPLTYWPHKALCOPILSSKTSAGEGITGAVTHYYGKKLGNITTTLYFIAFFVVVL
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IAYFLFLSLYLTGSWGDSLLTGQMSLDSHTLHQVWISIPWWFAFSHTPISTFAIDR
RENFGDQANDKCKLMKVAYLIIGLSVLFFVFSCLLSIPFSYIDARNEGVTILSALS
MMPNAPAWLSISGIIVAVVAMSKSFLGTYFGVISGATEMVRTTLQQVGVKKSRAFNA
LSIMLVSGITFIICCLNPAMSMIYALSGPLIAMILFIMPTLSTYLIPALKPYRSVGN
FTILVVGLLCVSVMFFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (5836, .6601)
/gene="STM3025"
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complement(4366. .4638)
                                                                                                                                                                                                                                                                                                                                                                                     complement (5836. .6594)
/gene="STM3025"
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/transl_table=11
/product="putati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="similar to E. coli orf, hypothetical (AAC75167.1); Blastp hit to AAC75167.1 (274 dentity in aa 1 - 274"
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protein_id="AAL21898.1"
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                                                                                                                                                                                                                                                                                                                                                           note="transcriptional regulator SprB (gi|5007028)"
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RBS for STM3025; RegulonDB:STMS1H003072"
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                                                                                                                                                                                                                 AsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheValSerSer
                                                                                                                                                                                                                                                                                                                                                                                      ArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGATACGTTGTATCGTATATCGCGCGCTACGGGAACCAGCGTGAAAGAACTGGCCCGA 18719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAla
  ATCGCTACGATGGGCAGCACGGATGCCGCATCCGTAAGACTACACTTCCAGATTCGCTAC 18221
                                    IleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArg
                                                                                   TACGCTCATAATGACACCATGCTGGTTAATAATGGACAAAGCGTTAAAGCGGGGCAAAAA 1828:
                                                                                                                         TyrlleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg
                                                                                                                                                                                                                                                            GGCGCGCGGAACGCCTGTTTATGCGGCGGGAGCGGGTAAAGTTGTCTATGTCGGGAAC
                                                                                                                                                                                                                                                                                                   GlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTGGGTATGGCCTGCTAACGGTAAAGTGATTTTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaHisThr---ProSerProValAlaValGlnSerSerArgProProValGlnGlnHis 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAGCGCAAAGAGTAGCACTTCAACACGCAAAACCAGCAATAAAACAGCAACAAAAACT 18602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyAspLeuLys------ValArgGluArgSerIleSerSerGlyValAsnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TCCAGTAATTCCGGCTCAGGAACGTAT----TCCGGCTCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGTATTGCGGTGCTGTTATGCACAGGGCTGCTGCTGGCGGGGTGT
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                                                                                                                                                                                                                                                                                                                                                ------AATAAGGGGATCGATATTGCG
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AUTHORS
TITLE
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ORGANISM
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AL627277/c
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davise, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella enterica servorar Typhi CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230050 bp DNA linear BCT 06-JUN-2002 Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18, complete chromosome; segment 13/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-OCT-2001) Submitted on behalf of sequencing team, Sanger Centre, Wellcome Trust Hinxron, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of S. typhi sequencing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Notes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/S_typhi/).
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ILYFAMSILVFPFVAALMLLALYLIPOMNGAALFLFDFDSAASTGNGLWMTLWIAIPAM
VFSFNHSPIISSFAVAKREEYCEGAEKKCSKILAFAHIMMVLTVMFFVFSCVLSLTPA
DLAAAKGNISILSYLANHFNAPIIAWAPIIAMAFIIAMITKSFLGHYLGAREGFNGMVIK
SLRGKGKSIEINKLNKITALFMLVTTWIVATLNESILGMIETLGGPIIAMILFLMPMY
                                                                                                                                                                                                                                                                                              Orthologue of E. coli sdaC (SDAC_ECOLI);
SDAC_ECOLI (429 aa), 95% identity in 429
                                                                                                                                                                                                                                                                                                                                                overtap
                                                                                                                                                                                                                                                                                                                                                                                      aa overlap
AIQKVPAMRKYSGHISNVFVVIMGLIAISAIFYSLFS"
                                                                                                                                                                                                                                 /transI_table=11
/product="putative serine transporter"
                                                                                                                                                                                                                                                                                                                                                                Fasta hit to TDCC_ECOLI (443 aa), 50% identity in 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STY3109"
/note="sdaC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Salmonella enterica subsp. enterica serovar
Tvohi"
                                                                                                                                                                                                                                                                                                                                                                                                           /note="Fasta hit to Q46940 (409 aa), 40% identity in 416
                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="STY3109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain="CT18"
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                                                                                                                                                                                                                                                                                                Fasta hit to
aa overlap"
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available

CDS

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gene
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                FEGURICASE)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF01367 5_3_exonuclease, 5'-3' exonuclease, score 120.40, E-value 3.3e-32" complement (4042. .5190) /gene="STY3112" /note="fuc0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454 aa overlap
Fasta hit to SDHL_ECOLI (454 aa), 77% identity in 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3201. .3947
/gene="STY3111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mlasprrecyptrfyventvaahllivdalnlirrihavqgsp
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rdyfqdkwldapfirefgylprqlfdywglagissskypgvagigfysatqllyqpq
nlegiyahldevpekwrkklethkemaflcrdiarlqtdlhidgnlqdlrlvr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIERGITTEGVLPGKLRVPRRAAALRRMLVSQDKTTTDPMAVVDWINMFALAVNEENA
AGGRVVTA PTNGACGI VPAVLAYYDKET REVNANSLARYMLVASAIGSLI YKMNASI SG
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IERNAIASVKAVNAARMALRRTSEPRVCLDKVIETMYETGKDMNAKYRETSRGGLAMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="Sptrembl:Q8Z434"
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                                                                                                                                                                                                                                                                                /product="1,2-propanediol oxidoreductase (lactaldehyde
reductase)"
                                                                                                                                                                                                                                                                                                                                            Orthologue of E. coli fuc
FUCO_ECOLI (383 aa), 91%
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fasta hit to ADH2_ECOLI (383 aa), 44% identity in 371 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (4042. .5190)
/gene="STY3112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Orthologue of E. coli exo (EX9_ECOLI); Fasta hit
X9_ECOLI (281 aa), 88% identity in 264 aa overlap"
'codon start=1
'trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="L-serine de
protein_id="CAD02797
db_xref="GI:16504051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="STY3110"
note="Fasta hit to TDCG_ECOLI (454 aa), 73% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657. .3024
'gene="STY3110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135. .3950
gene="STY3111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Fasta hit to EUTG_ECOLI (395 aa), 40% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135. .3950
gene="STY3111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="sdaB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ote="exo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xref="SPTREMBL:Q8Z433"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ologue of E. coli sdaB (SDHM_ECOLI); Fasta hit to
_ECOLI (455 aa), 94% identity in 455 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _table=11
                                                                                                                                                                                                                                                                                                                                                                                                      coli fucO (FUCO_ECOLI); a), 91% identity in 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dehydratase 2 (L-serine deaminase
                                                                                                                                                                                                                                                                                                                                                                                                      Fasta hit to
aa overlap"
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                                                                                                                                                                                                                                                               No.:
   18 LeuGlyLeuIlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysPro
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Percent Similarity:
Best Local Similarity:
Query Match:
US-10-018-706-2 (1-322) x AL627277 (1-230050)
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complement (4354..4416)
/gene="STY3112"
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| pyekliteshiveidadogheogklessemrehmaayqtrpdanavvhhhavhctavs
| ilmrripahityminaaggensipcayyattgtrelsubhyadlknrkatilqhhdlir
| Eenldkalmiaheyevlaqlyistlaivdpvpvlddeaiaivlektktyglriee"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMLLCLISAFSGGHIĞLLALTLCSAFMSIQYPTIFSLGIKNLGUNU
GGGIVTPVMGFVSDAAGKIPTAELVPALCFAVIFIFARFRSQAATN
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/traiblation="mgnttigtgsfravdaegskskrylipfallcslefemavannu 
fgaalfwapatelmnytitligtelijaegsgryfiiplagtgstraubefsgrifillagt 
fgaalfwapatelmnytitligtelijaegsgrapgryfiipval 
fusfgaliavveggslilsnvehgsgealdkytegdsaykhstvlsvogtpyniival 
vlvvallimutkepalgsdhysgobaldkytegdsaykhstvlsvogtpyniival 
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gwsyliryaleelfgmtegfaanvittgtmvoffigretgstwlssreahkvladyald 
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E-value 2e-97"
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/gene="STY3112"
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/gene="9fam match to entry PF00465 Fe-ADH, Iron-containing
/note="Pfam match to entry PF00465 Fe-ADH, Iron-containing
alcohol dehydrogenases, score 655.70, E-value 2.4e-193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to FUCP_ECOLI
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'note="Fasta hit to YGBL_ECOLI (212 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="PS00913 Iron-containing alcohol dehydrogenases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="PS00060 Iron-containing alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="STY3116"
/note="fucI"
7758. .9488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="STY3115"
note="fucP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="STY3115"
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protein id="CAD02800.1"
db_xref="61:16594054"
db_xref="SPTREMBL:082431"
                                                                                                                              0.00535
232.50
40.19%
24.44%
13.92%
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Pseudomonas putida p
O-methyltransferase
Pseudomonas putida.
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e (pcm) gene, partial cds; and NI
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                                                                                                                                                                                         613 CTGGTGATTGCATTGGCCATGGGCTCGCTTCTGGTGGGTTGCTCAAGC
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 73
                                                                         60 SerGlnValIleThrAspSerGlnGlyValProAsnArg-----
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Ojangu, E.-L., Tover,
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TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp
                                     GCGCGGGTGGTCGACCGCAACAACACCGTGCCCAAGCGCCCGGCGGTGACTTCTGGGCAA
                                                                                                                                                   AsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGly
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FSIAFRYGMYKELAARNGIQAPYTIRFQQAIRFSGSSSRTTTVVSSPSSSSRTTVTR
RPVGSTATAFASTSKPATSAPSAFAVVATVPAAAERAVGGWTWPANGVLIGKFASNGS
LNKGIDIAGDLGQPVFAASDGAVVYAGSGLRGYGELIIIKHSDTYVSAYGHNRRLLVR
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/protein_id="AAF70311.1"
/db_xref="GI:7839531"
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/transl_table=11
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response sigma factor RpoS
AF244357
2 (bases 1551 to 2609)
Seshadri, R. and Samuel, J.E.
Direct Submission
Submitted (10-MAR-2000) Medical
A and M Health Science Center, 4
Station, TX 77843-1114, USA
                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group; Coxiella Group; Coxiella.

1 (bases 1 to 2609)

1 (bases 1 to 2609)

Seshadri, R. and Samuel, J.E.

Characterization of a stress-induced alternate sigma factor, RpoS, of Coxiella burnetii and its expression during the development
                                                                                                                                                                                                                                                                         Coxiella burnetii.
Coxiella burnetii
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Station, TX 77843-1114, USA
Sequence update by submitter
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Seshadri,R. and Samuei,J.E.
Direct Submission
Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology and Immunology, Texas Submitted (01-JUN-2000) Medical Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And Microbiology And 
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                                                                                                                             AACGGCTGGCTTCAACCGAAGGCACGGTTA-GGTTCT
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pgtdffamnhhcvsitplrvdlthyeafdqlaswvkrlem"
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/db_xref="taxon:777"
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db_xref="GI:8141682"
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Apodaca, J., And
                Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, B.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
                                                                                                                                                                           Escherichia coli O157:H7 EDL933
Escherichia coli O157:H7 EDL933
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Perna, N.T., Plunkett, G. III,
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to residues 1 to 99 of 99 from Escher
Strain MG1655: B2862"
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                                                                                                                                                                                                                                                                                      complement (1492. .2097)
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#116; Region
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coli K-12 Strain
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Jegene="24205"

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/function="orf; Unknown function"

/function="orf; Unknown function"

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/function="orf; Unknown function"

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5921. .6799
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RGYGNLIMIKHSEDYITAYAHNDTMLVNNGQSXEGWAKNRHHGEHGCGICSPAFPDSL
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3652. 5910
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/function="putative structure; Not classified"
/note="Residues 1 to 192 of 223 are 98.95 pct identical to residues 22 to 213 of 259 from Escherichia coli K-12

Strain MG1655: B2865"
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/db_xref="GI:15517383"
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Best Local Similarity:
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                          AsnThrAlaHis---ThrProSerProValAlaValGlnSerSerArgProProValGln 150
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product="putative dehydrogenase"
/protein id="Au657997.1"
/protein id="Au657997.1"
/db_xref="GI:12517386"
/translation="MNHSETITIECTINGMPFQLHAVPGTPLSELLREQGLLSVKQGC
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CGFCTPGLIMATTANLAKPREKPLTITEIRRGLAGNLCRCTGYQMIVNTVLDCEKTK"
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/function="putative regulator; Not classified"
/function="Residues 1 to 592 of 592 are 99.32 pct i
/note="Residues 1 to 592 of 592 from Escherichia coli
wG1655: B2869"
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/gene="ygeV"
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/function="putative enzyme; Not classified"
/function="Residues 1 to 159 of 159 are 99.37 pct identical to
/note="Residues 1 to 159 of 159 from Escherichia coli K-12 Strain
MG1655: B2868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Z4207"
6796. .7275
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Conservative:
Mismatches:
Indels:
Gaps:
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Direct Submission
Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEBH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex.
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http://sequence.toulouse.inra.fr/R.solanacearum.html.
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                                                                                                                                                                                                                                                  predicted
                                                                                                                                                                                                                                                                                                                                                    complement (2152. .3216)
/gene="RSc1150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAWYEEGWLQLAGPGAH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MNELPLYAAARGVQPGLAAGRPAQLLGGLSPRDEMRTHWQKKPL
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FLLQAHGRRRWRISSQNDLTLVPDLPLKILANFTPEEEFILEPGDMLYLPPHYAHDGV
                                                                                                                                                                                                                      predicted by Codon_usage
predicted by FrameD"
                                                                                                                                                                                                                                                                           Gene name
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (2152. .3216):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VADEDDEEPPRTLH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBALDGHEQGFETKLQLEPDDAFGEYDQELIKIEPRDRFPEPLEVGMQFEGVPEDGDD
EDAIIYTVTDVAEDKVVLDGNHPLAGMALRFDLRVTDVREATAEEIEHGHVHGENGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEGDCMTYSVGFRSPSYRELAGHFLGFLSQTLEDNPDFEGRYTDPEQKPVERPGELPT
AMVRALAQKLNALRWTPELVGEFFGAYLTEPKDHVEFVTQPRLSLARFTARARKEGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (332. .1561)
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                                                                                                                                                                                                                                                                        /note="Product confidence : probable
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted by FrameD'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="cell processes; chaperoning"
/note="Product confidence : probable
Jene name confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDARTQALYDAQRFWINGDTFEPSDTLLAWLSALSDQRGASAEAVDAAADLPDLMDTI
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                                                                                                                  product="PROBABLE TRANSMEMBRANE
                                                                                                                                     /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                              note="RS04601"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="RSc1149; RS04602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="GI:17428162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="CONSERVED HYPOTHETICAL PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="RSc1148"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="RSc1148"
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strain="GMI1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                          function="miscellaneous; unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MKIAKNTVVSVAYKLSDAQGNVIEESDEPMVYLHGGYDGTFPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="probable fksp-type peptidyl-prolyl cis-trans somerase (rotamase) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EC_number="5.2.1.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="slyD"
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Homology
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CLASRITCFLDVLEARLAGGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (5960. .6853)

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/function="miscellaneous; not classified regulator"
/note="product confidence: probable
Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
/codon_start=1
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/gene="RSc1153"
/function="cell processes; transport
/note="Product confidence: putative
Gene name confidence: hypothetical
predicted by Codon usage
predicted by Homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (5960. .6853)
/gene="RSC1152"
/note="RS04599"
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synthesis, modification; dna - replication, repair,
restr./modif."
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DQAKERSYRENARWETGGVLFVTLNVPCDNNNYKTAGGRNGEYEDRLEANRQWLARAF
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EYDGAVLLIHGASQSFLLDRPLKDESGRPDPHVMRARTFGSPTLDQWLEVSVTFGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATHYEELTQLPQEFAQAANVHLSAVEHGDGIVFLHAVQEGPASQSYGLQVAQLAGVPQ
PVIRAARKKILMLEQHSADTGATPQLDLFALPSDPSDDDAAEAAAPAAPSALAEALDG
IDPDSMTPRDALDALYRLKALSDASA"
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                                                                                                                                      of small molecules"
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Best Local Similarity:
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysileAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGCCGCTGGAACCGCCTCCGCCCCGCTACTATCGGGTCAAGCGTGGCGATACGCTCTAC 70859
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                                                                                                                                                                                                                       ValValValLysLysProThrProThrProProValValGlnGlnProAlaProValAla 182
                                                                                                                                                                                                                                                                                                                                                                      GlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThrProProVal 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCCGAACCAGATCGAAGTCGACCAACTGATCCGCGTG------GTG 70961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysVal 122
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                                          ProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyr 202
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Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P.,
Borodovsky,M., Rudd,K.E. and Koonin,E.V.
Metabolism and evolution of Haemophilus influenzae
whole-genome comparison with Escherichia coli
                            Medical Center Dr. Rockville, MD 20850, USA
The H. influenzae sequence has been updated by R. Fleischmann.
database matches have been assigned, product names have been
improved, and a number of frame shifts have been corrected. We
gratefully acknowledge the work of Tatusov et. al. We have
                                                                                                                                                                                                                 White, O., Clayton, R.A., Kerlavage, A.R. and Fleischmann, R.D. Direct Submission Submitted (27-SEP-1997) The Institute for Genomic Research,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSer 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySer 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 11435)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 11435)
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their annotation
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Rd sec
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Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kerlavage, A.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 bp
section
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into the
                                                                                                                                                                                                                                                                                                                                                                                  20850,
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                                                                                                                                                                                                                                                                                                                                                                                                                       for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Fleischmann, R.D
                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 29-MAY-1998 complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                           9712
                                                                                                                                                                                                                                 9712
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-MAY-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 2085. Medical Center Dr, Rockville, MD 2085. The whole genome was shifted by 588 nucleotides for a new start On Sep 30, 1996 this sequence version replaced gi:1221405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 (bases 1 to 11435)
White,O., Clayton,R.A.,
Peterson,J., Hickey,E.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                           ALYVRKTDCNTLFVGEKLAKFAGVSERNMGYAGLKDRRAVTEQWFCLQMPGMETPDFS
QFELDGVEILTVTRHNRKIRTGSLEGNYFDILLRGAEESDELKARLDFVANFGFPNYF
TEQREGGHNLTQALRWAQGEIKVKDRKKRSFYLSAARSEIFNLVVAARIEKSTINQ
VLPNDIVQLAGSHSWFKADEKEDLTALQVRLENQDILLTAPLIGEDILAASEIENEIV
                                                                    identity: 56.50; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GB:L07942 SP:P36664 PID:1036739 PID:1036738 GB:U00096 percent identity: 44.24; identity: equence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKVEKNVVVSISYQVRTQDGVLVDEAPANQPLEYLQGHNNLVIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSKLAELQAETREIIEDLLNDGSEPNALYIIEHHIAHHDFDLLE
KIAVDAFKAGYEVSEAEEFKDDDGKPIFCFDIISEVELKAEIIDAQQKEILPLLEKHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:1790704 percent identity: sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (106. .678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (106. .678)
/gene="HI0699"
                                                                                                                                                                                                                                                                                                                                                                                  NQHSAFDPLMKQERMKAARRPLLMKAKGFSWAFEPEGLRLKFYLPAGSYATALVRELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HI0701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HI0701"
1328. .2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
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                                                                                                        note="similar to GB:U00096
dentity: 56.50; identified
                                                                                                                                                                                     gene="HI0702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MLEQLPYLALKTPPKTTALLKAECADFIVKEHLGYEMSGDGEFV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SP:P37163 GB:U14003 PID:537096 PID:1790704 percent identity: 54.20; identified k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="GI:1573703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="HI0700"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAC22358.1"
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Haemophilus"
db_xref="taxon:71421"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="peptidyl-prolyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="similar to GB:L13261 SP:P30856 GB:Z21496 PID:394720 DD:475995 percent identity: 68.25; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .11435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1219)
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                                                                                                    PID:1789101 PID:882637 percent by sequence similarity;
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gene

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3115. 3603
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3911. .5120
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DLPFEELKGYKVCRLGYRSSSVEVIKQRDPRDETIYWIGPSALPEDESEGTDFYAVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGIDVKELAALINILSEPYNISLGQULKISNODIKTUTTTVSVKOPAVTASTATPVKP
AVTYTPGANGTQIGSDGTIIGPIKSEAGTSEPSVPVATSSTQVTSSVNIANSTPINSNV
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3702. 3887
Jeane="H10704"
3702. 3887
Jeane="H10704"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identity: 72.25; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYVSITPIQADLTAYHSLLSLQNWLDQEFTK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'trans1_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGB:L10653 SP:P36684 PID:148929 percent identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
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gene

gene

SdC

gene

14

TKDLRAFGVEKSPLGLSAAGCLLQYAKETQRTALPHIQSISLIQNQDCIQLDAATRRN LELTQNLAGGTENTLASVLDKCVTPMGSTLLKRWIHQDVRDVEKLKQRQQSIABILNE DLVDELQPLLQLVGDMERILARVALKARRPRDLTRLETALBQIPALBAIVQQKTPPFL TALFSQIADFSEQCDLLQRALIETPPLLIRDGGVLABGYNAELDEWRMLSDGATQYLE KEYEDKVLKSKGAALALEKQLYDLFPLLLIRDGGVLABGYNAELDERWRLSDGATQYLE LEKERESTGIDTLKIGFNAVHGYYIQISQQQAKKAPIHYVRKQTIKNAERYITEPL LEYEDKVLKSKGAALALSELDVUNLAERDT LNYVMPTFCDEVSVKIKNGRHPVVEQVLKDPFIANPVELNHNRHLLVITGPNMGGKST

סט 5078	Qу 309	Db 5018	Qy 289	495	Ov 269	Db 4898	Qy .251	Db 4838	Оу 231	Db 4778	Оу 216	Db 4733	Оу 196	Db . 4673	Qy 176	Db 4613	Оу 161	Db 4562	Qy 151	Db 4517	Qy 131	Db 4463	Qy 111	Db 4403	Qy 91	Db 4343	Qy 71	US-10-018-706-	Pred. No.: Score: Percent Similarity: Best Local Similari Query Match: DB:
CGCTA	ß	B CAAGACATCGCAAAAATGGGTAGCTCTGGTACAAATACCGTGAAACTCCACTTTGAAATT 5077	- വ	AGTGCCTATGCGCATAACGACAAATTCTTGTCGCCGATCAACAAGAAGTCAAAGCAGGT 50		GGCAATGCTTTACGTGGTTACGGTAATTTAATTATCATCAAACATAATGATGATTTTTTA 4				B ACTTCAGGTAATATCATCCAAGGTTTCTCAAGCACAGATGGCGGTAACAAAGGAATTGAT 4837		AATGTCGTTGCGCCAATCGCCTCAAATGTTGTGTGGCAATGGCCG 4777	GlyValMetGlnPheArgTyrProValGlyAlaThrAsnPro	ACTTCATCAACACAGGTTACATCATCTGTAAATAATGCGAATAGCACACCAATTAA	6 GlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThrGlySerSer 195	GGTACTATTATTGGCCCAATTAAATCAGAGGCTGGCACATCGCCTAGTGTACCTGTGGCA 4672	ProValValValValLysLysProThrProTh	2CCAGCAGTCACTTATACTCCGGGCGCAAACGGTACTCAAATAGGATCTGAC 4612	GlnHisProAlaVal	7GTAAAACAACCTGCAGTCACAGCATCAACAGCAACGCCAGTTAAA 4561	ValAsnThrAlaHis	CAAGTTTTAAAGATTTCTAATTGTGACATAAAAACGGTTACTACAACGGTTTCT 4516	– ი	GATGTAAAAGAATTGGCGGCGTTGAATAACCTATCCGAACCTTATAATTTAAGTTTAGGG 4462		AATACCTATAAAGTAAACAAAGGCGATACAA	AsnArgTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLe	6-2 (1-322) x U32753 (1-11435)	0.00115 Length: 11435 219.50 Matches: 76 214.69\$ Conservative: 46 1milarity: 27.84\$ Mismatches: 114 13.14\$ Indels: 37 1 Gaps: 10

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REFERENCE
AUTHORS
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ORGANISM
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AE011804
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MEDLINE
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                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C., Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J., Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L., Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L., Cursino-Santos,J.R., El-Derry,H., Faria,J.B., Ferreira,A.J.S., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Formighieri,E.F., Franco,M.C., Greggio,C.C., Gruber,A., Katsuyama,A.M., Kishi,L.T., Leite Jr.,R.P., Lemos,M.V.F., Locali,E.C., Machado,M.A., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,B.C., Meidanis,J., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,B.C., Meidanis,J., Menck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Oliveira,M.R., Pereira Jr.,H.A., Rossi,A., Sena,J.A.D., Silva,C., Oliveira,V.R., Pereira,B.I.D., Trindade dos Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitaija, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quaggio, R.B., Monteiro-Vitorello, C.B., Van Sluys, M.A., Almeida Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C., Camargo, L.E.A., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B., Coutinho, L.L., Cursino-Santos, J.R., Bl.Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr., R.P., Lemos, B.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M., Martinez-Rossi, N.M., Martina, B.C., Meddanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, M.C., Oliveira, V.R., Pereira, Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F., Rakisa, M.A., Tamura, R.E., Texeira, B.C., Tezza, R.I.D., Trindade dos Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and Kitajima, J.P.
Comparison of the genomes of two Xanthomonas pathogens with differing host specificities

Mature 417 (6887), 459-463 (2002)
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AE011804.1 GI:21
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Xanthomonas axonopodis pv. citri str. 306
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas axonopodis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the complete genome. AE011804 AE008923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sao Paulo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kitajima,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1
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                                                                                                                                                                                                                                                                                 gene="pyrG"
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                                                                                                                                                                                                                                                       note="XAC1716"
                                                                                                                                                                                                                                                                                                                                                                                                              strain="306"
                                                                                                                                                                                                                                                                                                                                                    note="pathovar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:21107911
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                                                                                                                                                                                                                                                                                                                                                                                 xref="taxon:190486"
                                                                                                                                                                                                                             .1850
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                                                                                                                                                                                                                                                                                                                                                    citri"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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182 of 469 of
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                                                                                                                                                                                                                                                                                       CDS
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VLDVLQTPAFLVRQTDFIKNVCAAGKEVNIKGQFLAFWGAKSVGGGSSSGGQREFVPVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3514. .4806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3138.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAAVAVGISGLFAETHPDPSKALSDGPNAWPLDRMEELLETLMELDTVTKKHGFARFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGTLAREVYGKDVVAERHRHRYEFNNRYRTQLEDAGLVISGKSMDDTLVEVVELPRDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="kdsA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MTPLIFVTGGVVSSLGKGIAAASLASILEARGLKVTMMKLDPYI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GI:21107912"
                                                                                                                 codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="eno"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="XAC1718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="2-dehydro-3-deoxyphosphooctonate protein_id="AAM36584.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="XAC1717"
                                                                                                                                                                                      note="identified by sequence similarity; putative; ORF ocated using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                           gene="XAC1720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="identified by sequence similarity; putative; ORF
ocated using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="XAC1718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VADLDAANSTENDRQSPHPVIGLITEWRTATGEVEKRDEKSDLGGTMRLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="GI:21107913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="putative; ORF located using Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aldolase"
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translation="MRNWRWLLLVLAVLLAWLQYRFWFGPGNSGEVMMLEAQVAHQTQ

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                   US-10-018-706-2 (1-322) x AE011804 (1-11555)
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                                                                           50
                                                                                                                          30 LeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySerGlySerHisArg 49
                         ThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIleThrAspSerGlnGlyVal 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5976. ..6476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="XXC1721"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EASAPAQQAPEPVDPVDHP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNEGLRQRNQALAAEVKDLKDGEAAIEERARSELGMIKPGETFYRVVEDAPLPAPASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAM36589.1"
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ICERPKVGPHAVAMRERIADLLAIELDAVSVKATTSEQLGFTGRGEGIAAQAAVLLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (7951. .8490)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                               0.00116
219.50
40.07%
27.27%
13.14%
                                                                                                                                                                                                                                                                     Conservative: Mismatches: Indels:
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Matches:
                                                                                                                                                                                                                                     Gaps:
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Deinococcus radiodurans R1 section 198 of 229 of the complete chromosome 1.  AED02061 AED00513  AED02061 AE000513  AE002061.1 GI:6460095  Deinococcus radiodurans.  Deinococcus radiodurans  Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales; Bacteria; Deinococcus.  1 (bases 1 to 14193)  White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Vamathevan,J.J., Lan,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et al.	305 GlubheArgIleSetArgAsnGlyValTyrValAspProLeuThrValLeu 321 1390 CACTTCGAGATCCGCTACAACGGCAAGCCGGTCGATCCGTTGCTGTATCTG 11440	285 ValargThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPhe 304    :::      :::       1330 GTCAAAGCGGGGCAAATTGCCGAAATTGGCCGCGAGCGCGCGC	265 AsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThr 284 :::   :::::   :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::     :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :	247 ValileGlnAlaAspHisAsnMetAspGlyAlaSerIleValileGlnHisThr 264    :::         :::       :::         :::    1210 GTGGTGTATTCGGGCGCCGGCCTGGTCGGCTACGGCGAACTGATCATCATCATCAAGCACAAC 11269	227 AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThr 246	207 ThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSer 226	187 GluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAla 206	167 LysProThrProThrProProValValGlnGlnProAlaProValAlaProProValThr 186	147 ProProValGlnGlnHisProAlaValGlnLysProThrProProValValValValLys 166	127 IleSerSerGlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArg 146	107 IleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSer 126	87 ArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThr 106	70 ProAsnArgTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGln 86	0796 TCGTCGCGTCCCAGTGCC

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REFERENCE
AUTHORS
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MEDLINE
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White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Minton,K.W., Fleischmann,R.D., Ketchum,K.A., Nelson,K.E., Salzberg,S., Smith,H.O., Venter,J.C. and Fraser,C.M.
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20036896
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Location/Qualifiers
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Medical Center Dr, Rockville, MD 20850, USA
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64.29; identified by sequence similarity; putative"
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Complement (2232. . 3733)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGDDHRALITTEEDRAPGVPRLTREALVSLIEHARLAPLGALDLRGYWRAGDVDLDSA
ASVAELVSAHLAQRGTFTYVLLTLSQQPAQSLVNVSELAQRLGNGVSTDDMNAILDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VETVVKPYSTPRARQTGRQKPSGSGKTETPTKREEGRSEASRQGAASPSVREVRGQPA
GSLTGRRTAPSGGRNLSGLGEERRPATGEEGEPRPSGLKPIAPAFTPQVPQPGRQELT
LPASLASFGTRSREABPVAAPGAAESGPSDVPAALSPVPSGPVPAVQEVVSDPAPAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MCCDNVPRPSHPSWRTARVNPTRYILTRSCIEEGSMRLLKFNEA
SFPESGPVQFVDDRGKEYPAVVDRTQMQVLGLGELYHDHNLGVNDVLTVTPTEPGRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (90. .1598).
/gene="DR2286"
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/db_xref="GI:6460097"
                                                                                                                                                                                                                                                                          complement (4055. .4567)
                                                                                                                                                                                                                                                                                                                          complement (4055. .4567)
                                                                                                                                                                                                                                                                                                                                                    /gene="DRrrnaA16S"
/product="P<sup>1</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="transcriptional
/protein_id="AAF11834.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARPPFLAVTPLPNGQFLLRSTVTDLLADLADYAQGVRRLRAPGGGTEGPRG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQLGALEDQIVEFARLSGYRLTLLGRGLVRLTADLGPAYGYTVLLATDREALSSPEWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein_id="AAF11844.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (90. .1598)
/gene="DR2286"
                                                                                                                                                                                                                                                                                                      'gene="DR2288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to GB:AE000782 percent identity: 64.18; dentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="DR2287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:1299"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Deinococcus radiodurans"
|strain="R1"
                                                                                                                                                                                                                                                                                                                                                 product="Ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (5444), 1571-1577 (1999)
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                                                                                                                                                                                    start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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/gene="DR2293"
/note="similar to GB:D12650 SP:P30865 PID:1208970
/note="similar to GB:D12650 SP:P30865 PID:1208970
                                                                              /gene="DR2293"
7988. .8956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (5351. .6193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4567.
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//transl_table=1
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/db_xref="GI:6460098"
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                                                                                                                                                                                                   product="hypothetical protein"
protein_id="AAF11845.1"
db_xref="GI:6460107"
                                                                                                                                                                                                                                                                                                                                                                                                 gene="DR2292"
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db_xref="GI:6460100"
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transi_table=11
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'gene="DR2291"
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'cransT_table=11
'product="pseudouridylate synthase
'protein_id="AAF11837.1"
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transl_table=
                                                                                                                                                                                                                                                                                                                                                         gene="DR2292"
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gene="DR2291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="cell wall
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                                                                                                                                                                                                                                                                                                                             note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _xref="GI:6460099"
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/translation="MDADPRLYAPPPGFTRLRLTVAWDGRDYAGWQEQRNAVSVQET
LQTALHALGGEGALRPVSAGRTDAGYHAEAWFLHWDVDTTFRVDLVQLDRALINAWLPA
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AQSLIGLHDFAAFATREDRQTVRDLLRLEVQPQGELWDIHVAGESFLRHWVRGLVGTL
LLVGQGKLGAAEVEGILASRERARAGANVPPGGLYFAGAEYGVRRVEGRSGNGGEPGT
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GTPPQGRILIIVVTGASGVCKGTLRERWLAGQDVFYSTSWTTREER PGEVNGRDYVDFV
SPAEFLAKAQNGFLEHAQFVGNHYGTPIEBIEAALERGDVVTLEIEVEGAMQVKORN
GEQAILVFIMPPSLTELRRRLTGRATETPERIEKRLTRARDEIQAAHDFRYVIVNDNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLANVPLLSIRLQMKSSPFARPVLGPVTGILLAGALLLGGAGAE
$YRVKPGETLYRIALNAGLSEETVQQANPVLRGGHALYAGQMLTIPPKPLPPGTFRVR
KGEDLKKLAQRLGVSEGDIRRDNPQIDRRGSLNAGQVLRLPARLIAAQRAAEQAAQQK
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LDSPAQPGLALVASHWSGPLPELTPPAGAKHWTFRVLAQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'SDFGWRVLDGEREKHQGIDVAAPPGTPVIAARSGRVIQAHLDETYGWGWTVVIQHPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEYNPRLAGQTLNVGAVLSLVAPPLRPAPVAPARPAPVRLVVARPAPASPTPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYAHLSRISVEAGQLVRQGERVGAVGSTGRVTGPHLHFGLYRNWDPHNPLAFYA
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                  GlnLysProThrProProValValValLysLysProThrProThrProProValVal
                                                                                                                        ValAlaValGlnSerArgPro---ProValGln------GlnHisProAlaVal 155
                                                                                                                                                                                                                                                                                 AsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAsp
                                                                                                                                                                                                                                                                                                                                                ThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsn 99
             ACCTTCTACAGCGTCGCGGGGGCGTACGGCATCAACCCCATCGCCCTACAGGAGTACAAC
                                                                                                                                                                                                          LeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro 139
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/transl_table=11
/product="conserv
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/gene="DR2295"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="periplasmic divalent cation tolerance protein" /protein id="APF11840.1" /db/cref="GI:6460102" /db/aref="GI:6460102" /tamslation="MSLVVLVTLPPERAQELARTLVTERLAGCVNILPGIQSIYRWDG /tramslation="MSLVVLVTLPPERAQELARTLVTERLAGCVNILPGIQSIYRWDG EVAEDPESLLLIKTVGEQYPALEARIKSLHPYEVPEIVALPFDRASPEFQSWLRDSVG
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PGWTFPGLLLRIDHLLVRDLRPTRARVLSMAGSDHRPLLVEYRWGR"
complement (8987. 9295)
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complement(8987..9295)
/gene="DR2294"
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YNVARGSOGTAAALLSTLOASDADLILLOGETULDPAKGLALRSGLSGYSTALTGGREVUT
TLSRWPVLRQTQHAVPGSTRTFAETWVKGÞDGRTLRVVNAHLGTVLLTSALRGDTAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MLCSAPMDASPSPAPSAHRTWRETWRLRSRQLRRLPLTMMITCL
LLLLGSVQAAFQIGNNVYRSWTWTQETEQVRGRVAALQSDLHMLKDAEAAAQDPAYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="DR2295"
/note="identified by Glimmer2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="conserved hypothetical protein"
protein_id="AAF11839.1"
/db_xref="GI:6460101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by sequence similarity; putative"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="hypothetical protein"
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transl_table=
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Matches:
Conservative:
Mismatches:
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JOURNAL
PUBMED
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AUTHORS
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AE013686
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DEFINITION
ACCESSION
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7590
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I chases 1 to 10592)

I (bases 1 to 10592)

Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Liss, P., Perna, N. T., Rose, D. J., Mau, B., Zhou, S., Schwartz, D.C., Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.

Blattner, F.R. and Perry, R.D.

Genome Sequence of Yersinia pestis KIM

J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE013686
Yersinia
AE013686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia pestis KIM.
Yersinia pestis KIM
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                            Direct Submission
Submitted (21-FEB-2002) Genetics, 
Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                   i2142430

(bases 1 to 10592)

(bases 1 to 10592)

Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.F., Deng, W., Burland, V., Rose, D.J., Mau, B., Zhou, S., Schwartz, D.C., Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE013686.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrGlyAspThrValArgThrGlyGlnArgIleAlaSerMet-----LysAsnGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGTCATTCAGGCG-----CACCTCGACGAGACCTACGGCTGGGGCTGGACAGTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrValIleGlnAlaAspHisAsnMetAsp------GlyAlaSerIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCGGGCCGCACCTG---CACTTCGGGCTGTACCGCAACTGGGACCCTCACAACCCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCGGGCAACTCGTGCGCCAGGGCGAGCGCGTGGGCGGCGCAGCACGGGCCGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGCCCGCGTGGTGGTGCCGCAAACCAGCCACACTCTGTGGCAGTGGCCGCTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAspProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTCAGCACCCCGACGCTGGCAGACCCGCTACGCGCACCTCAGCCGTATCTCGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTACGGACGCATCACCAGCGACTTCGGGTGGCGGGTGCTGGACGGCGAACGCGAAAAA 7355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GlySerSerGlyValMetGlnPheArgTyrProValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pestis KIM section
AE009952
/gene="nlpD"
/function="membrane; macro
modification: Lipoprotein"
                                                                        /gene="nlpD"
/note="y0833"
                                                                                                                          /db_xref="taxon:187410"
                                                                                                                                                   organism="Yersinia pestis
strain="KIM"
                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:21957562
                                                                                                                                                                                            .10592
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ction 86 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA linear BCT 26-JUL-2002 415 of the complete genome.
                                                                                                                                                                                                                                                     University of Wisconsin,
                                                                                                                                                                          KIM
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7589 298 7529 280 7469 7415

245

225

260

5. 무 Ś 밁 Ş B ş В Ş g Ş 밁 Š

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/functions"enzyme; global regulatory functions"
/note="synthesis of many growth plase related proteins;
residues 1 to 330 of 332 are 92.46 pct identical to
residues 1 to 330 of 330 from E. coli Kl2 : B2741;
residues 1 to 332 of 332 are 97.28 pct identical to
residues 1 to 332 of 33 from GenPept : >gb|AAC43391.1|
(U16152) RpoS [Yersinia enterocolitica]"
                                                                                      AAELQTPLRQVGDLERI LARLALRTARPRDLARMRHAFQQLPEI HRLLQPI DVPHVQN
LLSQVQQFDELQDLLERA I VETPPVLVRDGGVI JASGXRAELDEWRALADGATDYLDRL
EIREREKLGLDTLKVGFNGVHGYY I QVSRGQSHLVP I HYVRRQTLKNAERY I I PELKE
YEDKVLTSKGKALAI EKGLYBEI FDLLLLPHLPELQLSANALAELDVLANLAERAETLN
YSCPTLSDKPGI KIMGGRHPVVEQVLKEPFI SNPLTLSPQRRMLI I TGPNMGGKSTYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="residues 5 to 851 of 851 are 84.09 pct identical to residues 5 to 853 of 853 from E. coli KI2: B2733; residues 5 to 851 of 851 are 84.09 pct identical to residues 5 to 851 of 851 are 84.09 pct identical to residues 5 to 853 of 853 from GenPept:

>gb|AAG57842.1|AE005501_11 (AE005501) methyl-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKNNI AEPYSLNVGQSI QLGNGSGGGMLAATDATSSGI AQPPSNI QNTTTI QNTTTTV
DSQSTSAYSGNSGKQNVGKMLPSSGAVVATTAPVTAPSSSVSEPASNGGPVSGWRWPT
DGKTI DSFSASEGGNKGI DI AGSRGQPILATASGRVVYAGNALRGYGNLI I I KHNDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="residues 1 to 333 of 333 are 58.65 pct identical residues 1 to 379 of 379 from E. coli K12: B2742; residues 1 to 373 of 333 are 58.65 pct identical to residues 1 to 379 of 379 from GenPept;
                                                                                                                                                                                                                                                         TRDLIGFGVEQAHLALRAAGCLLQYVKDTQRTSLPHIRGLTMERQQDGIIMDAATRRN
LELTQNLSGGSENTLAAILDCSVTPMGSRMLKRWLHMPIRDIRVLTDRQQAIGGLQDI
                                                                                                                                                                                                                                                                                                                        /translation="mkondkldshtpmmqqylrlkaqhpeillfyrmgdfyelfysda
KRASQLD151TKRGASAGEP1PMAGVPYHS1ENYLAKLVQLGSSAA1CEQ1GDPATS
KGPVERKVVLIVTPG71SDBALLQERQDNLLAA1MQDAKGFGYATLD1SGKRFRVAED
ADLETMAAELQRTNPAELLYPENFEPMSLIEHRHGLRRRPLMEFELDTAKQQLNLQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mismatch repair [Escherichia coli 0157:H7 EDL933]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2497. .5052)
/gene="mutS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (2497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERITSVDTPLGGDSEKALLDILSDENENGPEDTTQDDDMKQSIVKWLFELNAKQREVL
ARRFGLLGYEAATLEDVGREIGLTRERVRQIQVEGLRRLREILQTQGLSIEALFRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNQTRTIRLPIHIVKELNVYLRTARELSHKLDHEPSAEEIAEQLDKPVDDVSRMLRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELLAQGYTQRVLDATQLYLGEIGYSPLLTAEEEVYFARRALRGDVSSRRRMIESNLR
LVVKIARRYSNRGLALLDLIEEGNLGLIRAVEKFDPERGFRFSTYATWWIRQTIERAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="RNA polymerase,
/protein_id="AAM84419.1"
/db_xref="GI:21957564"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSAYAHNDTMLVREQQEVKAGQKIATMGSTGTSSVRLHFEIRYKGKSVNPLRYLPQR'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTMLSKANTDSSGGRIVYNRSYDNIPKGSYSGNTYTVKRGDTLFYIAWITGNDFRDLA
GVVNVHLDALEHGETIAFMHSVQEGAASKSYGLAVAALAGVPRDVIKRARQKLKELES
                                                              RQTAL I VLLAHLGS YVPADQAT I GP I DR I FTR VGAADDLASGRST FMVEMTETAN I LH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restriction/modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="rpos"
function="enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="rpos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="lipoprotein"
/protein_id="AAM84411.1"
/db_xref="G1:21957563"
/translation="MSTGSPMIRLRRVAACTVVSLWLVGCTNDNSTSAPISSVGGDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="methyl-directed mismatch repair protein"
'protein_id="AAM84420.1"
'db_xref="G1:21957565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transI_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="y0835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MSQSTLKVNELHEDADFDENSTETEIFDEKALVDDEPTESELAD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="y0834"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -gb|AAG57849.1|AE005502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="mutS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replication, repair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sigma S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDL933]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sigma38) factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="y0836"
5549. .5683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="rpiB"
                                                                                                                                                                                           nnocua]
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gene

gg

Sg

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/product="putative dehydrogenase"
/product="putative dehydrogenase"
/protein_id="AAM84423.1"
/db_xref="01:21957568"
/translation="MCDKKPLKESSMSHENLKGAQMAEGIPETMRAVVAYGPRDYRFE
/translation="MCDKKPLKESSMSHENLKGAQMAEGIPETMRAVVAYGPRDYRFE
RVPVPTIDAKEILVKVEGCGICAGDTKAFEGAPSFWGDDKQPAYIKAPMIPGHEFIGH
VVGLGADVEGFELGDRVTSEQIVPCWGCRFCNHGQYMWCBKHDLYGFQSNVNGAMEY
LKFTKEAINYHVPDHLPLEKAILIEFYACAFHAVQRAKIKLGDVVVLLAGSGTLGLGMI
GAIKKSGAAKLIVLDLSDDRLALAKKFGADLVLNPSRDDVNTLIKEMTGGYGCDIYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-oxidative branch, pentose pathway"

/note="residues 1 to 147 of 151 are 44.21 pct identical residues 1 to 146 of 149 from E. coli K12: B4090; residues 2 to 150 of 151 are 54.36 pct identical to residues 1 to 148 of 151 from GenPept: >gb|AAK03729.1|
(AE006201) RpiA [Pasteurella multocida]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to 2,3-butanediol dehydrogenase; residues 30 to 375 of 382 are 34.00 pct identical to residues 1 to 375 of 549 from GenPept: -dbj|BAB60856.1| (AB063194) acetylacetoin reductase [Bacillus cereus]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="y0838"
6751. .7899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="residues 1 to 42 of 44 are 39.53 pct identical to residues 84 to 126 of 698 from GenPept : 

>gb | AAF28325.1 | AF204952_3 (AF204951) ESV-1-144 [Ectocarpu
/transl_table=11
/product="putative dehydrogenase"
/protein_id="AAM84424.1"
/protein_id="AAM84424.1"
/db_xref="GI:21957569"
/translation="MPNDYKWFDTAFSLSGKVAAITGGATGIGHAIABLYLAKGARVV
LMDCADNVAEIAEQLDRDNAVGLHCDVSDSQSVRQAVAQAIGAFGQLDILVNSAGIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (5846. .6301)
                                                                                                                                                                                                                                                                /function="putative"
/note="residues 5 to 256 of 256 are 54.76 pct identical/
residues 3 to 254 of 254 from GenPept : >emb|CAC95595.1|
(AL596164) similar to dehydrogenase/reductase [Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIEGISNGDLPTEGVVTHILPLEKYAEGIELVKRGVDSLKVVLNPNLT"
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/protein_id="AAM84422.1"
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/note="y0837"
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AYCASKFGVJGITKVLALEWGPLDIQVBAISPTVVLTALGQKAWSGQLAEDMKLKIPA
RRFAYPAEVJAALFLASDAANMITGENLVIDGGYTIQ"
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Submitted (04-OCT-2001) Submitted on behalf of the Yersinia
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prentice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooke, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Davis, P., Dougan, G., Feltwell, T., Hamilin, N., Holroyd, S., Jagels, K., Leather, S., Karlyshev, A.V., Woule, S., Oyston, P.C.F., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Genome sequence of Yersinia pestis, the causative agent of plague Nature 413 (6855), 523-527 (2001)
                                                                                                                                                                                                                                                                                                                                                                        Details of Y. pestis sequencing at the Sanger Centre on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/Y_pestis/).
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Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSer-----IleValIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTAGATTGCATTTTGAAATTCGTTACAAGGGGAAATCCGTAAACCCGCTGCGTTACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACACAATGATGATTACCTGAGCGCCTACGCTCATAACGATACAATGCTGGTCCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTGGCCGGGTTGTGTATGCTGGGAACGCACTGCGTGGTTACGGTAATCTAATCATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSer-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACAAGAAGTGAAGGCGGGTCAAAAAATAGCAACCATGGGTAGCACCGGAACCAGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGGCAATAAAĞĞĞATTGATATCGCCĞĞTTCTCGTĞĞĞCAACCTATTCTCGCCACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 220050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 220050)
                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/Y_pestis/)
Location/Qualifiers
                                                                                                                                                       /organism="Yersinia pestis"
/strain="CO92"
/db xrefe="taxon:632"
/note="biovar: Orientalis"
/complement (191. .715)
/gene="YPO3215"
/note="aroL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220050 bp DNA li
pestis strain CO92 complete genome;
AL590842
             complement (191. .715)

(gene="YPO3215"

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BCT 06-JUN-2002 16/20

1072 321 1012 301 952 281 892 261

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Similar to Rhizobium meliloti phospholipid
N-methyltransferase PmtA TR:AAG10237 (EMB:AF201699) (200
aa) fasta scores: E(): 1.1e-07, 25.9% id in 185 aa, and to
Bradyrhizobium japonicum PmtA protein TR:Q9LCT2
(EMBI:Y09633) (199 aa) fasta scores: E(): 0.0057, 24.2% id
in 178 aa, and to Klebsiella pneumoniae hypothetical 22.7
kDa protein TR:O87755 (EMBI:AJ011907) (196 aa) fasta
scores: E(): 0, 52.9% id in 191 aa"
                                                                                                                                                                                  note="Similar to Escherichia coli hypothetical protein
YafE SW:YAFE ECOLI (P30866) (207 aa) fasta scores: E(): 0,
65.1% id in 169 aa, and to Pseudomonas aeruginosa YafE or
PA3119 TR:087011 (EMBL:U93274) (187 aa) fasta scores: E():
0, 55.2% id in 172 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (668. .691)
/gene="YPO3215"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(470. .544)
/gene="YPO3215"
/note="PS01128 Shikimate kinase
                                                                                                                                                                                                                                                                                                                   complement (2249. .2770)
/gene="YPO3218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mlnivrrnfksqfsylqrfiasprtygslvpsspwlcqamlnqi
DWTQNLNIAELGAADGVLTKRILSHMSANSSLQAYEIQFHFVHALHQLKDSRLQIADR
SAEQLDQEYDVVFCCLPLLSIPTKISIRILQQTQQRLRARNGVLVLFQYSHLSESLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (962. .1519)
/gene="YPO3216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="YPO3216"
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score 245.00, E-value 1.1e-69"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (209. .709)
/gene="YPO3215"
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VAEVVESEGWDGFRLRESMALQAVTAPKTVVATGGGAVLSSENRAFMRDHGRVIYLRA
SAAVLAKRLAEDPEEAQRPSLTGKPIVEEILDVLASREALYQDVAHHVLDGTQTPSLV
                                                                                                                                                                                                                                                                                                                                                                                             complement (2249. .2770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYFNWKKIRVVRNFPPALVYICHPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEQILQMLTGEMVK"
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/protein_id="CAC92450.1"
/db_xref="GI:15981151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shikimate kinase AroL or AroM SW:AROL_ERWCH (P10880) (173
,a) fasta scores: E(): 0, 63.7% id in 168 aa"
     translation="MQAAADKKLTNIEIQQGLAESLPFADQSFDIVISRYSAHHWHDV/
                              'product="conserved hypothetical protein"
'protein id="CAC92453.1"
'db_xref="G1:15981154"
'db_xref="SPTREMBL:08ZC12"
                                                                                                                                                                                                                                                                                                                                                                          /gene="YP03218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein"
/protein_id="CAC92452.1"
/db_xref="GI:15981153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="YPO3217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="putative methyltransferase"
/protein_id="CAC92451.1"
/db_xref="GI:15981152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="PS00017 ATP/GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=!
/transl_table=
                                                                                                                                   codon_start=:
table=
                                                                                                                                                                                                                                                                                                                                                                                                                            KNIASPHVLSIVACSIKKAAAKMRLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MIGTDVGIVVANVIMAETNDDRGRSISCHFFIQSSPNAHPLNVD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="no significant database hits"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="SPTREMBL:Q8ZC15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="YP03217"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xref="SPTREMBL:Q8ZC13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xref="SPTREMBL:Q8ZC14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _table=11
                                                                                                                                      table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signature."
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misc_feature
                                                                                                  misc_feature
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                        /note="Pfam match to entry PF00171 aldedh, Aldehyde dehydrogenase family, score -217.90, E-value 0.00013"
     complement (4776. .4841)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       trans
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/note="Similar to Serratia marcescens gamma-glutamyl phosphate reductase ProA SW:PROA SERMA (P17887) (417 aa) fasta scores: E(): 0, 85.1% id in 417 aa, and to Escherichia coli gamma-glutamyl phosphate reductase ProA SW:PROA ECOLI (P07004) (417 aa) fasta scores: E(): 0, 72.4% id in 417 aa"
complement (4572. .5744)
/gene="YPO3221"
                                                                                                                                                                                                                /product="gamma-glutamyl phosphate reductase"
/protein_id="CAC92456.1"
/db_xref="GI:15981157"
/db_xref="SPTREMBL:08ZC09"
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/translation="WMLLEHWGKAAKQASWQLAMLSTAKKNQALAVIANLLESESQTI
/translation="WMLLEHWGKAAKQASWQLAMLSTAKKNQALAVIANLLESESQTI
LQANERDMAAARESGMSEALLDRLLLTPARLAAIANDVRQVCRLNDPVGRVIDGSLLD
SGLKLERRKVPLGVIGVIYEARPNVTIDVASLCLKTGNAVILRGGKETHYTNQATVNV
                                                               IREHGTSHSDAILTRSLSHAEYFVRAVDSSAVYVNASTRFTDGGQFGLGAEVAVSTQK
LHARGPMGLDALTTYKWIGYGDDLVRS"
                                                                                                                            IQRALEQCGLPAAAVQAIESPDRQLVNELLKLDRYVDMLIPRGGASLHKLCREQSTIP
VITGGIGVCHTFVDENADFEKALLVIENAKIQRPSACNSLETLLVHQAVAKTFLPLLS
ARMHAFGVTLHASPLAMPYLADGKAKVVAVEAADYDDEWLSLDLNVDIVTDIDAAIDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4554. .5813)
/gene="YPO3221"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRILDIQPETNQFIFDFGSVENENVLALGAEQLTIIVBPTGAKIEFTCNKLKHVEYLS
LPAFSSAIPEQLYFIQRREYFRVSIPQWPAYYCSGKFPDGTQYKYTLADISLGGMGLY
AMKGSEFPLQGCSVLRDAAVDLCGFGLFKLDLQFIRALDKQVVNNKGEMLTVQRLSFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (3151. .3216)
/gene="YPO3219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3088. .3138)
/gene="YPO3219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="GI:15981155"
/db xref="SPTREMBL:Q8ZC11"
/db xref="SPTREMBL:Q8ZC11"
/translation="MEGSVMGISEEBSIRRLTNEKNAVGHSAKWVAIISAVYFIIMLF
YKHELGVLTLAGGIFLVSFTTWMKKRQKVKSYKNQLQQIEEDKTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLRLSPIQEKGLQRAIFELEKQQTAKARKFQEGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (3468. .4226)
/gene="YPO3220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="one of 2 probable for YPO3219 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="one of 2 probable transmembrane helices
for YPO3219 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTSDIMMIVAVRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKALREVKRVLRPGGKVI FMDVVSPGHPVLDI YLQTVEVLRDTSHVRNYSPGEWLSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similar to Escherichia coli hypothetical protein
rcgR SW:YCGR_ECOLI (P76010) (244 aa) fasta scores: E():
10.7% id in 241 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3468. .4226)
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/protein_id="CAC92454.1"
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/db_xref="GI:15981156"
/db_xref="SPTREMBL:Q8ZC10"
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'product="conserved hypothetical protein"
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGGGGGCGATCGTTCAGGTACGATGTTGÁGTAAAGCGAACÁCCGATÁGCTCTGGGGGGG 166106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerGlyGlyLeuAlaIleGly------SerGlnValIleThrAspSerGlnGly--- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTACCAATGAT-----AATTCAACATCTGCACCC-----ATCAGCAGT 166166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysAlaSerLysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGly 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAATGATTAGATTACGCCGAGTCGCGGCATGTACGGTTGTGAGTTTGTGGGTTAGTAGGT 166205
                                                                                                                      AGCAATGGTGGTCCAGTTAGTGGCTGGAGATGGCCAACCGAT-------
                                                                                                                                                    GlySerSerGly---ValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal 211
                                                                                                                                                                                         GCGGTTGTCGCTACAACAGCACCTGTTACCGCACCAAGCAGTTCTGTCAGTGAACCAGCC
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                                                                                                                                                                                                                                                                                                                               AATATTĆAĠAACACAACTACTATTĆAĠAACACAÁĊTACAACGGTTGATTCTCAATCAACT 165785
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                                                                                                                                                                                                                         ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCAATTGGGTAATGGGTCTGGTGGCGGTATGTTAGCCGCCACTGATGCCACATCAAGT
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                                                                                  ArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSer----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="yp03221"
/note="p601223 Gamma-glutamyl phosphate reductase
signature."
complement (5823 . 6926)
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/note="proB"
-AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn
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Conservative:
Mismatches:
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                                                    GGTAAAACGATCGATAGCTTCTCTGCTTCCGAA 165590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165589 GGGGGCAATAAAGGGATTGATATCGCCGGTTCTCGTGGGCAACCTATTCTCGCCACAGCA
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1433 bp DNA linear BCT 03-MAY-1994
Escherichia coli L-isoaspartyl methyltransferase (pcm) and katf
gene, partial cds and lipoprotein precursor (nlpD) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-18089.1 GI.433183
L-180aspartyl methyltransferase;
Escherichia coli (strain MP180) [
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1433)
(chikawa, J.K., Li,C., Fu, J. and Clarke, S.
A gene at 59 minutes on the Escherichia col
Lipoprotein with unusual amino acid repeat
Bacteriol. 176 (6), 1630-1638 (1994)
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AAACACAATGATGATTACCTGAGCGCCTACGCTCATAACGATACAATGCTGGTCCGGGAA 165410
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/map==59 min."
/trans1_tabl==11
/product="lipoprotein precursor"
/protein id="AAA17875.1"
/protein id="AAA17875.1"
/protein id="AAA17875.1"
/db_xref="01:433185"
/trans1ation="MSAGSPKFTVRRIAALSLVSLWLAGCSDTSNPPAPVSSUNGNAP
/trans1ation="MSAGSPKFTVRRIAALSLVSLWLAGCSDTSNPPAPVSSUNGNAP
/trans1ation="MSAGSSPKFTVRRIAALSLVSLWLAGCSDTSNPPAPVSSUNGNAP
/trans1ation="MSAGSSPKFTVRRIAALSLVSLWLAGCSDTSNPPAPVSSUNGNAP
/trans1ation="MSAGSSTYTVKAGOTLFYLAWITGNBTGDLAQRNNIQAPYALNVG
QTLQVGNASGTPITGGNAITQADAABQGVVIKPAQNSTVAVASQPTITYSESSGEQSA
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/map="59 min (
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                                                                                                                                                                                                                                   map="59 min."
97. 1326
                                                                                                                                                                                                                                                                                                                          note="putative"
                                                                                                                                                                                                                                                                                                                                                                                          'producT="L-isoaspartyl methyltransferase"
'protein_id="AAA17874.1"
'db_xref="GI:433184"
                                                                                                                                                                                                                                                                                                                                                                       translation="IDTVEAVRFVPLVKGELA"
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CTGTCAGCAGTACATCAACCAGTACGCCTATCTCCACCTGGCGCTGGCCCG-----ACTG 989
                         heAlaThrGly------SerSerGlyValMetGlnPheArgTyrProValGlyAlaT 207
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/db_xref="GI:476826"
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                                                                                                                                                                                                                                                                                                                      Submitted (22-OCT-2000) Laboratory of Genetics, Un
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 10573)
Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
Posfai,G., Hackett,J., Linn,A., Dimalanta,E., Potamousis,K.,
Grotbeck,E.J., Davis,N.W., Linn,A., Dimalanta,E., Potamousis,K.,
Apodaca,J., Anantharaman,T.S., Linn,J., Yen,G., Schwartz,D.C.,
Welch,R.A., and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of enterohaemorrhagic Nature 409 (6819), 529-533 (2001)
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Escherichia coli O157:H7 EDL933
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/gene="Z4048"
/function="putative regulator; Not classified"
/note="Residues 12 to 146 of 146 are 100.00 pc
                                                                                                                                nomologous
                                                                                                                                note="0-island #110; Region of the EDL933 nomologous to E. coli K-12 MG1655"
                                                                                                                                                                                            /note="enterohemorrhagic"
                                                                                                                                                                                                                                                            /organism="Escherichia
/strain="EDL933"
                                                                                        gene="Z4048"
                                                                                                                                                                                                                  db_xref="taxon:155864"
                                                                                                                                                                                                                                      serotype="0157:H7"
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gene

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transT_table=11
/product="RNA polymerase, sigma $ (sigma38) factor;
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MG1655: B2742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="rpoS"
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                                                                                                                                                                                                                     /transI tak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl for
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Strain MG1655: B2743"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="miaadslpgvymtlrnkafhQlfQQHtarwQhelpDltkpQ
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                                                                                                                                                                                                         protein
                                                                                                                                                                                                         carboxylmethyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcriptional
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gene

CDS

CDS

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to residues 1 to 159 of 159 from Escherichia cc
Strain MG1655: B2746"
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residues 1 to 349 of 349 from Escherichia co
//61655: B2745"
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strain MG1655: B2744"
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complement(3602. .4363)
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                                              protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pct identical to
coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli K-12
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Db 1884  Qy 285  Db 1884  Qy 285  Db 1824  Qy 305  Db 1764  RESULT 30  AECCESSION AND VERSION AND VERSION AND AND AND AND AND AND AND AND AND AN	Qy 247 alileGlnAlaAspHisAsnMetAspGlyAlaSerIleValileGlnHisThrA 265	Qy 227 snGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrV 247	Oy 207 hrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerA 227	2103 CTGTCAGCAGTACATCAACCAGTACGCCTATCTCCACCTGGCGCTGGCCGACTG	Qy 190 heAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaT 207	Db 2163 CAACTGCGACCACGGTCACAGCGCCTGTAACGGTACCAACAGCAAGCA	Qy 170 roThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProP 190	Db 2223 TTACGTATTCTGAGTCTTCGGGTGAACAGAGTGCTAACAAAATGTTGCCGAACAACAAGC 2164	Qy 170	Db 2282 AGGA-GTTGTGATCAAGCCTGCACAAAATTCCACCGTTGCTGTTGCGTCGCAACCGACAA 2224	Qy 152 isProAlaValGlnLysProThrProProValValValLysLysProThr- 169	Db 2324 CACTGGCGGAAAATGCCATTACCCAGGCCGACGACGCAGCAGCAGCA 2283	Qy 132 snThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnH 152	2359ACCTTACAGGTGGGTAATGCTTCCGGTACGCCAAT	112 nieuThrieuTrnSerGlyAen-LeuivsVallargGluArgSerTleSerSerGlyValla	Db 2417 CCCTCACCTTCACCCCAACAATATTCACCCACCATTACCCCTTCAACCTCACCTTCAACCACC	24// CTATACCGTGAAAAAAGGCGACACGCTTTTCTATATCGCCTGGATTACTGGCAACGATTT	72 gTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTr	CATCGTCTATAACCGTCAGTATGGGAACATTCCGAAAGGCAGTTATAGCGGCA	Qy 60 rGlnValIleThrAspSerGlnGlyValProAsnAr 72	Db 2597 ACAACCGCAAATCCAGCCAGTGCAGCCAGTAGCTCAGCAGCGGTACAGATGGAAAACGG 2538	Qy 41 SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeu-AlaIleGlySe 60	Qy 21 IlePheGlyVallleThrTyrSysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40 ::::::	US-10-018-706-2 (1-322) x AE005502 (1-10573)	12.78% Indels: 1 Gaps:	Arigument Scores: 0.00238 Length: 10573 Pred. No.: 213.50 Matches: 87 Score: 87 Percent Similarity: 42.01% Conservative: 55 Pest Incal Similarity: 42.01% Conservative: 55	CES	e complement (6598 /gene="Z4056"		LLAHPRVKRVVIAISPGDSRFAQUPLANHPQITVVDGGDERADSVLAGLKAAGDAQWV
							COMMENT	JOURNAL	AUTHORS	REFERENCE		JOURNAL	AUTHORS				MEDLINE	TITLE JOURNAL		AUTHORS	Decepance	SOURCE	ACCESSION VERSION KEYWORDS	DEFINITION	RESULT 30 AE000358/c	Qy . Db . 1	Db 1	δ	D 09	?

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /producE="putative transport protein"
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to 444 residues of an approx. 456 aa protein GNTP_BACLI
SW: P46832"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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יאַביטטטכנ="lipoprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "b2740"
                                                                                                                                                                                                                                                                                                                                                                                                                                      72. .2603)
Sigma70; 1
88. .3727)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted +1 start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at 2865614"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as gene
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                                                    Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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/translation="MVSRRVQALLDQLRAQGIQDEQVLNALAAVPREKFVDEAFEQKA WDNIALPIGQGQTISQPYMVARMTELLELTPQSRVLEIGTGSGYQTAILAHLVQHVCS VERIKCLQWQARRLKNLDLLHNVSTRHGDGWQGWQARAFFDAIIVTAAPPEIFTALMT QLDEGGILVLPVGEEHQYLKRVRRRGGEFIIDTVEAVRFVPLVKGELA" complement (4487. .5248) /gene="surg"
                                                                                                                                                                                                                                       /function "putative enzyme; Not classified"
/note="f349; was f292 and f255 before splice; This 3
/RF is 44 pct identical (8 gaps) to 338 residues of
approx. 344 as proteinY701_HAEIN SW: P44039"
/trans__table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3867. .4493)
/gene="pcm"
/BC number="2.1.1.77"
/functions="enzyme; Proteins - translation and modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTLQVGNASGTPITGGNAITQADAAEQGVVIKPAQNSTVAVASQPTITYSESSGEQSA
NKMLPNNKPTATTVTAPVTVPTASTTEPTVSSTSTSTPISTWRWPTEGKVIETFGASE
GGNKGIDIAGSKGQAIIATADGRVVYAGNALRGYGNLIIIKHNDDYLSAYAHNDTMLV
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ANTINSGMLITBPERMGTTSTAQOPQJCDPVQDPOQDATQOPQJCDPVQPVAQDPVQBNAD
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GAQREGIGGSNLQGAQRWAQTNTPVEDRNKESFWLSAARSALFNQIVAERLKKADVNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="factor Sigma70; predicted +1
complement (5229. 6278)
/gene="ygb0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mrillsnddgwhapgiqtlakalrefadvqvvapdrnrsgasns
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pdlfldkgirvtrggtrhpadqvipqdbrgntlymigppggkcdagegtdfaavd
egyvsitplhvdltahsaddvysdwlnsvgvgtqm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="phenotype; Not classified"
/note="f253; 100 pct identical to PIR: 169732; alternate
name ygbC; ORF1 of L07942, has different start due to
frameshift in L07942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REQQEVKAGQKIATMGSTGTSSTRLHFEIRYKGKSVNPLRYLPQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5229. .6278)
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/protein_id="AAC75786.1"
/db_xref="GI:1789101"
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'funrt:-
                                                                                                                                                                                     /product="putative hydrogenase subunit"
/protein_id="AAC75787.1"
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/db_xref="GI:1789100"
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trans1_table=
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luPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTATACCGTGAAAAAAGGCGACACACTTTTCTATATCGCCTGGATTACTGGCAACGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTCAGCAGTACATCAACCAGTACGCCTATCTCCACCTGGCGCTGGCCG-----ACTG
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                                                      TTAAGGCGGGGCAAAAAATAGCGACCATGGGTAGCACCGGAACCAGTTCAACACGCTTGC
                                                                                         alArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheG
                                                                                                                             ATGATTACCTGAGTGCCTACGCCCATAACGACACAATGCTGGTCCGGGAACAACAAGAAG
                                                                                                                                                             snGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrV
                                                                                                                                                                                                   TTGTTTATGCTGGTAACGCGCTGCGCGCCTACGGTAATCTGATTATCATCAAACATAATG
                                                                                                                                                                                                                                     allleGlnAlaAspHisAsnMetAspGlyAlaSer----IleVallleGlnHisThrA
                                                                                                                                                                                                                                                                         AGGGGATTGATATCGCAGGCAGCAAAGGACAGGCAATTATCGCGACCGCAGATGGCCGCG
                                                                                                                                                                                                                                                                                                             snGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrV
                                                                                                                                                                                                                                                                                                                                                   AGGGCAAAGTGATCGAAACCTTTGGC--
                                                                                                                                                                                                                                                                                                                                                                                 hrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerA 227
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25.74%
12.78%
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                                                                                                                                                                                                                                                                                                                                                   -GCTTCTGAGGGGGGC
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DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
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ECU29579/c
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                                                                                                                                                                                                                                                                                                                                         feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUN-1995) Guy P. Plunkett, University of Wisconsin, Laboratory of Genetics, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps with other sequence determinations are annotated. This entry should be considered somewhat provisional; it will be updated and merged with others at a later
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                               /translation="MNQVAVVIGGGQTIGAFICHGLAAEGYRVAVVDIQSDKAANVAQ
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GVGLTQSLALDLAEYGITVHSLMLGNLLKSPMFQSLLFQYATKLGIKFDQVEQYYIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="this sequence comprises the following lambda clones: DD609(EC30K446-3), DD612(EC19-195), DD615(EC27-240), DD618(EC22-172), and DD620(EC18-1463); M13Janus
                /translation="MVSALITVAVIAMCAQLALGGWQISRFNRAFDTLCQQGRVGVGR
SSGRFKPRVVVAIALDDQQRIVDTLFMKGLTVFARPQKIPAITGMHAGDLQPDVIFPH
DPLSQNALSLALKLKRG"
                                                                                                                                                                                                                                                                                                                                                            VPLKRGCDYQDVLNMLLFYASPKASYCTGQSINVTGGQVMF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="glucito1-6-phosphate
phosphate 2-dehydrogenase)"
/protein_id="AAA89214.1"
/db_xref="GI:882597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="gutD"
39. .818
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                                                             /protein_id="AAA69215.1"
/db_xref="GI:882598"
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/function="glucitol
/note="CG Site No. ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="gutD"
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                                                                                                                                                                                                                                                                                                                 note="similar to GenBank Accession Number X13463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="CG Site No. 153; alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar to
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                                                                                                                                codon_start=1
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                                                                                                          _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _table=11
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                                                                                                                                                     n activator"
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codon start=1
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note="alternate
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155. .3081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
transl_table=
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note="alternate name ygaB; ORF_f352"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                    US-10-018-706-2 (1-322) x ECU29579 (1-72221)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GenBank Accession Number M73326 (ECOASCBFG)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="4Fe-4S iron-sulfur protein"
protein id="AAA69223.1"
(db_xref="GI:882606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="electron transport from formate to hydrogen" note="CG Site No. 33521"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                omplement (9882. .10409)
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213.50
42.01%
25.74%
12.78%
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Mismatches:
Indels:
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GTCTACAGCGCAGCAACCGCAAATTCAGCCGGTGCAGCAGCACACAAATTCAGGCTACTCA 40814

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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                AP002562/c
                                                                                                                                                                                          RESULT
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                                                                                    270365
Escherichia coli O157:H7 DNA,
APO02562 BA000007
    Escherichia coli O157:H7 (strain:O157:H7, DNA.
                                                                      AP002562 BA000007
AP002562.1 GI:13
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                                                                                                                                                                                                                                                                                                                                TTAAGGCGGGGCAAAAAATAGCGACCATGGGTAGCACCGGAACCAGTTCAACACGCTTGC
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                                                                                                                  linear BCT genome, section 1
                     sub_strain:RIMD 0509952)
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Ohnishi,M., Kurokawa,K., Makino,K.,
Hayashi,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and Shinagawa,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Information Research Center; 3-1, Yamadaoka, Suita, Osa Japan (E-mail:ken@gen.info.osaka-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res.
21156231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete genome sequence of enterohemorrhagic 0157:H7 and genomic comparison with a laborato DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete nucleotide sequence of the prophage VT1-Sakai carrying Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli O157:H7 strain derived from the Sakai outbreak
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Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
20557356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete nucleotide sequence of the prophage VT2-Sakai carrying tverotoxin 2 genes of the enterchemorrhagic Escherichia coli O157 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URL:http://www.gen-info.osaka-u.ac.jp/,
Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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translation="MVLMSETKNELEDLLEKAATEPAHRPAFFRTLLESTVWVPGTAA/
QGEAVVEDSALDLQHWEKEDGTSVIPFFTSLEALQQAVEDEQAFVVMPVRTLFEMTLG/
STLFLNAKLPTGKEFMPREISLLIGEEGNPLSSQEILEGGESLILSEVAEPPAQMIDS
                                                                                                                                                                                                                                                     complement (435. .1220)
/gene="ECs3388"
                                                                                                                                                                                                                                                                                                     complement (435. .1220)
/gene="ECs3388"
                                                                                                                                                                                                           /note="similar to SSEB ECOLI
98 in 261 aa (Conserved in E
                                                                   /transl table=11
/product="enhanced serine
/protein_id="BAB36811.1"
/db_xref="GI:13362859"
                                                                                                                                                                                                                                                                                                                                               /sub_strain="RIMD 0509952"
/db_xref="taxon:83334"
                                                                                                                                                                evidence=not_
                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                               strain="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Escherichia coli 0157:H7"
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Yasunaga, T., Yokoyama, K., Makino, K.,
                                                                                                                                                                _experimental
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O157:H7 Sakai strai
                                                                                                                  sensitivity'
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a laboratory strain K-12
                                                                                                                                                                                                              gi|1788871
.coli K-12)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel:81-6-6879-8365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hattori,M.,
K., Shinagawa,H.
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complement (3364...5214)
/ gene="EC83392"
complement (3364...5214)
/ gene="EC83392"
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complement (3364...5214)
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/gene="EC83390"
/note="identical to YFHJ_ECOLI gi|1788873 (Conserved E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative peptidase"
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ACLVGKGITFDSGGYSIKQTAFMDSMKSDMGAATVTGALAFALTRGLMKRVKLFLCC
ADNLISGNAFKLGDIITYRNGKKVEVNNTDABGRLVLAADGLIDASAQKEBMIIDAATL
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TGAAKTALGBUNYHALFSEDDALAGRELLASASGENEPFWRIEDLASFHSVGLENWFAEL
TGAAAYPAGASTAAGFLSHFVENYQQGWLHIDCSATYRKAPVEQWSAGATGLGVRTI
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PIDICQVKKOEKGISHFITEHIAPFYERRWGGFLRDFKQNRII"
COMPLEMENT (1354...7724)
/gene="EC83389"
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/gene="ECs3391"
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/db_xref="GI:13362861"
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DPQASNEKILEAILLVWLDBAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2815. .3015)
/gene="ECs3390"
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//gene="EC3389"
//gene="EC3389"
/note="similar to PEPB ECOLI gi|1788872 percent identity
/poin 456 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/transl_table=11
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/translation="wpkTVILPHQDLCPDGAVLEANSGETILDAALRNGIEIEHACEK
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/gene="ECs3391"
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identity 100 in 111 aa (Conserved in E.coli K-12)"
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/transl_table=11
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'transl_table=11
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Alignment Scores: Pred. No.:
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AHLSEVAQGDDVDAIEQAIKNVDKQTQDFAARRMDQSVRRALKGHSVDEV"
complement (5231. .5746)
/gene="EC83393"
complement (5231. .5746)
/gene="EC83393"
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/protein_id="paB36817.1"
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VDEPTPEDIVFEDKGVKVVVDGKSLQFLDGTQLDFVKEGLNEGFKFTNPNVKDECGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (5842. .6165)
/gene="EC83394"
                                                                /transl_table=11
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/translation="MAYSERVIDHYENPRNVGSFDNNDENVGSGMVGAPACGDVMKLQ
/translation="MAYSERVIDHYENPRNVGKSLDEAQAIKNTDIAEELELPPV
                                                                                                                                                                                                                                                                                      complement (6182. .6568)
/gene="ECs3395"
                                                                                                                                                                                                                                                                                                                                  complement (6182. .6568)
/gene="ECs3395"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (5842. .6165)

complement (5842. .6165)

/gene="BC83394"

/note="similar to ISCA_ECOLI gi|1788877 percent identity

100 in 107 aa (Conserved in E.coli K-12)"

/codon_start=1
                                                                                                                                                                                            /evidence=not_experimental
/transl_table=11
/product="putative iron-bir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/transl_table=11
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                  214715 GTCTACAGCGCAGCAACCGCAAATTCAGCCGGTGCAGCAGCCACAAATTCAGGCTACTCA
                                                                          214595
                                                                                                                                                     214655 ACAACCGCAAATCCAGCCAGTGCAGCCAGTAGCTCAGCAGCCGGTACAGATGGAAAACGG 214596
214535 CTÁTACCGTGAÁAAAAGGCGACÁCGCTTTTCTATATCGCCCTGGATTACTGGCAACGATTT 214476
                                                                                                                                                                                              41
                                                                                                                                                                                                                                                                        21
                                                                                                                 60
                                                                                                                                                                                         SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeu-AlaIleGlySe
                                                                          ACGCATCGTCTATAACCGTCAGTATGGGAACATTCCGAAAGGCAGTTATAGCGGCAGTAC 214536
                                                                                                            rGlnValIleThrAspSerGln-----GlyValPro-----
                                                                                                                                                                                                                                                                        IlePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn 40
                                 gTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTr 92
                                                                                                                                                                                                                                                                                                                                                                   0.0852
213.50
42.01%
25.74%
12.78%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Parkhill,J., Dougan,G., James,K.D., Thomson,N.R., Pickard,D., Wain,J., Churcher,C., Mungall,K.L., Bentley,S.D., Holden,M.T.G., Sebaihla,M., Baker,S., Basham,D., Brooks,K., Chillingworth,T., Connerton,P., Cronin,A., Davis,P., Davies,R.M., Dowd,L., White,N., Farrar,J., Feltwell,T., Hamlin,N., Haque,A., Hien,T.T., Holroyd,S., Jagels,K., Krogh,A., Larsen,T.S., Leather,S., Moule,S., O'Gaora,P., Parry,C., Quail,M., Rutherford,K., Simmonds,M., Skelton,J.,
                                                                                                                                                                                                                                                                                                                                                                                                    AL627276 274050 bp DNA linear E Salmonella enterica serovar Typhi (Salmonella typhi) complete chromosome; segment 12/20.
                                                                                                                                                                                                                                                                 Salmonella enterica subsp. Salmonella enterica subsp.
                                                                                                                                                                                                                                                                                                                                                                           complete chromosome;
AL627276 AL513382
                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                        AL627276.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   luPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGATTACCTGAGTGCCTACGCCCATAACGACACAATGCTGGTCCGGGAACAACAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      snGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTTGAAATTCGTTACAAGGGGAAATCCGTAAACCCGCTGCGTTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAGGCGGGGCAAAAATAGCAACCATGGGTAGCACCGGAACCAGTTCAACACGCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allleGlnAlaAspHisAsnMetAspGlyAlaSer----IleValIleGlnHisThrA
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. enterica serovar Typhi
gamma subdivision; Enter
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Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing team, Sanger Centre,
Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-OCT-2001)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         World Wide Web.
                                                                            /product="putative RNA methyltransferase"
/protectn_id="CADD5832.1"
/protein_id="CADD5832.1"
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SDRQQALFSTTLPEKMVLVLGREYDYLPEAAREPDDLCVKINGTGNVESLNVSVATGV
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/note="PS00130 Uracil-DNA
complement (1013. .2050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosylase, score 376. .405
                                                                                                                                                                                                                                                                                                                                                                                                 /note="Orthologue of E. coli yfif (YFIF_ECOLI); Fasta hit
to YFIF_ECOLI (345 aa), 88% identity in 345 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="yfiF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="STY2840"
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                                                                                                                                                                                                                                                                                                                                                codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="STY2841"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="STY2841"
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in 228 aa ove
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9e-132"
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YFIP_ECOLI (232 aa), 88% identity in 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score 116.00, E-value 2419. .2475
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0, E-value 1.1e-33"
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y, score 181.50, E-value 1.4e-50"
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                       -----GlyValPro----
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SEFTALDVTLDIAPEDGDNESSLAVRPYPHQLEEWVENKNGDRCLFRPILPEDEPQLR
QEIAQVTKEDLYYRYFSEIUBETHEDLANMTQLDYDRENAFVAVRRMDNAEEILGVTR
AISDPDNVDAEFAVLVRSDLKGLGLGRRLMEKLIAYTRDHGLKRLNGIIMPNNRGMVA
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/gene="STY2845"
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/EC_number="2.7.8.8"
/BC_number="2.7.8.8"
/roote="Orthologue of E. coli pssA (PSS_ECOLI); Fasta hit
ro PSS_ECOLI (451 aa), 94% identity in 451 aa overlap"
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2 (bases 1 to 1290)
Paesold,G. and Krause,M.
Analysis of rpoS mRNA in Salmonella dublin: identification multiple transcripts with growth-phase-dependent variation transcript stability
J. Bacteriol, 181 (4)
                                                                                                                                                                                                                                               nlpD gene.
Salmonella enterica subsp. enterica serovar Dublin.
Salmonella enterica subsp. enterica serovar Dublin
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                          Submitted (18-MAY-1998)
Swiss Federal Institute
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  ProProVal---
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                                       GCACAGCAAGGAGTTGTGACCAGGTCTGCACAAAATTCCACCGTTGCAGTTGCGTCTCAA
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LOVGNASGMPITGGNAITQADAAQQGVVTRSAQNSTVAVASQPTITYSEGSGEGSANK
MLPNNKPAGTVVTAPVTAPTVSTTEPNASTSTSAPISAPWPTDGKVIENFGASEGG
NKGIDIAGSKGQAIVATADGRVVYAGNALRGYGNLIIKHNDDYLSAYAHNDTMLVRE
QQEVKAGQKIATMGSTGTSSTELHFEIRYKGKSVNPLRYLPQR"
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Sequence 4 from 1
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AR210638.1 GI:2:
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Potter, A.A., Rioux, C. and Schryvers, A.B.
Vaccine compositions comprising Haemophilus somnus transferrin-binding proteins and methods of use Patent: US 6391316-A 4 21-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
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           TyrGlnValLysGlnGlyAspThrValSerLysIlleAlaGlnArgTyrGlyLeuAsnTrp 92
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             Nature 413
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2 (bases 1
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1 (bases 1 to 20984)

McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,

Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M.,

Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A.,

Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,

Stoneking, T., Nhan, M., Waterston, R., and Wilson, R.K.
                                                                                                                                                                                            Salmonella typhimurium LT2.
Salmonella typhimurium LT2
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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AE008833.1 GI:16421460
                                                                                                                                                                                                                                                                                                       Salmonella typhimurium
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                                                                                 Complete genome sequence of Salmonella
                                                                                                                                                                                       Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                             ATTCGTTATAAAGGTCAATCAGTAGATCCAATGAGATATTTA
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gene CDS	gene	FEATURES		AUTHORS TITLE JOURNAL COMMENT
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gene CDS CDS		RBS RBS	RBS	gene CDS

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complement(4944. .6217)
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ACRRQPQKIRFVFSSSLAVYGGTLPECYTDTTALTERSSYGAQKAACELLVNDYTRKG
YVDGLALRLFTICVRPGKENRAASSFVSAIIREPLQGETTVCPVSESLRLWISSPATV
IHNLSLAATLPAPGEASSINLPGISVTVGEMLETLCQAGGQAARDRVTHQRDEGVEKI
VASWPGRIDNQRALALGFVADKRFDDIIERFRQDDMEGRS"
                                                                                                                                                                                                                                                                                                                  complement (4313. .4318)
                                                                                                                                                                                                                                                                                                                                            LATPTGSCLGNLDPQRLSKVDPQGEWLSGDKPSKEVRFHLALYRNNPCCKAVVHLHST
WSTALSCLEGLDPQNVIRPFTPYVVMRMGDIPLVPYYRPGDDRIARDLAALAARHQAF
LLANHGPVVCGENLQEAANNTEELBETAKLIFILGERPIRYLTTEEIAQLRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4309. .4947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INYPWLFRLFDDVGYRGWIGCEYQPRNTTQDGLGWFNAWR"
complement(4309. .4962)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ygbM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative RBS for
complement(3490..3495)
/gene="STM2914"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2543. .2548)
/gene="STM2914"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (2538. .3488)
/gene="STM2914"
                                                                                                                            complement (4944. .6206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2538. .3495)
/gene="STM2914"
/note="similar to E. coli orf, hypothetical protein (AAC75779.1); Blastp hit to AAC75779.1 (388 aa), 79% identity in aa 1 - 384"
                                                                                                 /gene="ygbK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative fuculose phosphate aldolase"
/protein_id="AAL21796.1"
/db_xref="G1:16421465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to E. coli putative epimerase/aldolase
(AAC75780.1); Blastp hit to AAC75780.1 (212 aa), 85%
identity in aa 1 - 211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to E. coli orf, hypothetical protein
(AAC75781.1); Blastp hit to AAC75781.1 (258 aa), 79%
identity in aa 1 - 258"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative RBS for complement(3528. .4318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGVVLINLLFGSGGSWLDPLLPIVVLAAIMLWVRWQAQGIKDKLVVKD"
                                                                                                                                                               'note="STM2917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="ygbL"
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'protein_id="AAL21794.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="similar to E. coli UDP-galactose-4-epimerase(AAC73846.1); Blastp hit to AAC73846.1 (338 aa), 25identity in aa 1 - 162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="ygbL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="STM2915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="ygbM"
                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MTILAKEEHALREEMVRIAASFFQRGYATGSAGNLSLLLPDGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MQIIITGGGGFLGQKLASALLNSSLAFNELLLVDLKMPARLSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db xref="GI:16421463"
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trans1_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STM2913; RegulonDB:STMS1H002970"
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-018-706-2 (1-322) x AE008833 (1-20984)
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                                                              CTGGCCCAGAGAAACAGTATTTCTGCCCCGTATAGCCTGAATGTAGGGCAAACTTTGCAA
                                                                                                                                                                                                                                                    TACAATCGCCAGTATGGGAATATTCCGAAAAGGTAGCTATACGGGTGGCAGTACTTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGCAACAAACGCCGCAACAAGCGCCGCAAATTCAACCCGTTCAGCGTCCTGTAACGCAG 12933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGlySerHisArgThrSerGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĊŢĠĠĊĀĠĠŢŢĠŢĀĊĊĀĠŢŢĊĠŢĊĀĀĀĊĊĊŢĊĊĠĠŢĊĀĊĠŢĊŢĠŢĠĠĀĊĀĠŢĠĠŢ
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                                                                                                                                                                                         ValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGlu
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                                                                                                                                                                                                                                                                                                                                                    CCCATGCAAACTCAACCGGTCACGGAACAACCCGTGCAGATGGAAAATGGGCGAATCGTA 12872
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                                                                                                            IleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeu---
                                                                                                                                                                                                                                                                                                                                                                                               ---IleGlySerGlnValIleThrAspSerGln---
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/protesin_id="AAL21797".1"
/protesin_id="AAL21797".1"
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/*AVVEALFSLLAARLAEGGITRFIVAGGETSGVVTQSLGITGFHLGPCISPGVPWVNAL
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/gene="ygbL"
/note="putative RBS for ygbL; RegulonDB:STMS1H002973"
complement (6200. .7134)
/gene="ygbU"
/note="STM2918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="3-hydroxyisobutyrate dehydrogenase"
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/protein id="ALI21798.1"
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ISSADAQEIAAALTALNLNMLDAPVSGAVKAAAAAMALAARAGLFUDVXTDVVTHAAG
NSWMFENRMQHVVDGDYTPRSAVDIFVKDLGLVADTAKALRFFLPLASTALNMFTSAS
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note "similar to E. coli putative dehydrogenase
(AAC75778.1); Blastp hit to AAC75778.1 (302 aa),
identity in aa 1 - 299"
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209.00
38.25%
22.95%
12.51%
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                -ThrLeuTrpSerGlyAspLeuLysValArgGluArgSer
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Matches:
Conservative:
Mismatches:
Indels:
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84
56
138
138
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VERSION
KEYWORDS
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AE004139
LOCUS
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MEDLINE
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316
                                                                                                                                                                                Batteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

1 (bases 1 to 10104)

1 (bases 1 to 10104)

Heidelberg, J. F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,
Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.,
Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.,
Gill, S.R., M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D.,
Nesrman, W.C. and White, O.

DNA sequence of both chromosomes of the cholera pathogen Vibrio
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Vibrio cholerae
2 (bases 1 to 10104)

Heidelbergy, F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.,
                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
Vibrio cholerae
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AE004139.1 GI:9654953
                                                                                                                                          Nature 406 (6795),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ProProValValValLysLysProThrProThrProProValValGlnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACAGCAAĠĠĀĠŦŦGTGĀĊĊAGGTCTGCACAAAATTCCACCGTTGCAGTTGCGTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleSerSerGlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCCGCTGCGTTATTTA 12057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGATGCTGGTCCGGGAACAACAGGAAGTTAAGGCGGGCAAAAAAATCGCTACTATGGGT 12135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArgIleAlaSerMetLys 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTAATCTTATTATCATCAAACATAACGATGATTACCTGAGTGCCTACGCCCATAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ser-----IlevalIleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProProVal----------GlnGlnHisProAlaValGlnLysProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspProLeuThrValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCACCGGCACCAGCTCTACACGCTTGCATTTTGAAATTCGTTACAAGGGGAAATCCGTA 12075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome
                                                                                                                                             477-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AATAAAGGGATCGACATTGCAGGCAGTAAGGGACAG 12315
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251 of the complete
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Submitted (14-JUN-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ermolaeva,M.D., Vamathevan,J., Bass,S., Qin,H., Dragoi,I.,
Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D.,
Nierman,W.C., White,O., Salzberg,S.L., Smith,H.O., Colwell,R.R.,
Mekalanos,J.J., Venter,J.C. and Fraser,C.M.
                                                                          /translation="mtdilsplaylcgkptakaklkalpehpqvnevlgysltghgeh
LMVRIRKTGENTSFVANELAKACGVPSRAVSWAGLKDRHAVTEQWLSVHLPNGETPDF
SAFLAQYPSIBILEVTRHDKKLRPGDLQGNEFYVTLSBYSDVAAVLSRLETVABLGVP
                            NYFGSQRFGRHGNNLSEARRWGRDNVRSRNQNQRSLYLSAARSWI FNQIVSKRIEQGC
FARFIEGDIALAEQQMFNVDGDLALWDQRLQAGEVAISAALAGDNALPTSGQALPLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:L42023 PID:1005557 PID:1220756
PID:1204923 PID:1573673; identified by sequence
  AELDAEPDLMALIRGNRMRHDRRAIALKAQNLSWQVQEDQITLRFSLDAGSFATSLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTPOMFRAQSLRERLFAALQQQVTITDEASAFEWRGEKPALVAGRADNLKITQPEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLIEHVVVAVSADDPYFANLPLAHHPRVIRVDGGKERADSVLSALEYVCQHRLSEWVL
VHDAARPCVTHADITQLITTALAHPIGAILASPVRDTMKRGDHLQQIVHTVDRTALMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mvmRvfALTLSULLVWLLYTLMWGKNGVMDfRAVQAEIEVQQQV
NANLHLRNQEMFAEIDDLRQGLDAIEERARNELGMVKDGETFYRIIGEESRQ"
                                                                                                                                                       product="conserved hypothetical protein"

protein_id="AAF93698.1"

db_xref="GI:9654957"
                                                                                                                                                                                                                                                                                                                                1573. .2658
/gene="VC0530"
                                                                                                                                                                                                                                                                                                                                                                                                                                         APKMAPYIQAMCAAIAEDLETDLGNINVKATTTEKLGFTGRKEGIACEAVVLLRKA"
                                                                                                                                                                                                                                                  /codon_start=]
/transl_table=
                                                                                                                                                                                                                                                                                                                                                               /gene="VC0530"
L573. .2658
                                                                                                                                                                                                                                                                                                                                                                                                                     1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="conserved hypothetical protein"
protein_id="AAF93697.1"
db_xref="GI:9654956"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAEFYLSRNKEKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="CDP-ribitol pyrophosphorylase-related
protein_id="AAF93696.1"
db_xref="GI:9654955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="conserved hypothetical protein"
protein_id="AAF93695.1"
db_xref="GI:9654954"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=]
transl_table=
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                                                                                                                                                                                                                                                                                                      note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDALLGATAAGDIGRHFPDTDDKWKGADSRELLKDVYRRVKAQGYVLGNADVTITAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="VC0527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MIRIGHGFDVHRFGGEGPIIIGGVKIPYEQGLIAHSDGDVALHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="VC0529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="VC0529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MNNMTAIVPAAGVGSRMQADRPKQYLTLLDKTVLEHTVEHLLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="VC0528"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="VC0528"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="biotype:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _xref="taxon:666"
                                                                                                                                                                                                                                                  _table=11
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                                                                                                                                                                                                                                                                                                   Glimmer2; putative"
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                                                                                                      gene
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                      complement (6140.
/gene="VC0535"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MANPKADRLIQPLTEQGITSPQVLAAIHALPREFEVAPAMMHQAYDNNALPIGQGQTISQPYIVAKMTELLALTPETKVLEIGTGSGYQTAVLAKLVNHVFT
VERIKTLQMBAKRELKQLDIYNVSTKHGDGMQGWPARGPFDAILVTAAAAKVPQSLLD
QLAEGGRMVIPVGEDEQYLYKIVRQGGQFISERVEAVRFVPLVAGDLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAPDRURSGASNSLTLEHPLRVSQIAENTYSVQGTPTDCVHFALNELMKDALPDLVLS
GINHGANLGDDVLYSGTVAAAMEGHFLGVQSIAFSLAGTTHFASAAHFVRQLVEQHLA
NPIPTNRLLNVNIPDRPLELIQGIEVTRLGARHHAESMIKQKDPRGHDIYMLGPPGKE
                                                                                complement(6140./gene="VC0535"
                                                                                                                                                                                                                /translation="msvsntvtkvebepdebealevletdaelfsdeelvavegased
vreeeddasksldatqmylsbigfsplltabeevlyarralkgdeaakkmiesnirl
vvkisrkysniglalldlieegnicdiravektdpergerfstyatmvirgtieralk
vqtrtirlpihvvkelniylrtarelsqrldheptpebialeldrpvddvtkmlrlne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQKIATMGSSGTNSVRLHFEIRYQGKSVNPKRYLP
5040. .6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAATVAVASSTSASVAKAATTATVAQTVSKSSNTKNVQNGSTNSQNLTKKDPVKTV
DQTKTKEYVEPVGKQNVNVNVAKAKPSDEKIAKWLWPTKGRVIKNFSAGDQGNKGIDI
AGQRGQAVVATADGTVVYSGNALRGYGNLIIIKHNEHYLSAYAHNDQLLAKEGQTVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTLYSFRLGLLLFCSLLFGCTAPTPAPVSGLGKDYNKVERGSYR
GSYYEVKKGDTLYFIAYLTDKDVNDLISYNDLAPPYTIHPGQKIKLMLPNYTPPAYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4031. .4966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GB:M63493 SP:P24206 PID:147115
PID:882636 GB:U00096; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDAGPGTDFHAIERGWVSLTPLQVDLTAHESLRSMDHWLKEKVNG"
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                                                                                                                                                                                                                                                                                                                             /product="RNA polymerase
/protein_id="AAF93702.1"
/db_xref="GI:9654961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5040. .6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/trans| table=11
/product="lipoprotein NlpD"
/protein_id="AAF93701.1"
/db_xref="GI:9654960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity; putative"
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/transT_table=11
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/protein_id="AAF93700.1"
/db_xref="GI:9654959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3405.
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/protein_id="AAF93699.1"
/db_xref="GI:9654958"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3405. .4031
note="similar to GB:M64730 SP:P23909 PID:146906
                                                                                                                                                                .ISSVDTPIGGDGDKALLDILPDSHNADPEFSTQDDDIRESLLNWLDELNPKQKEVLA
.RFGLLGYEPSTLEEVGREINLTRERVRQIQVEGLRRLREILVKQGLNMEALFNVEYD
                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="VC0534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="VC0534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="similar to GP:2897901; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="VC0533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="VC0533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="VC0532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="VC0532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MNKRAAIQRAKIKMKILLSNDDGVYAQGIHALADALRDLAEIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="VC0531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VC0531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to GP:2897902; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to GB:U00096 PID:1789101 PID:882637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   imilarity; putative"
                                                                                                            .8728)
                                                                                                                                                                                                                                                                                                                                                                                sigma-38 factor"
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Percent Similarity:
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         AlaValGlnLysProThrProProValValValValLysLysProThrProThrProPro
                                               GTGAGCAAAAGCTCTAATACCAAAAATGTACAAAATGGGTCAACGAATAGTCAAAATTTG
                                                                                        ValAlaValGlnSerSerArgProProValGln---
                                                                                                                                 GCTTCAAGCACAAGTGCAAGTGTTGCCAAAGCGGCGACGACGGCAACAGTTGCTCAAACC
                                                                                                                                                           -----ArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro
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/gene="VC0536"
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/db_xref="GI:9654962"
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Takayanagi,Y., Tanaka,K. and Takahashi,H.
Structure of the 5' upstream region and the gene of Escherichia coli
Mol. Gen. Genet. 243 (5), 525-531 (1000)
94268497
Submitted (06-SEP-1993) Hideo Takahashi, The University of Tokyo, Inst. of Mol. & Cell. Biosci.; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113,
                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                            Tanaka,K., Takayanagi,Y., Fujita,N., Ishihama,A. and Takahashi,H. Heterogeneity of the principal sigma factor in Escherichia coli: the rpoS gene product, sigma 38, is a second principal sigma factor of RNA polymerase in stationary-phase Escherichia coli Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3511-3515 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli (strain:pH1) DNA, clone:pKTF106
Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Ento
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D17549.1 GI:404097
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1612 bp DNA linear BCT 10-SEP-1999
Escherichia coli gene for RNA polymerase sigma factor, ORF-X
protein, L-isoaspartyl protein carboxy methyltransferase, partial
                                                                                                                                                                                                                                             Ichikawa, J.K., Li,C., Fu,J. and Clarke,S.
A gene at 59 minutes on the Escherichia coli chromosome
lipoprotein with unusual amino acid repeat sequences
J. Bacteriol. 176 (6), 1630-1638 (1994)
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                                                              CTGACACTTCAAATCCACCGGCACCGGTCAGCTCCGTTAATGGCAATGCCGCCTGCAAATA
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                                GlyValileThrThrCysIleLeu---
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/transI table=11
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/product="RNA polymerase sigma factor"
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/LISQGATQRVLDATQLYLGEIGYSPLLT"
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Direct Submission

Submitted (13-NOV-2001) Institute of Molecular Biology and Medicine, University of Scranton, Scranton, PA 18510, USA

3 (bases 1 to 12362)

Elzer, P.H. and Hagius, S.

Direct Submission

Submitted (13-NOV-2001) Department of Veterinary Science, LSU Ag Center, 111 Dalrymple Building, Baron Rouge, LA 70803, USA

(bases 1 to 12362)

Kapatral, V., Los, T., Ivanova, N., Anderson, I., Bhattacharyya, A., Iykidis, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Elykidis, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Haselkorn, R., Bernal, A., and Overbeek, R.

Direct Submission

Direct Submission

Park Drive, II. 60612, USA

Fark Drive, II. 60612, USA

Follows II. 1 12362)
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Direct Submission

Direct Submission

Submitted (13-NOV-2001) Unite de Recherche en Biologie Moleculaire,

Laboratoire d'Immunologie et de Microbiologie, Universite of Namur,

61 rue de Bruxelles, Namur 5000, Belgium

6 (bases 1 to 12362)

O'Callaghan,D.

Direct Submission

Submitted (13-NOV-2001) Faculte de Medecine, INSERM U431, Avenue

Yannedv. Nimes 30900, France
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1 (pelvecchio, V. G., Kapatral, V., Redkar, R.J., Patra, G., Mujer, C., Delvecchio, V. G., Kapatral, V., Bhattacharyya, A., Lykidis, A., Los, T., Jahlonski, L., Larsen, N., D'Souza, M., Bernal, A., Reznik, G., Jablonski, L., Larsen, N., D'Souza, M., Bernal, A., Mazur, M., Goltsman, E., Selkov, E., Elzer, P. H., Hagius, S., O'Callaghan, D., Letesson, J.-J., Haselkorn, R., Kyrpides, N. and Overbeek, R.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
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Proc. Natl. Acad. Sci. U.S.A. 99 (1), 443-448 (2002)
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complement (1943. 2512)
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A I FDKAKAGLPQTLHPA FLPMAL VPA YLNA VERLGAQAAQKVAD I SA I RKQWLMFRAN
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LMDVRVKGEPVADNKNK"
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NMASZ2491/c
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VERSION
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                                                                                                                                                 Neisseria meningitidis Z2491.
Neisseria meningitidis Z2491
                                                                                                                                                                                                    ALI62756 AL157959
AL162756.2 GI:73
                                                                                                                                                                                                                                                       Neisseria meningitidis serogroup A
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                                                                                                                                                                                                                                                                       NMA5Z2491
                                                                                                                                    Bacteria;
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                                                                                                 (bases 1 to 329861)
                                                                                                                                    Proteobacteria; beta
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                                                                                                                                                                                                                                                                      329861 bp
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Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Davies, R.M., Davies, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGATCAGGCCGCAGCGCCATCCTCAACCGGCATCTCGCAGATGCGTTGGCCGGTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGly 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTGCGCCGGCCAATGGAGGTGCAGAGGTAAAGCCTTATACGCCGCCGCAGGCCAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgProProValGlnGlnHisProAlaValGlnLysProThrProProValValValVal 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAla--- 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGly 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysLysProThrProThrProProValValGlnGlnProAlaProValAlaProProVal 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGCGCCGACACAGGTGGCCGCAATCACGCCGCCAGCCGGCAAACCCCGGCCAAAGCAGCC 11345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyValAsnThr------AlaHisThrProSerProVal---AlaValGlnSerSer 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSer 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThr 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LeuPheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrVal 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GTAATCGAGGATGCGGAA-----
                                                                                                                                                                                                                                                                                                                                         subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AAGTCGGGCATGAGCGGCAACGCCAAG 10925
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Z2491 co
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PUBMED
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Nature 404 (6777), 502-506 (2000)
20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Direct Submission
Submitted (30-MAR-2000) Submitted on behalf of the Neisseria Submitted (30-MAR-2000) Submitted on behalf of the Neisseria Sequencing team, Sanger Centre, Wellcome Trust Genome Campus, sequencing team, Sanger Centre, Wellcome Trust Genome Campus, sequencing team, Sanger Centre, Wellcome Trust Genome Campus, sequence Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Wellcome Campus, Sanger Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centre, Centr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notes:
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                                                                                                     /CHAILS LOCATE TO THE SYNTHASE "
/product = "putative threonine synthase"
/product = "putative threonine synthase"
/product = "putative threonine synthase"
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VFMLSPDGKWSAFGTRAGWFSLOGNUHNIAVKGMFDDCQDIVKAVQNDAAFKEKYHIG
TVNSINWGRIVTAQVVYYFAGYTKATQSNDEGVSFCVPSGMBTGNVCAGHIAKQMGLFVN
RLIVATNENDYLDEFFKTGAKRENSAHTYYTSSESMDISKASNTERFFYFDLMDRDPG
RLIVATNENDYLDEFFKTGAKRENSAHTYYTSSESMDISKASNTERFFYFDLMDRDPG
RLIVATNENDYLDEFFKTGAKRENSAHTYYTSSESMDISKASNTENDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="PS00013 Prokaryotic membrane lipoprotein lipid
attachment site"
complement (571. .580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="NMA1439, possible lipoprotein, len: 123 aa; unknown, contains a probable N-terminal signal sequence and an appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="sptrembl:09JU92"
/translation="makth.G1Lpva1LLGGCAAGGGNTFGGSLDGGTGMGGSIVKMAVE
SQCRAELNKRSEWRLTALAMSAEKQAEWENKICACVAQEAPNQLTGNDVMQMLDPSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQALAALTAKTVSACFKHLYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  noTe "NWA1440, thrC, probable threonine synthase, len: 485 aa, similar to many e.g. Sw:THRC_METGL (EMBL.D14071), thrC, wethylobacillus glycogenes threonine synthase (EC 4.2.99.2) (475 aa), fasta scores; E(): 0, 61.9% identity in 475 aa overlap. Contains Pfam match to entry PF00291 S. T. dehydratase, Pyridoxal-phosphate dependent enzymes "/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="thrC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Core DNA uptake
/label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Core DNA uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="NMA1439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative lipoprotein"
/protein_id="CAB84675.1"
/db_xref="GI:7380092"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Neisseria meningitidis Z2491"
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transI_table=
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db_xref="taxon:122587"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number="4.2.99.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gccgtctgaa"
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                                                                                                                  repeat_unit
                                                                                                                                                                                                                            repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2923. .2932)
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Stem loop containing DNA uptake sequences:
gccgtctgaa gccc ttcagacggc atata"
2909. 2918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to
Pyridoxal-phosphate
E-value le-65"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTVPNSADAVKGIIEQTLA"
875. .1780
                                                                                complement (3984. .4038)
/note="RS103"
                                                                                                                                                                                                   3964. .3983
/note=">= 9
                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pram match to entry PF00175 oxidored_fad, Oxidoreductase_FAD/NAD-binding domain, score 20.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="maafnTokvlsvHhwTdayfTfTCTRDESLRFENGOFVMVGLMV
DGRPLMRAYSVASANWEEHLEFFSIKVQDGPLTSRLOHLKVGDDVLISKKPTGTLVAG
DLNPGKHLYLLSTGTGIAFPLSITKDPEIYEOFEKIILVHGVRYKKDLAYYDRFTKEL
PEHBYLGDLVKEKLIYYPIVSREEFBEHGRLTDLMVSGKLFEDIGLPKINPQDDRAML
PEHBYLGDLVKEKLIYPPIVSPKTGVRGDYLIERAFVDQ"
                                                                                                                                                /note=">= 90% match to ATTCCCNNNNNNNNNGGGAAT"
/label=dR83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="NMA1442, fpr, probable ferredoxin--NADP reductase, len: 258 aa; similar to many e.g. Sw:FENR AZOVI (RMBL:L36319), fpr, Azotobacter vinelandii ferredoxin--NADP reductase (EC 1.18.1.2) (257 aa), fasta scores; E(): 0, 69.8% identity in 255 aa overlap. Similar to NMA1664, fasta scores; E(): 1.3e-30, 34.6% identity in 257 aa overlap. Contains Pfam match to entry PP00175 oxidored_fad, Oxidoreductase FAD/NAD-binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEIQKLIAATVKPILPIRRLEHPRWGRDALRLAASISLISLADMPP"
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NARWRYALLGMVARYLKLGVLKPVPSLGGEPAIATESKRLYELRAAGIAVPELLAVRK
NALWFGNLEGIPLDTQIRGAEAGKADAWLAGLEAIARVKDQGLSQAFARNMMSDG
KNISFLDFEDDPSLYLTIAQCQARDWLCYIHSTALILKNGGILEAAAEKWGGVLSDQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative ferredoxin--NADP reductase"
/protein id="CAB84678.1"
/db_xref="SPTREMBL:Q9JRE3"
                                                                                                                                                                                                                                                                               )866. .3875
'note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                 3-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
transl_table=11
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(trans[ table=1]
(product="hypothetical protein NMA1441"
protein_id="CAB84677.1"
db_xref="GI:7380094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    094. .2888
gene="NMA1441"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                       label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                076. .3852
gene="fpr'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EC_number="1.18.1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label=DUS
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                                                                                                                                                                                                                                                                                                                                                                                 8.4e-05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hrC"
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  283427 CATACTATTGTGCGCGGCGACACGGTGTACAACATTTCCAAACGCTACCATATCTCTCAA 283368
                                                                                                                                                                            283280
                                                                                                                                                                                                                                                               283313
                                             173
                                                                                                                                                                                                                    133
                                                                                                                              153 ProAlaValGlnLysProThrProProValValValLysLysProThrProThrPro 172
                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp 92
                                                                                        GCTGCCGTGCAAACCCCTGTG---
                                                                                                                                                                                                                ThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHis 152
                                                                                                                                                                                                                                                                                                                                                                                         ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
CCTGTGCAGTCCGCGCCGCAACCTGCCGCGCCCCGCTGCGGAAAATAAAGCGGTTCCCGCG 283143
                                           ProValValGlnGlnProAlaProValAlaPro------ 183
                                                                                                                                                                                                                                                                                                 LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn 132
                                                                                                                                                                       ------CCGAAAGCCGCAGCCGTAAAA---AGCAGGCCCGCCGTACCG----- 283242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="NMA144, probable P-type cation-transporting ATPase, len: 823 aa; similar to many e.g. SW:COPA_ENTHR (EMBL:L13292), copA, Enterococcus hirae copper/potassium-transporting ATPase A (EC 3.6.1.36) (727 aa), fasta scores; E(): 0, 34.0% identity in 744 aa overlap. Similar to NMA1539, fasta scores; E(): 0, 34.4% identity in 735 aa overlap. Contains hydrophobic, probable membrane-spanning regions. Contains two Pfam matches to entry PF00122 E1-E2 ATPase, E1-E2 ATPases and PS00154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E1-E2 ATPases phosphorylation site"
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/gene="NMA1444"
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/gene="NMA1444"
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/protein_id="CAB84680.1"
/db_xref="G1:7380097"
/db_xref="SPTREMBL:Q9JU88"
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'protein_id="CAB84679.1"
'db_xref="GI.738096"
'db_xref="GI.738096"
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'transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159. .4320
gene="NMA1443"
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203.00
43.46%
27.31%
12.16%
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Matches:
Conservative:
Mismatches:
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71
42
97
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184 ProValThrGluAlaProPheAla------ThrGlySerSerGlyValMetGln 199

ZBZBIZ GAGGCTICTAGAACGCAGGTICATTICGAGGTGCGGCAAAACGGCAAACCGGTTAATCCG Z	Ď
	3
298 ProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAspI	Ş
282872 CTGGTCGGCGAAGGCCAGCAGGTCAAACGCGGGCAGCAGGTCGCTTTGATGGGCAATACC 282813	망
278 GlnValLysThrGlyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnG	Ş
282932 TTGGTCATCATCCAGCATAATTCTTCCTTCCTGACCGCATACGGGCACAACCAAAAAT	당
259IleVallleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAla 277	Ş
282992 TTGGCGGCTGACGGCAAAGTGGTTTATGCAGGTTTCCGGTTTGAGGGGATACGGCAAT 282933	뮹
240 AsnAlaSerAsnAlaGlyThrVallleGlnAlaAspHisAsnMetAspGlyAlaSer	8
283037AACAACAAGGGTGTCGATATTGCAGGAAATGCGGGACAGCCCGTT 282993	뮹
220 AlaGlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIle 239	Ş
283082 TGGCAGCGTCCGACGCAAGGTAAAGTGGTTGCCGATTTCGGCGGC	뭥
200 PheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrVal 219	Ş
283142 CCCGCCCGCAATCTCCTGCCGCTTCCGGCACGCGTTCGGTCGG	밁

Search completed: July 3, 2003, 21:18:47 Job time: 2677 secs

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Minimum DB seq length: 0
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-Q=/cgn2 1/USPTO spool/USI0018706/runat_30062003_091104_23784/app_query.fasta_1.519
-DB=N Geneseq_101002 -QFWT=fastap_-SUFFIX=rng_-MINWATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UMITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICH=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=000000000
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=000000000
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-NO_MMAP -LARCHQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO.MALP -MARN TIMEOUT=30 -THEADS=1 -XGAPDXT=0.5 -FGAPDP=6
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -XGAPDXT=0.5 -FGAPDP=6
-PGAPEXT=7 -YGAPDP=10 -YGAPDXT=0.5 -DELDP=6 -DELEXT=7
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

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4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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1670
                         2185239 seqs,
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Listing first 45 summaries
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
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XX Y conflict Moraxella catarrhalis BASB110; infection; otitis media; pneumonia; gene therapy; diagnosis; antibacterial; antimicrobial; genetic immunisation; Moraxella catarrhalis DNA encoding BASB110 protein. 23-APR-2001 AAF30046; AAF30046 standard; DNA; 969 BP. (first entry) Location/Qualifiers replace(310,G)

ALIGNMENTS

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US-10-018-706-2 (1-322) x AAF30046
                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                       Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of the coding region of the BASB110 CC gene of Moraxella catarrhalis Mc2331 (ATCC 43617), a causative agent of oticis media in children and pneumonia in adults. The CC agent of oticis media in children and process (see AB20106). It differs from a BASB110 DNA PCR amplification product (see AB20106). It Dy having A at position 310 rather than G. This would cause an anion acid change from Ser-104 to Gly in the translated sequence. The invention provides BASB110 polypeptides, and polynucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB110 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB110 polypeptide, or a polypeptide, an immunogenic fragment of a BASB110 polypeptide, or a polypeptide having at least 8% amino acid sequence identity to BASB110, or comprising a polynucleotide encoding such a polypeptide. A claimed having at least 18% amino acid sequence identity to BASB110, or a basB110 polypeptide and method of diagnosing a Moraxella infection involves identifying a BASB110 polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises polynucleotides also have utility in diagnosis of the stage and type of infection, and also for therapeutic or prophylactic purposes, in particular genetic immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 969 BP; 265 A; 214 C; 242 G; 248 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel BASB110 polypeptides of Moraxella catarrhalis, useful as vaccine for treating Moraxella catarrhalis infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 81; 88pp; English.
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P-PSDB; AAB20106.
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                                                                                                                       ATTTTTGGTGTGATCACCACTTGCATTTTGGCAGGATGTGCCAGTAAGCCAACCTATAAT
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                                                               AGTACCTCAGGTTCGGGCAGTCATCGTACTTCAGGTTCAGGTGGTTTTGGCCAATAGGTTCA
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16-JUN-2000; 2000WO-US16649.
                                                                                                                Genomic library; bacteria; human upper airway; otitis media; bronchopulmonary; endocarditis; meningitis; ss.
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                                                                                                                                                                                                                                                                                                                     CTTAAA 966
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Best Local Similarity:
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Claim 10; Page 83; 88pp; English.

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AAGGTGCGTGAGCGTAGTATCAGCTCTGGTGTGAATACAGCTCACACACCTTCGCCTGTG
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21-APR-1995;
07-JUN-1995;
                                Haemophilus influenzae Rd genome recorded on computer readable medium - useful for identifying commercially important nucleic acid fragments by homology searching
                                                                                                                                                                                                                                     Genome; bacterium; Haemophilus influenzae; computer readable medium; expression modulating fragment; regulation; gene expression; vector; organism; open reading frame; ORF; ds.
                Claim 1; Page 77.2-77.1091; 1291pp; English
                                                                                                                                                                                                                 Haemophilus influenzae.
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                                                                   WPI; 1996-485782/48.
                                                                                                                                                                    22-APR-1996;
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                                                                                                                                                                                                     WO9633276-A1.
                                                                                                                                                                                                                                                                        Haemophilus influenzae complete genome sequence.
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95US-0426787.
95US-0476102.
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GlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIle
                                                                                                                                                              SerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGly
                                                                                                                                                                                                                            AspHisAsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheVal
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                                                                                                  AGTGCCTATGCGCATAACGACAAAATTCTTGTCGCCGATCAACAAGAAGTCAAAGCAGGT
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                                                                                 The present sequence encodes the Haemophilus somnus lipoprotein LppB. CR Recombinant vaccines containing H. somnus lipoproteins LppA, LppB cand LppC have been described. H. somnus transferrin-binding proteins Tbpl and Tbp2 have also been found to be effective in vaccines against cand Tbp2 have also been found to be effective in vaccines against cand Tbp2 have also been found to be effective in vaccines against cand Tbp2 have also been found to be effective in vaccines against cand Tbp2 in the somnus infection. Clones expressing Tbp epitopes were identified by screening a genomic expression library of H. somnus strain HS25 in CR. coli with polyclonal antiserum raised against affinity-purified Tbp1 CR. only with polyclonal antiserum raised against affinity-purified Tbp1 and Tbp2 were obtained by inverse PCR. The nucleotide sequence encoding Tbp1 and Tbp2 may be used for the recombinant production of Tbp1 and Tbp2, which may then be used to manufacture vaccine compositions for immunising against H. somnus infections. The antibodies raised against the transferrin binding proteins may also be used diagnostically to identify the presence of that causes a number of diseases in cattle such as thromboembolic meningencephalitis (TEME), myocarditis, septicaemia, arthritis and
   Sequence 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 11; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding Haemophilus somnus transferrin binding proteins useful for vaccinating against and diagnosing H. somnus infections e.g.
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           Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                 Neisseria meningitidis ORF 025 partial DNA sequence SEQ ID NO:111-1
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Petersen J,
Tettelin H,
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02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
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, Pizza M, Rappuoli
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                                                     -ATTGTTÄÄÄĠTĊAAACCGGCAGGATATGCCGCA---
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Scalato E, Scarselli M;
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09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
 Petersen J,
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                                                                                                                                                                                                                                                                                   30-APR-1999;
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                                                                             CHIRON CORP.
                                                          INST GENOMIC RES
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                 Galeotti C,
 Pizza M,
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                                                                                                            98US-0083758.
98US-009486.
98US-0098994.
98US-0099062.
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Rappuoli R,
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meningitis; septicaemia;
Masignani V, Mora M;
Scalato E, Scarselli
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 205-206; 1453pp;
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    216
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    other;
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Length:
Matches:
Conservative:
Mismatches:

1014 66 45 109 32

Indels: Gaps:

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TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp
IleGlnAlaAspHisAsnMetAspGlyAlaSer---
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                                                           GGTGTCGATATTGCCGGCAATGCCGGACAACCCGTTTTGGCGGCGGCTGACGGCAAAGTG
                                                                                                                   GlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrVal
                                                                                                                                                                                  GGTAAAGTGGTTGCCGATTTCGGCGGCGGC--
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   ---IleValIleGlnHisThrAsn 265
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RESULT 4
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
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09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 206- ; 1453pp; English.
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P-PSDB; AAY74312.
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31-JUL-1998;
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, Pizza M, Rappuoli R,
, Venter JC;
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Scalato E, Scarselli
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                                                              SerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGly
                                                                                                             HisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArgIleAla
                   ValTyrValAspPro
                                          TTGATGGGCAATACCGATGCTTCCAGAACGCAGCTTCATTTCGAGGTGCGTCAAAACGGC
                                                                                                                                        GCGGGACAGCCCGTTTTGGCGGCGGCTGACGGCAAAGTGGTTTATGCCGGTTCAGGTTTG
                                                                                                                                                                                                             AspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHisAsnMet
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                                                                                                                                                              AspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheValSerSerTyrIle
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                                                                                                                                                                                                                                                                                    GTCGGCGGCATTGTTTGGCAGCGTCCG-----ACGCAAGGTAAAGTGGTTGCCGATTTC
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                                                                                         CACAACCAAAAATTGCTGGTCGGCGAGGGGCAGCAGGTCAAACGCGGTCAGCAGGTTGCT
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27.17%
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RESULT 9
AAA81766/c
ID AAA81766 standard; DNA; 6100 BP

04-DEC-2000 AAA81766;

(first entry)

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Query Match:
DB:
                                    Percent Similarity:
Best Local Similarity:
                                                                                                            Alignment Scores:
                                                                                                                                                                           sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The medicament) for treating, preventing or diagnosing infection due to medicament) for treating, preventing or diagnosing infection due to Meisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have falled mainly due to antigen tolerance. Multivalent vaccines have falled mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences, AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frazer CM, Hickey E,
Masignani V, Galeott
Rappuoli R, Pizza M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present
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30-APR-1999;
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                                                                                                                                               Sequence 6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 1588-1590; 1760pp; English.
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Galeotti
                                                                                                                                               BP; 1552 A; 1757
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99US-0132068.
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C, Mora
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Ratti G, So
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Scarselli
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US-10-018-706-2 (1-322) x AAA81766 (1-6100)

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T10 c10/c AAF21610 standard; DNA; 349980 BP. AAF21610; AAF21610; 13-MAR-2001 (first entry) Neisseria meningitidis B nucleotide sequence SEQ ID NO:111. Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial; ds. Neisseria meningitidis.	SerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGly 312	AspGlyAlaSer	GlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGlyArg 234	ProThrProThrProProValValGlnGlnProAlaProValAlaPro	TTCCGTGCGTGGAACGGCATGACCGACAATATGTTGAGCATCGGTCAGATT ValasnThralaHisThrProSerProValalaValGlnSerSerArgPro	

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Query Match:
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                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes the full length genome of CC Neisseria meningitidis B (NMB). The sequences in AAF21644 and AAF21607 CC to AAF21613 represent fragments of the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 cquences which overlap each other at the beginning and end of each CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21647 are repeated at CC the beginning of AAF21607, the last 49980 bp of AAF21547 are repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the CC Neisseria proteins given in AAB58550 to AAB58553 and AAF21599 to CC AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have cC Neisseria nucleic acids, proteins and/or antibodies which binds to the CC proteins can be used in compositions for treating or preventing infection CC due to Neisserial bacteria or as a diagnostic reagent for detecting the proteins can be used in a search to identify open reading frames (ORF8) cor coding sequences within the NMB genome. The DNA sequences provide CC more effective in vaccines than the outer membrane proteins which are cc used.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 349980 BP; 86771 A;
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Galeotti C, Mora M,
Frazer CM, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Appendix A; 692pp; English.
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08-OCT-1999; 99WO-US23573
28-FEB-2000; 2000GB-0004695
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-----ValAsnThrAlaHisThrProSerPro---ValAlaValGlnSerSerArgPro 147
                                                                                                                                        ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                                                                                                                                                                     CATACTATTGTGCGCGGCGACACGCTGTACAACATTTCCAAACGCTAC-----
                                                                                                                                                                                                      TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp
                                                                                LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly-----
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Rappuoli R;
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RESULT 11
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08-OCT-1999;
28-FEB-2000; 2
Pizza M, Hickey E,
Galeotti C, Mora M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
                                                                                                                                                                                                                                                                              Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection other Neisserial infections, for example, N.gonorrhoea -
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04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
                                                                                          Sequence 1885
                                                                                                                                        The DNA sequence is that of the Haemophilus somnus lppB gene LppB can be used in vaccines for preventing or treating H. s infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in vertebrates. See also AAQ51080-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis;
                                                                                                                                                                                                                                                                              Claim 8; Fig 9; 119pp; English.
                                                                                                                                                                                                                                                                                                                             and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                   Haemophilus somnus immunogenic proteins used in vaccines -
selected from haemin-binding protein, haemolysin, LppB and
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C. Theisen M;
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                      Antibacterial; infection; ds.
Listeria innocua
                                                        Listeria innocua contig DNA sequence #9
                                                                               29-AUG-2002
                                                                                                        ABQ67196;
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                                 food contamination; mutational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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sThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVa 155
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                                                                                                                                     The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in
                   anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genomic sequences from Listeria species, useful for detection treatment and prevention of infection, also related polypeptides,
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                                                                                                                                                                                                                  ------GTATCCGCTGC
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US-10-018-706-2 (1-322) x ABA90521
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Best Local Similarity:
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ABA90521/c
                                                                                                                                                                                                                                                                                                                                               The present invention is related to a lactbococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB5521). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactbococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                            Sequence 2365589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 1; 2504pp; French.
                                                                                                                                                                                                                  Match:
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CysAlaSerLysProThrTyrAsnSerThr----SerGlySerGlySerHisArgThr
                                                                                             ATTATGCTAAAGCTTGGCGAGCAAACGCGGCAACCTATCAAGCTGCAACCGCAGCCTTAA
                                                                                                                 TGGTATTCCAGTTGATCCA 2664956
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20-JUN-2001
                                                                                         Coryneform bacterium; amino organic acid synthesis; ds.
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                                                         Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                  GGACTTTCACAAAAATCTGGTAGCCCAATTGCTTCAATTAAG 268810
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                                                                                                                                        sequence fragment SEQ ID NO: 2741.
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                                                                                                        acid synthesis; vitamin;
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----TCGGTCACTCCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 615
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P-PSDB; AAG92487.
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                           192 ThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal
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HisAsnMetAsp---GlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSer
                                 GCAAACTCAATCGGCACCCCAATCTACGCCGTCATGGCCGGCACTGTCATCAGCTCTGGC
                                                              SerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAsp
                                                                                                 CCACGTTGGGGAACC-
                                                                                                                            ArgargPheGlyThralaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPhe 231
                                                                                                                                                                                                                             AAGCTGCAGGAGTCGCAACCACCGCCGTC-GCACCAGCCGCCACCGTAGCGCGCCCAGCA
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; 2000JP-0159162.
; 2000JP-0280988.
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Tateishi N,
                                                                                          analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. Tare useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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07-APR-2000; 2000TP-0159162
03-AUG-2000; 2000TP-0280988
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da M, Ozaki A;
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Alignment Scores:

43.3 146.50

Length: Matches:

Sequence 349980 BP; 80900 A;

98397 C; 92139 G;

78544 T; 0

other,

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RESULT 20
AAF59421/c
AAF59121/c
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                                                                                                                                                                                                                                                                          Actinobacillus actinomycetemcomitans; microbial; infection; vaccine; identification; localised juvenile periodontitis; antibacterial; antiinflammatory; ds.
                                                                                                                                                                                                                                                                                                                                                              Actinobacillus actinomycetemcomitans clone nucleotide sequence #8.
                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF59421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF59421 standard; DNA;
                        (IVIG-) IVIGENE CORP
                                                                06-AUG-1999;
                                                                                                       04-AUG-2000;
                                                                                                                                                      15-FEB-2001.
                                                                                                                                                                                                                                Actinobacillus actinomycetemcomitans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGACGGCGTCACCCCAGTCGACCCA 250131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HisAsnMetAsp---GlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysProThr------ProProValValValValLysLysProThrProThrPro 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleAlaSerMetLysAsnGlnPro---SerGlyAlaAlaLeuPheGluPheArgIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrlleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg
                                                                                                          2000WO-US21340
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method (M1) for identifying a polynucleotide (I) of a microbe (M) that is expressed in vivo. (M1) comprises: (a) absorbing antibodies (Ab) against antigens that are expressed by (M) in vivo and in viro with cells or cellular extracts of (M) that have been grown in vito; (b) isolating unadsorbed Abs; and (c) probing an expressed in vivo is identified. The method can be used for identifying antigens expressed during an actual microbial infection. The identified polynucleotides are useful for vaccine design, diagnostics and antibiotherapy, in particular for the diagnosis and therapy of Actinobacillus actinomycetemcomitans infection, which is the etiologic agent for localised juvenile periodontitis. The present sequence represents an Actinobacillus actinomycetemcomitans clone invarione incortice sequence, which is used in an example from the present expression expressed which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying microbial polynucleotides, useful for vaccine design, diagnostics and antibiotherapy, comprises isolating clones of a microbe's expression library reactive with antibodies against microbe proteins produced during in vivo growth -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 949 BP; 170 A; 236 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 63; 68pp; English.
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  224 ValThrSerAsnGlyMetTrp-
                                                                                                                                                                                           193
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                                                                                                                                                                                                                                                                                                                                                              153 ProAlaValGlnLysProThrProProValValValValLysLysProThrProThrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp
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                                                                GGCGTAGGTACTGCTGCACCGGCAACCAATCAGCCGATAACCCAAGCGGGCACCGCACCG
                                                                                           ArgPheGlyThrAla--
                                                                                                                                                                                           GlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArg
                                                                                                                                                                                                                                                                             ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp
                                                                                                                                                    GGCACA------CĀĀTATGGTTCCGACGGCACGATTACCGGCCCGATTAAAAGCC
                                                                                                                                                                                                                                     CCGGCTACGCAAGGTGGTGAACCGACC---
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145.00
37.04%
26.39%
8.68%
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                                                                                                       ThrValAlaGlySerThr---
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DB:
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 178-186; 1150pp; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to nucleic acid sequences (ABG67188-ABG71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1163020 BP; 388339 A; 197589 C; 235612 G; 341474 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
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                                                                                                                                                                            Genome; bacterium; Haemophilus influenzae; computer readable expression modulating fragment; regulation; gene expression; organism; open reading frame; ORF; ds.
07-JUN-1995;
                               22-APR-1996;
                                                                     24-OCT-1996
                                                                                                        W09633276-A1.
                                                                                                                                                                                                                                                 Haemophilus influenzae complete genome
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Best Local Similarity:
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAAAAAAACAACAACAAGCATTGCAAAAAGCACAGCAAGAGCATCAA----
                                                                                                                            GlySerSerGlyVal------MetGlnPheArgTyrProValGlyAlaThrAsn
                                                                                                                                                                                                                                AAAGCTGAAGAAAAACGAACA-
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                                                                                               AGTACAAGCGGTTTAGGGGCGCCAAAAAAAACAATATTCCTTACCAGTTTCTGGTTCA---
                                                                                                                                                                                             ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr
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                              ---ATTTTGCATACTTTTGGT-----TCTATCCAAGCAGGCGAAGTACGTTGGAAAGGT
                                                           ProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGly
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                                                                                                                                                                                                    New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial infection such as otitis media, delayed speech learning and inflammation of middle ea
                                                                                       The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. influenzae infection, which can cause otitis media in infants and
                                                                                                                                                              Claim 13; Page 88;
                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                       Thonnard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; auditory; antiinflammatory; gene; ds.
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DB; AAO17658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAlaAspHis---AsnMetAspGlyAlaSerIleValIleGlnHisThrAsnGlyPhe
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children, pneumonia in elders, sinusitis, nosocomial infections, invasive diseases, chronic critis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed splearning, infections of the upper respiratory tract and inflammal the middle ear. The present sequence is a version of the BASB201

spiratory tract and inflammation of is a version of the BASB201 coding

speech

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sequence

of,

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US-10-018-706-2 (1-322) x AAL46626
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Best Local Similarity:
H influenzae BASB201 coding sequence
                                     05-AUG-2002
                                                                                                     AAL46624 standard;
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                                                                                                                                                                                                                                                                                                           TTAAGTTTATATGGCTTCAATCAAGCGGTATCAGTGAAAGTTGGTCAGCTTGTTTCAGCA
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of several versions of the BASB201 protein from non-typeable Haemophilus influenzae. These can be used in the production of vaccines against H. influenzae infection, which can cause outtis media in infants and children, pneumonia in elders, sinusitis, nosocomial infections, or invasive diseases, chronic otitis media with hearing loss, fluid accumulation in the middle ear, auditive nerve damage, delayed speech learning, infections of the upper respiratory tract and inflammation of the middle ear. The present sequence is a version of the BASB201 coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated non-typeable Haemophilus influenzae BASB201 polypeptides, useful as components of vaccines for treating bacterial inflection such as otitis media, delayed speech learning and inflammation of middle ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 87; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASB201; otitis media; pneumonia; sinusitis; nosocomial infection; auditive nerve damage; delayed speech learning; vaccine; antibacterial; auditory; antiinflammatory; gene; ds.
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DB; AAO17656.
                                                                                                                   114
                                                                                                                                                                                     94 GlulleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeu 113
                                                                                                                                                                                                                                                       74 GlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArg
                                                 AlaHisThrProSerProValAlaValGlnSerSerArgProProVal---GlnGlnHis 152
                                                                                                             ThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsnThr 133
                                                                                                                                                       ----TCTACGCTGÄÄTGAACTCÄÄTAAAAATTTAGCCCTAGATCAAGATAAA-----
                 ĠĊTGAACAAGCAGCACGCGAACAAGAAAAACGTGAAÁGÁGAGGCACTTGCTCÁÁCGCCAA
                                                                                                                                                                                                                         CAAAAAAAACAACAACAAGCATTGCAAAAAGCACAGCAAGAGCATCAA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 466 A; 224 C;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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  09-APR-1992;
04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus somnus; immunogenic; haemolysin; LppB; thromboembolic meningoencephalitis; septicaemia; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTAAGTTTATATGGCTTCAATCAAGCTGTATCAGTGAAAGTTGGTCAGCTTGTTTCAGCA 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCAGGTTATTGCTCAAGTAGGAAATACAGGGGAAATATCACGTTCTGCGCTTTAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnAlaAspHis---AspMetAspGlyAlaSerTleValIleGlnHisThrAsnGlyPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIle 248
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  92US-0865050.
92US-0893424.
92US-0893426.
93US-0038287.
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93US-0038719.
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/note= "leukotoxin
2773..3573
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                        'note= "LppB peptide (split)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The lppB gene encoding llpB was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid pAA352. The lppB gene fragment was taken from pMS11. The lppB can be used in vaccines for preventing or treating H. sommus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and request in the large sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumonia in vertebrates.
See also AAO51080-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3646 BP; 1257 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 11; 119pp; English
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P-PSDB; AAR42385-6.
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249 lnAlaAspHisAsnMetAspGlyAlaSer------IleValIleGlnHisThrAsnGlyP 267
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                                                              GATATTAGCGGTTCTCGTGGACAAGCTGTTAATGCAGCAGCTGCATGGACGCAGTTGTAT 3537
                                                                                                                                                                                      ValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMet
                                                                                                                                                                                                                                                                                                                                                     ProThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                  GlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProVal 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrLeuTrpSerGly------AspLeuLysValArgGluArgSerIleSerSer
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                                                                                                                                                 AAAATTAATCAA----GGATTTTCCAGTGCTGATGGAGGC-----AATAAAGGTATT
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                                                                                                                                                                                                                                                                      PheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnPro
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                                                                                                   TrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThr---ValIleG
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                                                                                                                                                           In situ production of a homologous autolysin or a heterologous autolysin from a food grade Gram positive bacteria, can be used in a process for the lysis of a culture of lactic acid bacteria. The cultures of lactic acid bacteria e.g. cheese, where the culture is lysed following the completion of fermentation. The enhanced induction of the autolysin is performed some hours after the fermentation is finished. No extra lysin needs to be added and the lysin does not need to be isolated or encapsulated. The time of lysis can be precisely controlled.
                                                                                                                                       Sequence 1929 BP; 619 A; 378 C;
                                                                                                                                                                                                                                                                                        Claim 14; Page 51-54; 103pp; English.
                                                                                                                                                                                                                                                                                                              Lysis of a culture of lactic acid bacteria in, e.g. cheese production - by in situ prodn. of an auto:lysin, regulated by inducible promoter.
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P-PSDB; AAR85285, AAR85288, AAR85289.
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                                                                                                                                                                   ThrVal------ArgThrCdyGlnArglealaserMetLyg------Asm 296
                                                                                                                        GlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrVal
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                                                                                                                                                                                                                                                                                     AlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHis 263
                                                                                                                                                                                                                                                                                                                                  ValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn 243
                                                                                                                                                                                                                                                                                                                                                                             ValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThr 223
                                                                                                                                                                                                                                                                                                                                                                                                                          GluAlaProPheAlaThrGlySerSerGlyValMetGln-----PheArgTyrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTCTGTGACACCTGCA-----AAACCAACTTCACAAACAACTGTTAAGGTTAAATCC
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inhibition activity. The proteins may be administered to patients as vaccines, and the nucleotides may be used as part of a gene therapy regime. Diseases or conditions that may be treated using the proteins or nucleotides of the invention include autoimmune diseases; genetic disorders; haemophilia; cardiovascular diseases; cancer; bacterial, fungal and viral infections, especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary inflammation; Guillain.Barre syndrome; insulin dependent diabetes mellitus; and allergic reactions such as asthma and anaemia. They may also be used for treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis (ALS). Proteins with activiny inhibin activity may additionally may also be used for the sclerosis (ALS).
                                                                                                                                                                                                                                                                                                          cytokine activity; cell proliferation; differentiation; immune modulation; haematopoiesis regulation; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; h
                                                                                                                                                                                                                                                                                                                                                       The invention relates to 40 human secreted proteins (AAY94981-Y95020), and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins of the invention include those that are thought to be only partially secreted, i.e., transmembrane proteins. The proteins of the invention may exhibit one or more activities selected from the following:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New secreted or transmembrane proteins and polynucleotides encoding them, useful for treating neurodegenerative disorders, autoimmune diseases and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; cancer; tumour; cardiovascular disorder; blood disorder; haemophilia; autoimmune disease; diabetes; inflam infection; fungal; bacterial; viral; HIV; allergy; arthritis; neurodegenerative disease; asthma; contraceptive; ss.
Sequence: 4093
                                                           additionally be useful as contraceptives. Nucleic acid sequer invention may be used in chromosome mapping, and as a source
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 72; Page
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09-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11115 BP; 1521 A;
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(FARN/) FARNET
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Streptomyces venezuelae vep ORF1 (AAT68715) comprises the polyketide synthase (PKS) gene cluster encoding a polyene of 12 carbons (see also AAM16829-30 and AAW00918). It contains 5 PKS modules, with a 5' loading module and a 3' end domain. Each of the sequenced modules includes a keto-ACP, an acyltransferase, a dehydratase, a keto-reductase and an acyl carrier protein domain. He gene cluster was cloned using a heterologous hybridisation strategy from a genomic DNA library. A novel expression cassette encoding the first module

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCAGGTCGCCCAGGTGGGCGGGGGGGGGGCGCGCGGGGGTCGGAGGAGCAGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrAsp-----SerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GlyGlyLeuAlaIleGlySerGlnValIle 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGTCGCGCCCC-----TCGGCGACGAGCCGCCACAGGTCCTCGGGGGAG 315:
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GCGGAGACCGCCGTGGCGGCCTCCTGGTCGCGTACGGAGTCCGCCGCCATCGCGGAGCAG
                           AlaGlyThrValIleGlnAlaAsp---HisAsnMetAspGlyAlaSerIleValIleGln
                                                                                          Ser----AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn
                                                                                                                         CCGGTGCTCCCGTGCGCGGCGGTCCAGTCGACGTCGTGGCCCCGGACGAAGACGGTGGTG
                                                                                                                                                     ArgArgPheGlyThrAlaThrValAlaGlySer------
                                                                                                                                                                                    CCGTCGAACCAGTGGCGTTCGCGCTGGAAGGCGTAGGTCGGCAGGGGCACCCTGACCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGGCAGGCGCAGTCCCGTGTCGACGAGCGCGCTTCCGCAGC-----
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                                                                                                                                                                                                                   ---SerGlyValMetGlnPheArgTyrPro-----ValGlyAlaThrAsnProValVal
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RESULT 31
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The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not cerived from the eryC gene cluster of Saccharopolyspora erythraea or CC Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide compounds. Recombinant or augmented cells comprising the desosamine CC compounds. Recombinant or augmented cells comprising the desosamine CC compounds. Recombinant or augmented cells comprising the desosamine CC and/or macrolide biosynthetic gene clusters are useful for the corolides. The macrolide biosynthetic gene clusters are useful for the compounds are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide cynthesis may be useful to prepare novel antibiotics and cc synthesis may be useful to prepare novel antibiotics and cc recombinant host cells are useful as biopolymers, e.g., in packaging or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desosamine and macrolide biosynthetic synthesis of methymycin and pikromycin
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neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase
biopolymer; antibiotic; chemotherapeutic; immunosuppressant; ast
chronic obstructive pulmonary disease; respiratory inflammation;
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ArgArgPheGlyThrAlaThrValAlaGlySer
                                             CCGTCGAACCAGTGGCGTTCGCGCTGGAAGGCGTAGGTCGGCAGGGGCACCCTGACCGTG
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                                                                           ---SerGlyValMetGlnPheArgTyrPro-----ValGlyAlaThrAsnProValVal
                                                                                                         CCGGTGCCCGCACCGGTGCCGATCGGCCGCCGTGAGCGGCGCCGCCGTTCGCGCGGCG
                                                                                                                                         ProValAlaProProValThrGluAlaProPheAlaThrGlySer----
                                                                                                                                                                                                     ProProValValValLysLysProThrProThrProProValValGlnGlnProAla
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                                                                                                                                                                                                                                                                       The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent w0200177334 (published 18-OCT-2001) which is available in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 1; 2504pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluating strain variation of Mycobacterium tuberculosis, comprise determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monitoring.
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                                                                                                                                                                                                                                                                                                                                                       GATGTCGATGTTCAACCTCGGCCTGGGAAACATCGGCCAATTC 430321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACCTGGGCGATACCGTCTCGGGCGTATTCAACACCGGCATCGGGGCACCGGCCAACGT
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                                                                                                                                                                                                                                                                                                                                                                                        yAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyr 314
                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGGGCATGTTCAACATCGGCAGCAACCTCGCGGGGTTCTTCCACGACCAGGCGACCGG 430364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCAAGCGTCGGTCCCTTCGATGTCACGTTCGTCAACATTGCGGCTACCACGGGCTTTTT 430643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             eAlaSerMetLysAsn----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ACCTCGGGCTTC---AACAACTACGGCTCGCTGCAATCGGGACTGGC 430484
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                              tuberculosis
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                                                                                                                                                                            strain H37Rv genome SEQ ID NO 1.
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and 137Rv (AAI99682). The method is useful for evaluating strain variation M. tuberculosis and has valuable application in the fields of M. tuberculosis genetics, epidemiology, patient treatment and epidemic monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monitoring.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evaluating strain variation of Mycobacterium tuberculosis, compute the nucleotide sequence of the strain at positions genome corresponding to positions where M. tuberculosis strains 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
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ValGln-SerSerArgProProValGlnGlnHisProAlaValGlnLysProThrProPr 161
                                                                                                                                                                                               GGCAATTTCAGTACGGGCTTTGCCAACCAGGGTGATATCGCCACCGGGGCTTTCATCACC 430949
                                                                                                                                                                                                                                                                                                                                                                       LysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIle 95
                                                                                                                         GGCGACATGGGCAACGGCGCCTTCTGGCGCGGCGAC------CAGCAGGGCCTATTC 430898
                                                                                                                                                                                                                             ---AsnLeuAsnSerSerTyrThr------IleTyrThrGlyGlnTrpLeuThr 114
                                                                                                                                                                                                                                                                GGCGACACCAACACCGGCATCGCCAACCTGGGCGACTTCAACACGGGCTTCTACAACACC 431009
                                                                                                                                                                                                                                                                                                   GlyHisIleAsn-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGly 59
                                                     AGCGCGGGCTATCGGGTCCATGTTCCCGAAATACCCGCACACGTCACCGTGGAAGTTCCC 430838
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                                                                                 The present sequence is a Achromobacter lyticus DNA encoding the present sequence is used in the production of altered genes which The present sequence is used in the production of altered genes which The present sequence is used in the production of altered genes which allow expression and preferably secretion of active protein in mammalian cells/tissues. The altered gene is produced by operably linking the beta-lytic protease coding sequence with mammalian promoter, signal beta-lytic protease coding sequence with mammalian promoter, signal beta-lytic protease to translation initiation sequences. The modified sequence peptide and translation initiation sequences. The modified sequence ruminants, e.g. goats, sheep, and cows. It is also used to produce transgenic animals which are resistant to staphylococcal infections.
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21-JUN-1999;
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                                                            Sequence 1520
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                      CACACCGGCGGCTGGTCGACGACCTACTACCACCTGATGAACATCCAGTACAACACCGGC 1176
                                             HisThrAsnGlyPheValSerSerTyrTleHisTleLysAspAlaGlnValLysThrGly 282
                                                                         GCCGCCGGCTCGTTCAAGCGC-
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20-JUN-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                           AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clayton R, White OR;
                                                                                                                                                                                                                     Sequence 111309
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97US-0050359.
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                                                                                                                                    Borrelia burgdorferi; spirochete; bacterium; epidemic relapsing fever; endemic relapsing
                                                                                                                                                                                                          04-MAY-1999
            18-JUN-1998;
                                        30-DEC-1998.
                                                                                          Borrelia burgdorferi
                                                                                                                                                                             Borrelia burgdorferi polynucleotide sequence
                                                                                                                                                                                                                                                              AAX20248 standard;
                                                                                                                                                                                                                                     AAX20248;
                                                                                                                       infection; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCATTTCTCACAGCAACGGATTCCAAACTTTATATGCACATTTGAATTCTTTTGCCGTT
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                                                                                                                                    pathogen; Lyme disease;
fever; Lyme borreliosis;
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
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                                                                                 GTATTAGGGGAGACTTTTATTTATCCTGTGCAGGGTGTTATTACTTCGGGGTATGGCTAT
                                                                                                            ValLysLysProThr-----ProThrProProValValGlnGlnProAlaProVal
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{\tt TyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGly}
                                                                                                                                                                                                                     ArgSerIleSerSerGlyValAsnThrAlaHisThrProSerProValAlaValGlnSer 144
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                       Peptidase was purified from Achromobacter lyticus by a Sepharose CL-4B column, a Sephadex G-75 column, and by reverse phase HPLC. The first 25 N-terminal amino acids were found to be identical to those of the beta-lytic protease from Lysobacter enzymogenes. The beta-lytic protease from Lysobacter enzymogenes. The beta-lytic protease of A. lyticus was cloned using PCR primers full length sequence of the L. enzymogenes beta-protease. The full length sequence of the gene encoding the A. lyticus enzyme was determined by dideoxy sequencing. The beta-lytic protease is expected to be an enzyme which can decompose not only Gram-positive See also AAQ25084-6.
                                                                                                                                                                                     Claim 1; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                              Beta-lytic protease gene and DNA encoding it Gram-positive and some Gram-negative bacteria
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AsnAlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGln
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                                                          GACATGTCGCGCGGCGGCTGGGGGCAGCAACCAGAACGGCAACTGGGTGTCGGCCTCG
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                                                                                                                                                                         ValArgArgPheGlyThrAlaThrValAlaGlySer----------
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US-10-018-706-2 (1-322) x AAZ00266 (1-7277)
                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                             The invention provides a method for detecting a US (sub)type hepatitis E virus (US-HEV), or its naturally occurring variants in a sample by treatment with a binding partner specific for a marker of the virus, and then detecting any complex formed. The method is used to diagnose infection with US-HEV. Polypeptides from US-HEV, antibodies specific for open reading frames (ORF) in US-HEV and host cells expressing these ORFs are useful in vaccines or for passive immunisation. The polypeptides are also used to raise specific antibodies (useful as immunoassay reagents). Fragments of nucleic acid from US-HEV are useful as primers and probes in usual hybridisation and amplification assays for detecting infection. The present sequence represents a HEV-US2 full length gene sequence.
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                                                                                                                                                                                                                            Sequence
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ACGACGGTGGTTGATGGCGCCCATCTTGAAGCGAATGGCCCTGAGGAGTATGTTCTGTCA 1814

ThrCysIleLeuAlaGlyCys-----AlaSerLysProThrTyrAsnSerThrSer 43

	299 SerGlyAlaAlaLeuPheGluPheArgIleSerArgAsm 311      ::::   :::    2631 ATCCATGCAGTGGCTCCCGACTATAGGGTTGAGCAAAAC 2669	
298 2630	280 LysThrGlyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnPro	
279 2570	260 VallleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnVal :::	
259 2528	240 AsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIle               2493 AATGCCTCAAACCCTGGCCATCGCCCCGGGGGTGGC	
239 2492	220 AlaGlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIle	
219 2453	yThrAlaThrVal AAGGTGTAT	
199 2423	180 ProValAlaProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGln	
179 2390	160 ProProValValValValLysLysProThrProThrProProValValGlnGlnProAla     :::   :::       2337 AGCCCTATTGTGCTTACCCCCCCCCCCCCCCCCCC	
159 2336	150GlnGlnHisThr 	
149 2276	140 ValAlaValGlnSerSerArgProProVal	
139 2234	120 LeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro	
119 2174	101 LeuasnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAsp    :::	
100 2114	94AsnAsn	
93 2054	83TypSlleAlaGlnArgTyrGlyLeuAsnTpArg	
82 1994	77 GlnGlyAspThrValSer 1935 CCYGGTGGCGCCCTAGCGCCGCGGGGGGAGGTGGCSGCCTTCTGCAGTGCTCTTAT	
76 1934	59GlySerGlnVallleThrAspSerGlnGlyValProAsnArgTyrGlnValLys	
1874	1815 TTTGACGCCTCTCGCCAGTCTATGGGGGCCGGGTCGCACAGCCTCACTTATGAGCTCACC	

Search completed: July 3, 2003, 22:55:31 Job time: 8697 secs

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Result
No.
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-Q=Cgm2 1/USPT0.spool/USL0018706/runat 30062003 091105 23816/app query.fasta_1.519
-DB=ISSUEd Patents NA -QPMT=fastap -SUPFTX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10018706 @CGN 1 1 32 @TUNAT 30062003 091105 23816 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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US-09-405-728-4
US-08-619-812-3
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US-08-737-716-1
US-08-737-716-11
US-09-103-840A-1
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Sequence 139, App Sequence 7, Appli Sequence 7, Appli	129	Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli	18,18	Sequence 1, Appli Sequence 9, Appli Sequence 9, Appli Sequence 2, Appli Sequence 221, App Sequence 221, App Sequence 37, App	700012121	Sequence 2, Appli

## ALIGNMENTS

RESULT 1

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PCT-US96-05320A-707
; Sequence 707, Application PC/TUS9605320A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3
COMPUTER: HP Vectra 486/
COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
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APPLICANT:
TITLE OF II
NUMBER OF S
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CLASSIFICATION: PRIOR APPLICATION NUMBER:
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                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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STREET: 1100 New York Avenue,
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Owen White
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Johns Hopkins University
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Rockville, MD
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e, Suite 600
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,42
PILING DATE: JUNE 7, 195
ATTORNEY/AGENT INFORMATION:
NAMB: Eric K. Steffe
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488

08/487,429 , 1995

L488.014PC01

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TELEFAX: (202) 371-260

FILEFAX: (202) 371-2540

FINFORMATION FOR SEQ ID NO: 707:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
FYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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GGCAATGCTTTACGTGGTTACGGTAATTTAATTATCATCAAACATAATGATGATGTTTTTTTA 1047
                          AspHisAsnMetAspGlyAlaSer-----IleValIleGlnHisThrAsnGlyPheVal 268
                                                          ATTAGTGGTTCACGAGGACAAGCTGTAAAAGCGGCTGCAGCAGGGCGAATAGTGTATGCA
                                                                                   PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrVallleGlnAla 250
                                                                                                                                                                               AATGTCGTTGCG------CCAATC---GCTCAAAT---GTTGTGTGGCAATGGCCG
                                                                                                                    ÁCTTCAGGTAATATCATCCAAGGTTTCTCAAGCÁCAGATGGCGGTAACAAAGGÁATTGAT 927
                                                                                                                                               ThrAla-----ThrValAlaGlySerThrValThr-----SerAsnGlyMetTrp 230
                                                                                                                                                                                                                                           GGTACTATTATTGGCCCAATTAAATCAGAGGCTGGCACATCGCCTAGTGTACCTGTGGCA 762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGTAAAAGAATTGGCGGCGTTGAATAACCTATCCGAACCTTATAATTTAAGTTTAGGG
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Conservative:
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Sequence 4, Apy...

Sequence 4, Apy...

Patent No. 6391316

PARTENT INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Schryvers, Anthony B.

APPLICANT: Schryvers, Anthony B.

TITLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS SOMNUS

TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS

FILE REFERENCE: 9000-0049-2.0

CURRENT APPLICATION NUMBER: US/09/405,728

CURRENT FILING DATE: 1999-09-24

EARLIER APPLICATION UNMEER: US 09/267,749

RARLIER APPLICATION UNMEER: US 09/267,749

EARLIER FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 2179

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US-09-405-728-4
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Best Local Similarity:
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Pred. No.:
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                                                                     ProThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaPro
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Conservative:
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US-08-619-812-3
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GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/038,719
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: PORTING PATENTAL
                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
                                         MOLECULE TYPE:
                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                               NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
      NAME/KEY:
                                                                                STRANDEDNESS:
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STATE: CALIFORNIA
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THEISEN, MICHAEL
HARLAND, RICHARD J.
RIOUX, CLEMENT R.
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                                                          Sequence 7, Application US/08619812
Patent No. 6100066
GENERAL INFORMATION:
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APPLICANT:
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POTTER, ANDREW A. THEISEN, MICHAEL HARLAND, RICHARD
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Best Local Similarity:
Query Match:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION DATA:
FILING DATE: 15-MAR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/038,719
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBLNS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0019.20
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 3646 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Pred. No.:
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TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LOCATION:
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STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
CCUNTRY: UNITED STATES OF AMERICA
3271 TCAGAGGTGACACAAAATACAGTCAATGAG---ACATGGAATGCTAATAAACCAACAAAT 3327
                                                                                                                                                                                                                                                                                   3211
                                                                                                                                                                                                               3151 AAAGAATTGGCCACACTAAATAATATGTCTGAGCCATATCATCTGAGTATTGGACAAGTA 3210
                           150 GlnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThr 169
                                                                                                     130 GlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProVal 149
                                                                                                                                                                               113
                                                                                                                                                                                                                                               93 ArgGlulleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                                                                                                              LeuThrLeuTrpSerGly------AspLeuLysValArgGluArgSerIleSerSer 129
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2776..3570
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131.00
43.75%
23.08%
7.84%
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 5 US-08-737- SEQUENCE PACENT N APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPLI APPL	B & B & B & B & B & B & B & B & B & B &
ULT 5 General 1. Application US/08737716 General No. 595258 General No. 595258 GENERAL INPOGNATION: APPLICANT: Girbs BUIST APPLICANT: Girbs BUIST APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANT: Jerkox APPLICANTON LARA APPLICANTION NUMBER: USA. APPLICANTON UNMBER: USA. APPLICANTON UNMBER: USA. COMPUTER RADABLE FORM: APPLICANTON UNMBER: USA/377,716 FILING DATE: 12-ARX-1994 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP9420153.3 APPLICANTON UNMBER: EP94201	170 ProThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaPro 189

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LOCATION:
FEATURE:
NAME/KEY:
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                                                                                                                AlaGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHis 263
                                                                                                                                                                                                                                                                     ValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThr 223
                                                                                                                                                                                                                                                                                                           TGGAATCATTTAAGTTCAGATACCATTTATATTGGTCAAAATCTTATTGTTTCACAATCT 1272
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  ACTICITATOTAACTCAAATGCCTCAATTCAT----
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                                                                                                                                                                                                                                                                                                                                               GluAlaProPheAlaThrGlySerSerGlyValMetGln-----PheArgTyrPro
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                                    ThrAsnGlyPheValSerSerTyrTleHisIleLysAspAlaGlnValLysThrGlyAsp 283
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-AAGGTCGTTAAAGGAGAT 1380
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Best Local Similarity:
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: 12-MAY-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 9
FILING DATE: 12-MAY-1994
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/737,716
FILING DATE: 22-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL95/00170
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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CLONE: Fig.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                  No.:
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LOCATION:
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VENTION: acid bacteria by means of a lysin, and uses
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Sequence 1, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Sherman, D.H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT APPLICATION NUMBER: 05/09/105,537A
; CURRENT FAILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 15872
; TYPE: DNA | ORGANISM: Streptomyces venezuelae
US-09-105-537-1
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3195 GCGTCGCGCCCC------TCGGCGAGCGAGCCGCCACAGGTCCTCGGGGGAG 311
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                                                             ACCCCGTCGGGACCGAGCTCCAGGAAGGTGTCGGCGCCCCGATTCCTCCAGGGTGCGTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT EPPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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TITLE OF INVENTION: DNA SEQUENCES FOR
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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  430881 TACAGCGGCATAACGCTTGAGCÁAATCAÁCTTCGGTTTCACCÁTCGACATCGCÁGGGATC
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                                      oValValVal-----ValLysLysProThrProThrProProValValGlnGlnProAl
                                                                                   GTCAACATCCCCATCACCGCCAGCT-
                                                                                                                                                                AGCGCGGGCTATCGGGTCCATGTTCCCGAAATACCCCGCACACGTCACCGTGGAAGTTCCC
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                                                                               US-10-018-706-2 (1-322) x US-09-103-840A-1 (1-4411529)
                                                                                                                                           Query Match:
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                          Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAITITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT PEPLICATION UNDER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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APPLICANT: WHITE, Owe
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                             AsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGly 59
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Matches:
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RESULT 10
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
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                                                                                                                    GATGTCGATGTTCAACCTCGGCCTGGGAAACATCGGCCAATTC
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WITE, Owen R.
APPLICANT: WITE, Owen R.
APPLICANT: VENTER, Olaire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAM SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH 14150
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
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Matches:
Conservative:
Mismatches:
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US-08-276-213-6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Thomas, Steven
APPLICANT: Laymon, Robert
APPLICANT: Himmel, Michael
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HYPOTHETICAL: N
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
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CITY: Golden
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TOPOLOGY: linear
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--GlnTrpLeuThrLeuTrpSer------
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                                                   CGTGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCCAATACGGTGCGGACAGCT 1886
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(307) TD NO: 6:
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US-09-136-574A-1
                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09136574A Patent No. 6294366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 APPLICANT: Farrington, Grah
Anderson, Paige
Gibbs, Moreland
                                                                                 NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
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STATE: PA
COUNTRY: USA
ZIP: 19477
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                                               CITY: Spring
                                                                    STREET:
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                                                                                                                Gibbs, Policy
Bergquist, Peter
Bergquist, Roy
Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
Williams, Diane P.
OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fal
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                                                                 Spring House Corporate Center, P.O. Box
                                                   House
                                                                                                                                                                                                                                                                                        Graham
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PRIOR APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, MATY E.
REGISTRATION NUMBER: 1997US001/CIP
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELEPONMUNICATION: INFORMATION:
TELEPONE: 215-540-9200
TELEPONE: 215-540-9210
TELEPONE: CUNKnown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Best Local Similarity:
Query Match:
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Pred. No.:
9258 ACACCCACTCCGACTCCTTCTGTCACAGATGATACAAATGATGATTGGTTATTTTGCGCAG 9317
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                                                                      9198 ACACCAACAGCAACGCCAACACCTACACCTTCTATCACGATAACACCAGCGCCAACTGCA 9257
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                              159
                                                                                                            179 AlaProValAlaProPro----- 189
                                                                                                                                                                                                                                                        140 ValAlaValGlnSerSerArgPro---ProValGlnGlnHisProAlaValGlnLysPro 158
                                                                                                                                                                                                                                                                                                                                 122 ValArgGluArgSerIleSerSerGlyValAsnThrAlaHis-----ThrProSerPro 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 SerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeu 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 SerGlySerGlyGlyLeuAlaIleGlySer------
                                                                                                                                                  ACACCGACTGTGACGGTGACCCCAACTTCTACACCCACACGGTTTCATCATCCACTCCT 9197
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119.50
32.62%
25.32%
7.16%
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Qy 217 AlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGlyArgAspGly 236	Qy 206 AlaThrAsnProValValArgArgPheGlyThr 216	Qy 190 PheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGly 205	Qy 174ValValGlnGlnProAlaProValAlaProProValThrGluAlaPro 189	Qy 155 ValGlnLysProThrProProValValValValLysLysProThrProThrProPro 173	Qy 135 HisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAla 154	US-10-018-706-2 (1-322) x US-09-103-840A-2 (1-4403765)	Alignment Scores:  Pred. No.:  Score:  118.50  Percent Similarity:  Best Local Similarity:  Query Match:  7.10\$  DB:  Page 10	SULT 13 -09-103-840A-2 Sequence 2, Application US/09103840A Patent No. 6294328 PATENT INFORMATION: APPLICANT: WHITE, Owen R. APPLICANT: WHITE, Owen R. APPLICANT: VENTER, JOHN C. TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYS TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-2007.00 CURRENT FILING DATE: 198-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: A403765 TYPE: DNA ORGANISM: Mycobacterium tuberculosis FEATURE: OTHER INFORMATION: CDC 1551 OTHER INFORMATION: represent a, t, c or g -09-103-840A-2	Qy 233 GlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGly 245  Db 9423 AATCTTAAAAAGTGCATTAGCTGAGATTGCAAACAGAGGA 9461	Db 9372 TGGTTTGGATTTAATACAGGAACGAATGTGTTTGATGGTGTGTGGGAGTTGT 9422	Qy 213 ArgpheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSer 232	Qy 193 GlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArg 212

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US-09-462-606-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 5127
; TYPE: DNA
; ORGANISM: Hepatitis
US-09-462-606-1
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SEQ ID NO 1
TONGTH: 5127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Emerson, Suzanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS
FILE REFERENCE: 20264267US1
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT FILING DATE: 2000-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/053069
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: PCT/US98/14665
PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
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        1942 TTTTGCAGTGCCCTTTATAGATATAATAGGTTCACCCAGCGGCATTCGCTGACCGGTGGG 200:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetThrValThrIleAlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeu
                                                                                  TGCACAGCCACATTCCCCCCCGGCGGCGCCCCTAGCGCTGCGCCGGGGGAGGTGGCGGCC 1941
                                                                                                                                                                                                                                                                                                                                                                                               CTAACGGCTACTGTTGAGCTCACTGCAAGCCCAGACCGTTTAGAGTGCCGCACTGTGCTT
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                                                                                                                                                                                                                                                                              ThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAla 57
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                                                                                                                    AsnArgTyrGlnValLysGlnGlyAspThrValSer-----
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118.00
31.54%
20.26%
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                                                                                                                                                                                                  GlySerGlnValIleThrAspSerGlnGlyValPro 70
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                                         -LysIleAlaGlnArgTyrGlyLeuAsn-----
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Sequence 3, Application US/09462606
Patcent No. 6432408
GENERAL INFORMATION:
APPLICANT: MENG, XIANG-JIN
APPLICANT: Emerson, Suzanne U.
APPLICANT: Emerson, Suzanne U.
APPLICANT: PURCELL, Robert H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS ANI
FILL REFERENCE: 20264267US1
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT EILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: US 60/053069
PRIOR APPLICATION NUMBER: PCT/US98/14665
PRIOR FILING DATE: 1998-07-17
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Hepatitis E virus
US-09-462-606-3
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 3
LENGTH: 7207
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                                  ProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgŢγr 202
                                                                            ATTGTGCTTACCCTCCCCCCCCCCCCCCCCCTCCCTGTGCGTAAGCCCACCAACACCC-----
                                                                                                               ValValValLysLysProThrProThrProProValValGlnGlnProAlaProValAla 182
                                                                                                                                                      TCTCAGGTCGATGCGGCATCTGTGCCCCCCTGCTCCTGAGCCCGCTGGATTACCCAGCTCC
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31.54%
20.26%
7.07%
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Matches:
Conservative:
Mismatches:
Indels:
-TCCCGCACTCGTCGTCTCCTACACCTAT
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PATEBLE NO. 5994099

APPLICANT: Lewis, Randolph V

APPLICANT: Hayashi, Cheryl Y

ITILE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA

TITLE OF INVENTION: CODING THEREFOR

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 GATEHOUSE RD. SUITE 500E

CITY: FALLS CHURCH
STATE: VIRGINIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                   COMPUTER RENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ANAME: MUTPHY Jr., Gerald M
REGISTRATION NUMBER: 28977
REGISTRATION NUMBER: 28977
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 1447-109P
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPER: DISTANCE CHARACTERISTICS
LENGTH: 2830 base pairs
US-09-010-928B-1
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US-09-010-928B-1/c
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                  FEATURE:
NAME/KEY:
LOCATION:
                                                                   NAME/KEY:
LOCATION: 1..2830
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGly 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAT-----GCTTTTTACCAACGTTTCCCAGAGGCGTTTTACCCGACTGAG 2553
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                                                                       /note= "Flagelliform DNA sequence taken from the 5' region. The putative position 219"
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US-10-018-706-2 (1-322) x US-09-010-928B-1 (1-2830)
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Best Local Similarity:
Query Match:
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                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09125287B Patent No. 6114602
                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/125,287B
CURRENT FILING DATE: 1998-11-09
EARLIER APPLICATION NUMBER: PCT/IL97/00051
EARLIER APPLICATION NUMBER: PCT/IL97/00051
EARLIER FILING DATE: 1997-02-13
NUMBER OF SECTION NUMBER: PCT/IL97/00051
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD FOR THE INTRODUCTION OF GENETIC PARTHENOCARPY IN TITLE OF INVENTION: PLANTS
FILE REFERENCE: INTRO GENETIC PARTHENOCAPRI IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: BARG, Rivka
APPLICANT: SALTS, Tehiam
                           FEATURE:
                                            TYPE: DNA
ORGANISM: TPRP-F1 PROMOTOR
    NAME/KEY: unsure
                                                                                          LENGTH: 4518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTGCACTTCCGGGTCCGGAACCACCAGGACCGTAAGGTCCTCCAGCACCACCGGGTCC 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCACCTGGTCCGTAGGGTCCACCAGCACCTGGACCGTAGGGTCCACCAGCACCACC 2160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GATCCTCCTGCTCCACCAGCACCTCCTGCTCCACCAGCACCTCTAGCT 1658
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US-10-018-706-2 (1-322) x US-09-125-287-1 (1-12839)
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; OTHER INFORMATION: "n"'s are any nucleic residue US-09-125-287-2
                                                                 Query Match:
                                                                                        Best Local Similarity:
                                                                                                             Percent Similarity:
                                                                                                                                                           Pred. No.:
                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                          US-09-125-287-1
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US-09-125-287-1
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SOFTWARE: PatentIn Ver
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09125287B Patent No. 6114602
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: INTRO GENETIC PARTHENOCAPRI CURRENT APPLICATION NUMBER: US/09/125,287B CURRENT FILING DATE: 1998-11-09 EARLIER APPLICATION NUMBER: PCT/IL97/00051 EARLIER FILING DATE: 1997-02-13 NUMBER OF CEO. TO NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD FOR THE INTRODUCTION TITLE OF INVENTION: PLANTS FILE REFERENCE; INTRO GENETIC PARTHENOCAPRI IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BARG, Rivka APPLICANT: SALTS, Tehi
                                                                                                                                                                                                                                          NAME/KEY: unsure LOCATION: (5)..(113 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: TPRP-F1
                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 12839
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/895,367
FILING DATE: 09-JUNE-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. ROCKY
REGISTRATION UNMBER: 34053
REFERENCE/DOCKET NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smit
APPLICANT: Bing
APPLICANT: No.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3300 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 12-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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           881
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                                        63 IleThrAspSerGlnGly---
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                                                                                                                                       GGCGCCCTGTCGACCGACAACGCGGCTGGCGTGAACCTGTTCACCGCCTATCCGTCGTCG
                                                                                                                                                                     GlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThr 42
TGACGGGCACCGCCAACAACGACGCTTCGTTGCGGGTGAAGTCGCCGGCGCTGCGACC
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No. 5976864ellini,
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POLYPEPTIDES FROM CAULOBACTER
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EXPRESSION AND SECRETION OF
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                                     ValProAsnArgTyrGln
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APPLICANT: BINGLE, Wade H.
APPLICANT: No. 6210948ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION
FILE REFERENCE: 08106/002002
CURRENT APPLICATION NUMBER: US/09/142,648B
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: PCT/CA97/00167
PRIOR APPLICATION NUMBER: US 07/614,377
PRIOR APPLICATION NUMBER: US 07/614,377
PRIOR APPLICATION NUMBER: US 07/614,377
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US-09-142-648B-6
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                SEQ ID NO 6
LENGTH: 3300
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                                                                                    PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                            SOFTWARE:
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TYPE: DNA
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SECRETION OF
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Pred. No.:
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lSerSerTyrTleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGl
                           GGCCGTGACGGTCACCCAAACCGCCGCCGCCGCCACCGGCGCGCTACGGTCGCCGGTCGCGT
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Sequence 15. Application US/09311626B

Patent No. 6399347

GENERAL INFORMATION:
APPLICANT: JOTGGENERAL PET Lina
APPLICANT: Schnorr, Kirk
APPLICANT: Schnorr, Kirk
APPLICANT: Schulein, Martin
APPLICANT: Outtrup, Helle
TITLE OF INVENTION: No. 6399347el Rhamnogalacturonan Hydrolases
FILE REFERENCE: 5572.204-US
CURRENT APPLICATION NUMBER: US/09/311,626B
CURRENT FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08/98
PRIOR APPLICATION NUMBER: 60/084,358
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ORGANISM: Streptomyces coelicolor
                                                                                                                                                            1420 GCGGGCGCCGAGTCCTGGTCGTCCGCGGAGAGCGGCATCCGCAACCCCAAGGGCACCGTC 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1075 ACCAACTCCTCCACCAACAGCGGCAAGGGCTACGACGGCCAGGGCAACCACCACCACCTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1300 GAGGACGGCTCGAAGCCCTCGTCGTACCTGGCGGACGCCCGCACGGGCCAGATCCTCTGG 1359
                                                      138 rProValAlaValGln----
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                                                                                                                                                                                                                                                                                                                                                                  TCCACCGGCGAGCGGCGACAACGGCCGCGGTGTCTCCGGGGGACATCTGGTCGGGCAGC 1415
                                                                                                                                                                                                                                                            LeuLysValArgGlu---ArgSerIleSerSerGlyValAsn-ThrAlaHisThrProSe 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisIleAsnAsnLeuAsnSerSerTyr-----ThrIleTyrThrGlyGln-----Trp 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAC-----AACGGCTACGCCTGTGGACCACCAGGAACGGCCACGGCGAC 1239
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Matches:
-SerSerArgProProValGlnGlnHisProAl 154
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Score:
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US-09-308-375-1
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DB:
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Best Local Similarity:
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CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394-PCT
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                      111 GlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGly 130
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                                                                                                                                 HisIleAsnAsnLeuAsnSerSerTyr----
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                                                                                                                                                                                                                                                                GCCCTTATTGCAGCTGTAATTCAGCAAGAATCAGGGTTT-----AATGCTAAAGCACGA 4476
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                                                                                                                                                                               TCTGGTGTAGGTGCCATGGGATTAATGCAACTGATGCCAGCAACAGCAAAAAGCTTAGGA 4536
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APPHARMAN AND ANTE: 19-UUN-LING DATE: 19-UUN-LING DATE: 19-UUN-LING DATE: 19-UUN-LING APPHARMAN NUMBER: JP 158677/1996
APPHARMAN NUMBER: JP 158677/1996
THE DATE: 19-UUN-1996
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/878,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KIKUCHI, NORIHISA
APPLICANT: ODA, KOHEI
TITLE OF INVENTION: NOVEL PROTEINASE INHIBITOR AND
TITLE OF INVENTION: GENE ENCODING THE INHIBITOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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STREET: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGCTGCAAAAGCAGGTACAGCAATTAAATCTCTTCAAAGTGGTAAAGTCCAAATTGC
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                                                                                                                                                                                                  Version
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Percent Similarity:
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; NAME/KEY: CDS
; LOCATION: 1477..1911
US-08-878-546-9
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Pred. No.:
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ATTORMEY/AGENT INFORMATION.
NAME: DAVIDSON, CLIFFORD M.
REGISTRATION NUMBER: 32.728
REFERENCE/DOCKET NUMBER: 382.1009
TELEFOON [212) - 768-3800
TELEFHONE: (212) - 768-3800
TELEFONE: (212) - 362-2124
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: STREPTOMYCES PLATENSIS
ORGANISM: STREPTOMYCES PLATENSIS
FEATURE:
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APPLICATION NUMBER: JP 224104/1996
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
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                            542 CAGTGCTCGGCGGCCGGTCGTCGGCGGGGGTCAGCGACCGGCGGGCCGTCCGCTCCAGCA 483
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                                                                                                CCACÁCCGCACGCAGCGCGGATCGCCCGGCATCGCCCGCAGCCACCGGGTCCAGCG
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                                                               -----ThrValThrSerAsnGlyMetTrpPheSerGlyArg------
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03-MAR-1997
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112.50
33.61%
23.77%
6.74%
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Matches:
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NAME/KEY: variation LOCATION: replace(1267, "t") EATURE: NAME/KEY: variation	ON:	NAME/KEY: CDS LOCATION: 6226495 FEATURE:	Ē	F.	있照	LENGTH: 8438 base pairs TYPE: NUCLEIC ACID	¥8	×N	ATTORNEY/AGENT INFORMATION: NAME: Ribando, Curtis P	91	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/945,283	SOFTWARE: PatentIn Release #1.0, Version #1.25	IBM PC CO	두照	COUNTRY: USA ZIP: 61604	eoria	T:	CE ADDRE	OF INVENTION: Pseudo	:-07-945-283-1/c Sequence 1, Application US/07945283 Patent No. 5352596 GRMERAL INFORMATION:	299 GCTCCGTGAA 290	302 aLeuPheGlu 305	338 ¢GGCA¢ĠGGCGATCT¢CT¢GGCGGTGA¢GGĠĠĠ¢¢Ġġ	282 yAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAl 302	385CTCCTTGGTGCGGAAGTAGCGGTAGAAGGTGCGCAGCGCGACCCCGG 339		422 GCCGCACCCCGTCGGCGAGCAGCGGGACCACCGCGTC 386	249GÍnAlaAspHisAsnMetAspGlyAlaSerIleValIleGl 262	#82 CCTCGCGCACGGAGGGCGCTCCGGGGCCGGGTGCGGGGCGGCCAGGTCGATCCACT 423

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Best Local Similarity:
Query Match:
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US-08-923-137-2/
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US-07-945-283-1
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application Patent No. 6083716
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,700
APPLICATION NUMBER: US 60/024,700
APPLICATION NUMBER: US 60/024,700
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APPLICANT:
APPLICANT:
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NAME/KEY:
LOCATION:
                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                 APPLICATION NUMBER:
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Spring House
Pennsylvania
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33.90%
6.74%
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Krishna J.
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Matches:
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Sequence 221, Application US
PATENT NO. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Ente
NUMBER OF SEQUENCES: 496
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INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 36519 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
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                                                                                                                                                                     6801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 SerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnVallleThr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 ThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSer---ThrSerGly 44
                                                                                                                                                                     -ACTCGCATGCCATTTTCCGCCAGATCGTCT
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                                                                                                                                                                                                     lThrGluAlaProPheAlaThrGlySerSer 195
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                                                                                                                                                                                                                                                                                                                  CTAGTCACCGCCGAGCTCGCCAAGCTGCAAGACTCCTACGCCCACTTCATCCGCGAC
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                                                                                             Application US/09071035
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20850 Maryland

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US-10-018-706-2 (1-322) x US-09-071-035-221 (1-867)
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TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Vert
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
  144 SerSerArgProProValGlnGlnHisProAla---ValGlnLysProThrProProVal 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 LeuilepheGlyVallleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyr
                                              ACGCCAAGTAAGCCAGAGCAACCAACAGAGCCAACAACGCCAAGT---
                                                                      uArgSerIleSerSer-GlyValAsnThrAlaHis-ThrProSerProValAlaValGln
                                                                                                                                                     rTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGl
                                                                                                                                                                                          CCAACCGAACCTAGTGAGCCTTCAAAACCGACGGATCCTTCGTTACCAGACGAACCGAGC 297
                                                                                                                                                                                                                                                                  GAGCAACCAACAGÁGCCAAGTACACCÁGAGC-----ÀACCATCGGAACCGTCAACA
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DB:
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Best Local Similarity:
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US-09-134-001C-1165
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Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLETATION FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEPLETATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR PRIOR DATE: 1997-08-14
SEQ ID NO 1165
LENGTH: 993
TYPE: DNA
TYPE: DNA
TYPE: DNA
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                                                  ---GTATCAGGCTCATCTTCAAGAGCAACGTCAACAAATAGT 264
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Matches:
Conservative:
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Percent Similarity:
Best Local Similarity:
Query Match:

Alignment Scores: US-09-071-035-221

No.:

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60 91 40 31

Alignment Scores: 0.394 Length: 2077 Pred. No.: 0.394 Length: 74 Score: 110.50 Matches: 74		; FEATURE: ; NAME/KEY: CDS ; LOCATION: 2992077 ; FEATURE:	E SOU	: T	; LENGTH: 2077 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double : TOPOLOGY: linear	2 x 2	; REGISTRATION NUMBER: 27,386 ; REFERENCE/DOCKET NUMBER: 1122990831 ; TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 608-251-5000	- H H C	<b>≯</b> ഗ	LICATION DATA: ON NUMBER: US/08/217,327 TE:	TYPE: FIR: FIR: IBM FIR: IBM FIR: IBM FIR: FIR: FIR: FIR: FIR: FIR: FIR: FIR:	; STATE: W1 ; COUNTRY: USA ; ZIP: 53701-2113 ; COMPUTER READABLE FORM:	; CORRESPONDENCE ADDRESS: ; ADDRESSE: Quarles and Brady ; STREET: P.O. Box 2113 ; CITY: Madison	; APPLICANT: John, Maliyakal E ; APPLICANT: Barton, Kenneth A ; TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber ; NUMBER OF SEQUENCES: 16	US-08-217-327-7 ; Sequence 7, Application US/08217327 ; Patent No. 5474925 ; GENERAL INFORMATION:	397 GTTTCTGGTAAAGCGACGAGTTCCAGTCGTGCAAAAGCTAGTGGG		95 IleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThr	Db 265 GGCACAGTT
264 rAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspTh 	1057 CTGGCAAACCGCAACTATCGATGTGGATTTGGTACAGGGCAATAATATTGTGCAGTTGTC  244 aGlyThrVallleGlnAlaAspHisAsnMetAspGlyAlaSerIleVallleGlnHisTh	Db 997 TAACGGCGGCAGCAACGGTAACTATACGGTGAGTTTGCCCACGACCGGCGCCTGGACCAC 1056	Qy 219 lAlaGlySerThrValThrSerAsnGlyMetTrpPheSe 232	199 nPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrVa	Qy 183 oProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGl 199	Db 827 ACCATCGATAATAACCACACCGGCTTTACCGGCAGTGGCTTTGCCAACACCACAATGCC 886	767 AGTGTGGCCTCCGCA	Db 710 ACCAGCTCTGTGGCTTCCAGCTCTTCAACCACCACCACCAGTTCATCTTCTGCATCC 766  Qy 166 168	147 oProValGlnGlnHisProAlaValGlnLysProThrProProValValValVal	Qy 129SerGlyValAsnThr-AlaHisThrProSerProValAlaValGlnSerSerArgPr 147	Qy 115 LeuTrpSerGlyAspLeuLysValArgGluArgSerIleSer	Qy 95 IleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThr 114	75 506	Qy 55 GlyLeuAlaIleGlySerGlnValIleThrAspSerGlnGlyValProAsnArgTyrGln 74	Qy 35 SerLysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGlySerGly 54	Qy 17 ArgLeuGlyLeuIlePheGlyValIleThrThrCysIleLeuAlaGlyCysAla 34	Qy 1 MetThrValThrIleAlaIleAsnSerGlnAsnGlnLysProIleLys 16	US-10-018-706-2 (1-322) x US-08-217-327-7 (1-2077)	Percent Similarity: 34.49% Conservative: 45 Best Local Similarity: 21.45% Mismatches: 125 Query Match: 6.62% Indels: 102 DB: 1 Gaps: 16

•	US-10-018-706-2 (1-322) x US-09-136-574A-2 (1-6416)  QY	Pred. No.:       2.26       Length:       6416         Score:       10.50       Matches:       74         Percent Similarity:       33.96%       Conservative:       34         Best Local Similarity:       23.27%       Mismatches:       99         Query Match:       111       111         DB:       4       Gaps:       18	SEQUENCE DESCRI- -136-574A-2	; LENGTH: 6416 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear	TELEFAX: 215-540-5818  TELEX: <unknown> INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:</unknown>	TRATIC ENCE/D ICATIO HONE:		APPLICATION NUMBER: US/09/136,574A  FILING DATE: 19-Aug-1998  CLASSIFICATION: <unknown>  PRIOR APPLICATION DATA:</unknown>	MEDIUM TYPE: Diskette ; COMPUTER: IBM Compatible ; OPERATING SYSTEM: DOS ; CURRENT APPLICATION DATA:	STATE: PA COUNTRY: USA ZIP: 19477 COMPUTER READABLE FORM:	PONDENCE ADDRES DDRESSEE: Howse TREET: Spring Hou	; TITLE OF INVENTION: Compositions and Methods for Treating Cellulose Containing Fabrics Using Truncated Cellulase Enzyme Compositions ; NUMBER OF SEQUENCES: 49	Hergqust, Peter  Daniels, Roy  Morgan, Hugh W.  Williams, Diane P.	; GENERAL INFORMATION: ; APPLICANT: Farrington, Graham K. ; Anderson, Paige ; Gibbs, Moreland	RESULT 30 US-09-136-574A-2 ; Sequence 2, Application US/09136574A ; Patent No. 6294366	Qy 284 rValArgThrCly 288	1166
	Anderson, Paige Globs, Moreland Bergquist, Peter Daniels, Roy Morgan, Hugh W. Milliams, Diane P. Milliams, Diane P. TITLE OF INVENTION: Compositions and Methods for Treating Cellulose Containing Fabrics Using Truncated Cellulase Enzyme Compositions	RESULT 31 US-09-136-574A-46 ; Sequence 46, Application US/09136574A ; Patent No. 6294366 ; GENERAL INFORMATION: APPLICANT: Farrington, Graham K.	Qy 299 SerGlyAlaAlaLeuPheGluPheArgIleSerArgAsnGlyValTyrValAsp 316	Qy 284 ThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnPro 298	Qy 265 AsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAsp 283	Qy 250 AlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHisThr 264	Qy 245 GlyThr	Qy 225 ThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAla 244	Qy 205 GlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrVal 224	. Qy 188AlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProVal 204	Qy 180 ProValAlaProProValThrGlu	Qy 160 ProProValValValLysLysProThrProThrProProValValGlnGlnProAla 179	Qy 140 ValAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThr 159	Qy 122 ValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro 139	Qy 102 AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLys 121 Db 4159 4173	Qy 82 SerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeu 101	Db 4063 AAGGGCAGTGGCAGCTACAATCAGTCAAATGACTATTCGGTAAGAAGT 4110

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 46: US-09-136-574A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 2029 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
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                                                                                                                                                                                            316
                                                                                                                                                                                                                                                            286
   472
                               132
                                                               433 GGTGTTCTGGTATGGGGG---
                                                                                                                           253 TACCTGGAGGTAGGATTTAGCAGTGGAGCTGGG------
                                                                                                                                                         94 GluIleGlyHisIleAsnAsnLeu-----AsnSerSerTyrThrIleTyrThrGlyGln 111
                                                                                                                                                                                                                         84 IleAlaGlnArgTyrGlyLeuAsn-----
                                                                                                                                                                                                                                                                                       64 ThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThrValSerLys 83
                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                  AlaSerLysProThrTyrAsn------SerThrSerGlySerGlySerHisArg 49
   ACCCCAACTTCTACACCCACACCGGTTTCATCATCCACT----
                                                                                                                                                                                            ATACAGGTAAGGTTTAACAAGAATGACTGGAGCAATTACAATCAGGCAGACGACTGGTCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Howson and Howson STREET: Spring House Corpora CITY: Spring House
                            AsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGln 151
                                                                                             TrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyVal 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/932,571 FILING DATE: September 19, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <Unknown>
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109.50
33.47%
23.67%
6.56%
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Matches:
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Indels:
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                                                               -CAGGAGCCGGGAGGAGCGGTG
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Alignment Scores:
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                                                                                                                                                                        TELEX: 380816 CooleyPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: April 18, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 25-AUG-199
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
                                                                                             MOLECULE TYPE:
                                                                              FEATURE:
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooley Godward of STREET: 5 Palo Alto Square CITY: Palo Alto
                                                                                                              TOPOLOGY:
                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                     NAME: Luann Cserr
REGISTRATION NUMBER: 31,822
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                                                                                                                                                         3833 base pairs
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Sequence 18, Application US/08917320
Patent No. 5824508
GENERAL INFORMATION:
APPLICANT: Spaete, Richard and J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Spaete, Richard and Jackman, Winthrop, TITLE OF INVENTION: No. 5824508 Splicing Variants NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent In Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 HisProAlaValGlnLysProThrProProValValValVaLLysLysProThrProThr 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAGATGATACAAATGATGATTGGTTATTTGCGCAGGGTAACAAAATAGTCGACAAGGAT 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GGAACGAATGTGTTTGATGGTGTGTGGAGTTGTAATCTTAAAAGTGCATTAGCTGAG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAAACCTGTATGGTTAACAGGA-----GTTAATTGGTTTGGATTTAATACA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAlaThrValAla 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProProValValGlnGlnProAlaProValAlaProProValThrGluAlaPro-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooley Godward Castro Huddleson & Tatum
                                                                                                                                                                                                                                                                                             US/08/917,320
                                                                                                                                                              08/229,291
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AVIR-003/00US
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                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
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Query Match: DB:

Pred. No.:

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RESULT 33
PCT-US95-04611A-18
; Sequence 18, Application PC/TUS9504611A
; GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                                                                                                                                              ACAGGCCAACATAA-CATAACTTCAAGTTCAACCTCTTCCATGTCACTGAGACCCAGTTC 302
                                                                                                       AAACCCAGAGACACT
                                                                                                                                       LysThrGlyAspThr
                                                                                                                                                                                                VallleGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnVal 279
                                                                                                                                                                                                                                                                                                                                           GlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn-----Ala 244
                                                                                                                                                                                                                                                                                                                                                                                                                 AsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCCCAAATGCCACCAGCCCCACC------TTGGGAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThr
                                                                                                                                                                                                                                    GGAACAAGTCCCACCCCAGTAGTTACCAGCCAACCAAAAAATGCAACCAGTGCTGTTACC 2966
                                                                                                                                                                                                                                                                                                       GGCCTACTGTG---GGAGAAACAAGTCCACAGGCAAATGCCAACCAACCAACCTTAGGA 2908
                                                                                                                                                                                                                                                                                  GlyThr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pro-----ThrProProValValGlnGlnProAlaProValAlaProProValThrGlu 187
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Conservative:
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS; LOCATION: 101-
PCT-US95-04611A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,291
APPLICATION NUMBER: 08/229,291
FILING DATE APTIL 18, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR-00
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-843-5163
TELEPAC: 415-843-5163
TELEPAC: 415-843-5163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-857-0663
TELEX: 380816 COOLEYPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: OCDDS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04611A
FILING DATE:
FILING DATE:
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TITLE OF INVENTION: Non Splicing Variants of gp350/220
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: un
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TYPE: nucleic acid
STRANDEDNESS: double
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STATE: California
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                                                                                                         ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                                                                                                                                     GCACCTGCAAGCACAGGCCCCACTGTATCC-----
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Conservative:
Mismatches:
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RESULT 34
US-08-783-774-1
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                   FILING DATE: 15-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790-9990
                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Spaete, Richard APPLICANT: Jackman, Winthro
                                                                                                                                                                                                                   COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                             APPLICATION NUMBER: FILING DATE: 15-JAN CLASSIFICATION: 435
                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                    CITY: New York
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   212-869-8864
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NON-SPLICING VARIANTS
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No.:
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NAME/KEY: Coding Sequence
LOCATION: 1014...3734
OTHER INFORMATION:
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                                      GGCCCTACTGTG----GGAGAAACAAGTCCACAGGCAAATGCCACCAACCACACCTTAGGA
                                                                      GlyMetTrpPheSerGlyArgAspGlyAspLeuIleAspAlaSerAsp--
                                                                                                            AGCCCC--
                                                                                                                                                                                                                   AlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThr
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Qy 74GlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp. 92 Db 2391 GCACCTGCAAGCACAGGCCCACTGTATCC	Scores	Db 2907 GGAACCAGTCCCAGTAGTTACCAGCCAAAAAATGCAACCAGTGCTGTTACC 2966  Qy 260 ValileGlnHisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnVal 279  Db 2967 ACAGGCCAACATAA-CATAACTTCAAGTTCAACTTCAATGTCAACTGAGACCAGTTC 3025  Qy 280 LysThrGlyAspThr 284  Db 3026 AAACCCAACATAA-CATAACTTCAAGTTCAACCTCTTCCATGTCAACTGAGACCCAGTTC 3025  US-09-556-706B-1  Sequence 1, Application US/09556706B  Patent No. 6458364  PAPLICANT: Spacte, Richard APPLICANT: Spacte, Richard APPLICANT: Spacte, Richard APPLICANT: Spacte, Richard APPLICANT: Spacte, Richard APPLICANT: Spacte, Richard APPLICANT: Spacte, Richard APPLICATION NUMBER: US/09/556,706B  CURRENT FILING DATE: 1997-01-15 PRIOR FILING DATE: 1997-01-15 PRIOR FILING DATE: 1997-01-15 PRIOR FILING DATE: 1994-04-18 SOFTMARE: PatentIn version 3.0  SEQ. ID NO 1  LENGTH: 5931 TypE: DNA ORGANISM: Virus FEATURE: OTHER INFORMATION: gp350/220
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOWNITER: IBM PC compatible
TOWNITER: TOWNERM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CTTY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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RESULT 38
US-08-751-230-9
                                                                                                                                                                                                                                              Sequence
Patent No
                                                                                                                                                                              Patent No. 6117633
GENERAL INFORMATION:
APPLICANT: Garkavtsev,
APPLICANT: Riabowol, K
                                                                    APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
COUNTRY: USA
ZIP: 22313-1404
                                                    TY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-751-230-9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pair
TYPE: nucleic acid
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APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: FLOPPY BC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 15-NG CLASSIFICATION: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                         AspLeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSer
                                                                                            AGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGCGCGGACAGGC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATCHTIN Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                     ATTORNEY AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
                        INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
APPLICANT: 1
                                                                                                                                                                                                                PRIOR APPLICATION NAMER: US/08/828,158
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                            TELEFAX:
                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 08-DEC
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Johnston, Randall N.
Garkavtsev, Igor
   2061 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Burns, Doane, Swecker & Mathis
699 Prince Street
                                                          650-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helbing, Caren C.
Riabowol, Karl
                                                                                                                                                                                    UMBER: US 08/569721
08-DEC-1995
                                                                                                                                                                                                                                                                                           US/08/828,158
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-09-499-082-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double TOPOLOGY: linear
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229 MetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrVallle
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                                                                                                                                                                                                                                    ProThrPro---ProValValGlnGlnProAlaProValAlaProProValThrGluAla 188
                                                                                                                                                                                                                                                                          CGGGCACACCCAAGGAGAAGAAGCCAAGACCTCCA-----AGAAGAAGAAGAAGCGCT
                                                                                                                                                                                                                                                                                                          GlnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThr 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspLeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSer 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGCCAAGGTTGGCGCGGACAGGC
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                                                                                        ProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGly
                                                                                                                                                               ProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsn
                                                                                                                                                                                                   CCAAGGCCAAGGCGAGCGAGAGGCGTCCCCTGCCGACCTCCCCATCGACC--
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Query Match:
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REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 16..900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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STATE: VA
                                   101 CGGACCGCCTCCCCGCGACCCGCGGGCCGGCTCGGAGACAGTTTCAGGCCGCATCTTTGC 160
54 yGlyLeuAlaIleGlySerGlnValIle-----ThrAspSerGlnGly-ValProAsnA 72
                                                                                                       1 TTCCCAGATATAGCAGTAGCAGTGATCCCGGGCCTGTGGCTCGGGGGCCGGGGCTGCAGTT 100
                                                                                                                                    22 PheGlyVallleThrThrCyslleLeuAlaGly-CysAlaSerLysProThrTyrAsn-- 40
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Mismatches:
Indels:
Gaps:
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Matches:
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66
42
102
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824 AGTGCC 829	Ъ
249 GlmAla 250	8
779 GCGTGGGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCA 823	Дb
229 MetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrVallle 248	Qy
734 GCTGCGACAACGACGACGACGACGACGAGGGGTTCCACTTCTCGT 778	Db
209 ProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGly 228	γQ
680CCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCG 733	DЬ
189 ProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrproValGlyAlaThrAsn 208	γQ
629 CCAAGGCCAAGGCGAGCGAGCGTCCCCTGCCGACCTCCCCATCGACC 679	ממ
170 ProThrProProValValGlnGlnProAlaProValAlaProProValThrGluAla 188	γŞ
578 CGGGCACACCCAAGGAGAAGAAGGCCAAGACCTCCAAGAAGAAGAAGAAGCGCT 628	Db
150 GlnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThr 169	γ
521 GCAACAACGAGAACCGTGAGAACGCGTCCAGGAACCACGACCACGACGACGACGACGACGACGACGA	В
139ProValAlaValGlnSerSerArgProProVal 149	οy
461 CCAATGGCGATGCGCAGTCTGACAAGCCCAACAGCAAGCGCTCACGGCGGCAGC 520	DЪ
119 AspLeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSer 138	Q.
401 AGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGCGCGGACAGGC 460	Db
118Gly 118	ρŞ
341 AGATGGTGGAGCTGGTGGAGAACCGCACGCGCAGGTGGACAGCCACGTGGAGCTGTTCG 400	Дb
100 snLeuAsn-SerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSer 117	Ş
281 TGCAGCGCGCTGATCCGCAGCCAGGAGCTGGGCGACGAGAAGATCCAGATCGTGAGCC 340	DЪ
85 laGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnA 100	δ
221 GCTACGAGCGCTTCAGTCGCGAGACAGACGGGGCGCAGAAGCGGGGGATGCTGCACTGTG 280	Д
72 rgTyrGlnValLysGlnGlyAspThrValSerLysIleA 85	γŞ
161 TGACCCGAGGGTGGGCCGTGGAAACAGATCCTGAAGGAGCTAGACGAGT 220	Db

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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-Ge/Ggn2 1/USFTO Spool/USI30018706/runat 30062003 091107 23899/app_query.fasta_1.519
-DB=Published_Applications_NA -QFMT=fastap -SUFFTX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALION=200 -THR SCORR=pct -THR WAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=USI0018706 @CGN 1 118 @runat 30062003 091107 23899
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NOSE_SCORS=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                   219.5
209
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext .
Delop 6.0 , Delext
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US-10-098-808-4
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RESULT 1 US-10-329-960-1

ALIGNMENTS

Sequence 1, Application US/10329960 Publication No. US20030099277A1

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GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragn
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
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PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
PEATURE:
NAME/KEY: misc feature
LOCATION: (4747)...(4747)
COTHER INFORMATION: n equals a, t, g or c
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LOCATION: (51805)...(51805)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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LOCATION: (51334)..(51334)
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LOCATION: (45732)..(45732)
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216 ThrAla-----ThrValAlaGlySerThrValThr------SerAsnGlyMetTrp 230
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                                                                                                                                                                                                                                                                                                                                                                         GATGTAAAAGAATTGGCGGCGTTGAATAACCTATCCGAACCTTATAATTTAAGTTTAGGG
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                                                                 GlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGly 215
                                                                                              GlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThrGlySerSer 195
                                                                                                                                                                                                         -----CCAGCAGTCACTTAT---ACTCCGGGCGCAAACGGTACTCAAATAGGATCTGAC 74991
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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APPLICANT: Potter, Andrew A.
APPLICANT: Rioux, Clement
APPLICANT: Schryvers, Anthor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10098808
Publication No. US20030007981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/098,808

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/405,728

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-24

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/267,749

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 5

SOFTMARE: PAtentin Ver. 2.0
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NAME/KEY: CDS
LOCATION: (872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schryvers, Anthony B.
TITLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS
TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEINS
FILE REFERENCE: 9000-0049.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2179
TYPE: DNA
ORGANISM: Haemophilus somnus
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                                                      1349
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                                                                                                                                                        1289 AAAGAATTGGCCACACTAAATAATATGTCTGAGCCATATCATCTGAGTATTGGACAAGTA 1348
                                                                                                    113
130 GlyValAsnThrAlaHisThrProSerProValAlaValGlnSerSerArgProProVal 149
                                                                                                                                                                                                    93 ArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrp 112
                                                                                                  LeuThrLeuTrpSerGly------AspLeuLysValArgGluArgSerIleSerSer 129
                                                                                                                                                                                                                                                               TACAAAGTACGCAAAGGCGATÁCCATGTTTCTTATTGCTTATATTTCAGGCATGGATATA 128
                                                                                                                                                                                                                                                                                                TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrp 92
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                                                   TTGAAAATTGCAAATAATATTCCCGATAGCAATATGATACCAACACAGACAATAAATGAA 1408
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Arigiment Scores: 3.23e-05 Length: 9025608 Pred. No.: 3.23e-05 Matches: 88 Score: 187.00 Matches: 88	; LOCATION: (4187716) ; OTHER INFORMATION: a, t, c, g, other or unknown US-10-156-761-1	ORGANISM: Streptomyces avermitilis FEATURE: NAME/KEY: misc_feature		PRIOR APPLICATION NUMBER: JP 2001-204089  PRIOR FILING DATE: 2001-05-30  PRIOR APPLICATION NUMBER: JP 2001-272697  PRIOR FILING DATE: 2001-08-02	TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29	APPLICANT: HORIKAWA, HIROSHI APPLICANT: SHIBA, TADAYOSHI APPLICANT: SAKAKI, YOSHIYUKI APPLICANT: HATTORI, MASAHIRA	n	RESULT 3 US-10-156-761-1/c US-10-156-761-1/c ; Sequence 1, Application US/10156761 ; Publication No. US20030119018A1	Qy 308 IleSerArgAsnGlyValTyrValAspProLeuThrValLeu 321	Qy 288 GlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArg 307       :::           :::                         1796 GGTCAACAATTGCTAAAATGGGAAGTTCTGGAACAACACAATCAAACTCCATTTTGAA 1855	Qy 268 ValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrValArgThr 287	Qy 250 AlaAspHisAsnMetAspGlyAlaSerIleVallleGlnHisThrAsnGlyPhe 267	Oy 230 TrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGln 249	Qy 210 ValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrSerAsnGlyMet 229 ::::::::       :::       :::       :::         :::           :::	Qy 190 PheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnPro 209 Db 1559ACAAATGGAAAA 1570	Qy 170 ProThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaPro 189	Db 1466 GAACAAATGAAACCCGTTGCTACACCAACACATTCAACAATGCCAATCAAT	Db 1409 TCAGAGGTGACACAAATACAGTCAATGAGACATGGAATGCTAATAAACCAACAAAT 1465  Oy 150 GlnGlnHisProAlaValGlnLysProThrProProValValValVaLLysLysProThr 169
Qy 286 ArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeu 303	266 GlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspThrVal 285	Qy 247 VallleGlnAlaAspHisAsnMetAspGlyAlaSerIleVallleGlnHisThrAsn 265	Oy 234ArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThr 246	Qy 216 ThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPheSerGly 233	Qy 196 GlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGly 215	Qy 176 GlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThrGlySerSer 195	Qy 156 GlnLysProThrProProValValValLysLysProThrProThrProProValVal 175	Qy 136 ThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVal 155 :::	Qy 127 IleSerSerGlyValAsnThr	Qy 107 IleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSer 126	Qy 87 ArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThr 106 Db 2009362 GAGCAGAGCGTC 2009351	Qy 73TyrGlnValLysGlnGlyAspThrValSerLysIleAlaGln 86	Qy 67 GlnGlyValProAsnArg72  Db 2009482 GCGGCCGTCTCCGGAAAAGGTCTCCGCAGCCCCCGTTGCCGGAAGCAGGGGGCCGCCGAG 2009423	Qy 55 GlyLeuAlaile	Qy 47 SerHiBArg	Qy 27 ThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySerGly 46	US-10-018-706-2 (1-322) x US-10-156-761-1 (1-9025608)	Percent Similarity: 34.35% Conservative: 36 Best Local Similarity: 24.38% Mismatches: 117 Query Match: 11.20% Indels: 120 DB: 9 Gaps: 16

2008858 GCCGAGGCCGGCAGCTCGGCCTCTCTGGTGCGACCGGCAATGTCACGGGACCGCACCTG 2008799

Qy       66 SergInGlyValProAsnArg	Gaps: 15  -10-018-706-2 (1-322) x US-10-156-761-1629 (1-903)   46 GlySerHisArg	US-10-156-761-1629  US-10-156-761-1629  Alignment Scores:  Pred. No.:  2.52e-10  Best Local Similarity:  34.50%  Best Local Similarity:  34.27%  Matches:  Conservative:  35  Best Local Similarity:  34.27%  Misches:  107  Cuery Match:  10.93%  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Indels:  Ind	PRIOR PILING DATE: 2001-204089 PRIOR PILING DATE: 2001-05-30 PRIOR PILING DATE: 2001-05-30 PRIOR PILING DATE: 2001-05-30 PRIOR PILING DATE: 2001-05-30 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR PILING DATE: 2001-08-02 PRIOR	ISHIKAWA, ISHIKAWA, HORIKAWA, SHIBA, TAD SAKAKI, YO SAKAKI, YO HATTORI, M NVENTION: NO ENCE: 249-26 PLICATION NU	RESULT 4  US-10-156-761-1629 US-10-156-761-1629 ; Sequence 1629, Application US/10156761 ; Publication No. US20030119018A1 ; GENERAL INFORMATION: ; APPLICANT: OMURA, SATON	322 Lys 322 ::: 2008738 CGC 2008736	Db 2008858 GCCGAGGGCCGGCAGCTGGGCCTCCTCGGTGCGGACCGGCAATGTCACGGGACCGCACCTG 2008799  Qy 304PheGluPheArgIleSerArgAsnGlyValTyrValAspProLeuThrValLeu 321
APPLICANT: ISHIKAWA, JUN APPLICANT: HORIKAWA, HIROSHI APPLICANT: SHIBA, TADAYOSHI APPLICANT: SHIBA, TADAYOSHI APPLICANT: SAKAKI, YOSHIYUKI APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-05-30 PRIOR FILING DATE: 2001-08-02 NUMBER OF SEQ ID NOS: 15109 SEQ ID NO 4684 LENGTH: 609 TYPE: DNA	SULT 5 -10-156-761-4 Sequence 4684 Sequence 1684 Sepulation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderation to Moderatio	Qy 285 ValArgThrGLVGINATGILEALASETMETLYBASNGINPROSETGLYALAALA 302	Db 577 CACACCGGCGTCGACTTCGTGGTCCCAACCGCACCATCAAGGCCGTCGCCGCGCGC 636  Qy 246 ThrValileGlnAlaAspHisAsnMetAspQlyAlaSerileValileGlnHisThr 264	195 SerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPhe	Qy 155 ValGinLysProThrProProValValValValLysLysProThrProProVal 174	135 HisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAla :::	Qy 126 SerIleSerSerGlyValAsnThr

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RESULT 6
US-10-156-761-1
US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
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; FEATURE;
; NAME/KEY: CDS
; LOCATION: (1)..(609)
US-10-156-761-4684
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Pred. No.:
ANT: OMURA, SATOSHI
ANT: IKEDA, HARUO
ANT: ISHIKAWA, JUN
ANT: HORIKAWA, HIROSHI
ANT: SHIBA, TADAYOSHI
ANT: SHIBA, TADAYOSHI
ANT: SAKAKI, YOSHIYUKI
ANT: HARTORI, MASAHIRA
ANT: HARTORI, MASAHIRA
DF INVENTION: NOVEL POLYNUCLEOTIDES
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
INUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 1
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                                GCCTTCCTCCGG 5729281
                                                                                                CCGCACCTGCACTTCGAGATCCGTACGACCCCGAACTACGGGTCCGGCATCGACCCCGTC 5729269
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                                                                ThrValLeuLys 322
                                                                                                                             AlaAlaLeu---PheGluPheArgIleSerArgAsn---GlyValTyrValAspProLeu 318
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Matches:
Conservative:
Mismatches:
Indels:
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; ORGANISM: Xanthomonas campestris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(2353)
US-09-927-827-41
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TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas
FILE REFERENCE: 38-10(15824)B
CURRENT APPLICATION NUMBER: US/09/927,827
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/279,493
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 41
LENGTH: 3353
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Publication No.
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                                       ValArgThrGlyGlnArgIleAlaSerMet----LysAsnGlnProSerGlyAlaAlaLeu
                                                                                                                                                           SerSerTyrIleHis------IleLysAspAlaGlnValLysThrGlyAspThr 284
                                                                                                                                                                                                  TCCGACTGGATGACCGGCTACGGCATGATCCTGATCGTGGATCACGGCAATGGCTACATG
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No. US20030036176A1
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/189162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 2741
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US-09-738-626-2741
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ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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376 CCAGCATCCGGCTATGGACAGTGGATCCGCATCCAGCACGACGACGGATCCATCTCCATC 435
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TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                           SerGlyArgAspGlyAspLeuileAsnAlaSerAsnAlaGlyThrValileGlnAlaAsp 251
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ANDO, SEIKO
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; TYPE: DNA
; ORGANIAM: Corynebacterium glutamicum
US-09-738-626-1
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: HAVASHI, MIKIRO
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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                                                                        ThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal
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APPLICANT: Hillman, Jeffrey D.
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ThrAlaHisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHis
                                                                      LeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn 132
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US-10-156-761-7229
                                                                                                                             Best Local Similarity:
                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7229
LENGTH: 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HATTORI, MASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
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ORGANISM: Streptomyces
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SAKAKI, YOSHIYUKI
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FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
                                                                                                                          APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus
TITLE OF INVENTION: Thereof, and Uses Thereof
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PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
TYPE: DNA
ORGANISM: Haemophilus influenzae
EPATTE: DA NAME/KEY: misc feature LOCATION: (51334)...(51334) OTHER INFORMATION: n equals a, NAME/KBY: misc_feature LOCATION: (47036)..(47036) OTHER INFORMATION: n equals a, FEATURE: NAME/KEY: misc feature LOCATION: (45593)..(45593) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (4747)..(4747) OTHER INFORMATION: n equals a, TRATURE:

VAME/KEY: misc_feature

OCATION: (51602)..(51602)

THER INFORMATION: n equals a, t, g or c PEATURE:

JAME/KEY: misc_feature

JOCATION: (45732)..(45732)

JOHER INFORMATION: n equals a, VAME/KEY: misc_feature LOCATION: (44975)...(44975) DTHER INFORMATION: n equals a, UAME/KEY: misc_feature LOCATION: (36636)..(36636) DTHER INFORMATION: n equals a, EATURE:
IAME/KEY: misc feature
LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a, FEATURE:
NAME/KEY: misc feature
LOCATION: (9921)..(9921)
THER INFORMATION: n equals a,
FEATURE: NAME/KEY: misc_feature OCATION: (40808)..(40810) THER INFORMATION: n equals a, NAME/KEY: misc_feature OCATION: (36543)..(36543) THERE INFORMATION: n equals a, NAME/KEY: misc_feature OCATION: (10150)..(10150) THER INFORMATION: n equals a, AME/KEY: misc feature OCATION: (29298)..(29298) WHER INFORMATION: n equals a, AME/KEY: misc_feature OCATION: (44905)...(44905) THER INFORMATION: n equals a, AE/KEY: misc_feature CATION: (44416)...(44416) HER INFORMATION: n equals a, t, g ţ, 'n ŗ 'n t, g or c t, g or t, g or t, g or t, g or t, g or c t, g or c g or g.or g or Ω φ ω or or 9 or c

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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER_INFORMATION: n equals a,
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LOCATION: (145058)..(145058)
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                                                                                                    AlaHisThrProSerProValAlaValGlnSerSerArgProProVal----GlnGlnHis 152
                                                                                                                                                                                                                                                        GlnValLysGlnGlyAspThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArg
                                                                                                                                                    ThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsnThr
                                                                                                                                                                                                     GluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeu 113
 ProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAlaThr 192
                                                 ProAlaValGlnLysProThrProProValValValValLysLysProThrProThrPro
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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    ThrAsp---
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RESULT 14

US-09-988-384B-1/c

Sequence 1, Application US/09988384B

Publication No. US20030073824A1

GENERAL INFORMATION:

APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Zhao, Y.

APPLICANT: Zhao, LDNA encoding methymycin and FILE REFERENCE: 600.536US1

CURRENT APPLICATION NUMBER: US/09/988,384B

CURRENT FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: ECT/US99/14398

PRIOR APPLICATION NUMBER: US 09/105,537

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 1998-06-26
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; LENGTH: 15872
; TYPE: DNA
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Best Local Similarity:
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        HisThrAsnGlyPheValSerSerTyrIleHisIleLysAsp---AlaGlnValLysThr
                                                                                                                                                                                               CCGGTGCTCCCGTGCGCGGCGGTCCAGTCGACGTCGTGGCCCCCGGACGAAGACGGTGGTG
                                                                                                                                                                                                                                                                       CCGTCGAACCAGTGGCGTTCGCGCTGGAAGGCGTAGGTCGGCAGGGGCACCCTGACCGTG
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                                              GCGGAGACCGCCGTGGCGGCCTCCTGGTCGCGTACGGAGTCCGCCCATCGCGGAGCAG
                                                                            AlaGlyThrVallleGlnAlaAsp---HisAsnMetAspGlyAlaSerIleVallleGln
                                                                                                                      AGTGCGGCGAGCAGCGACTGGGGGCTCCGGGCGGCCC------
                                                                                                                                                     Ser-----AsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn
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US-10-018-706-2 (1-322) x US-09-836-821-1 (1-15872
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/836,821
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: DNA
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  ProProValValValLysLysProThrProThrProProValValGlnGlnProAla 179
                                                                                                                                                                                   IleSerSerGly-----
                                                                                                                                                                                                                                                                       LeuTrpSerGlyAsp----
                                                                                                                                                                                                                                                                                                                                                          IleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThr 114
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                                                                                        ValAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThr 159
                                                                                                                                                                                                                             -----TCGACGGACATGAGGGAGTCGAAGCCCAGCTCCTTGAAGGTGAGGCCGAGTTCG
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Matches:
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
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                                                                                                                                                                                                                        US-10-018-706-2 (1-322) x US-09-861-289-1 (1-15872)
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                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09861289 Patent No. US20020110897A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600. 438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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                                            3150 GTGACGCCGCGGGGTAGCGGCAGGCCATGCCGATGATCGCGATGGGCTCGGCGGTGGTG 3091
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ThrAsp----SerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThrVal 81
                                                                                                                                       GCGTCGCGCCCC-----
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                                                                                                                                    -----TCGGCGACGAGCCGCCACAGGTCCTCGGGGGAG 3151
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Matches:
                                                                                      --GlyGlyLeuAlaIleGlySerGlnValIle 63
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_	RGANISM: Staphylococcus simulans	ID NO 4 ENGTH: 1520	SEQ ID NOS: 10	NT: Kerr, Davi F INVENTION: TR FERENCE: Mastit	Ă	US/10087667	282 GlyAspThrValArgThrGlyGlnArgIleAlaSerMetLy8AsnGlnProSerGlyAla 301	HisThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThr		នី 🖁 🖁	195SerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal 211		rProThrPro :   :::    GCCCTCGCCC		115 LeuTrpSerdlyAspLeuLysValArgGluArgSer 126 2925TCGACGGACATGAGGGAGTCGAAGCCCAGCTCCTTCAAGCTTCCTTC	3030 AGCAGGTCGCCCAGGTGGGCGGCGCGCGCGCGCGCGCGCG	
	1009 GACATETCGCGGGGGGGGGGGGGGGGGACCAGAACTGGGTGTCGGCCTCG	223 ThrVa		QY 191 AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210	, 838 CGAW			Db 658 AGGTCGCGCTGGCGCTGCGCGAGTCGCTGTACGAGCGCGAATCCCGACGCGCCAAGGGGCC 717  Qy 176	ନ :	Db 520TGGGCCGGCTACAGCGGGATCAGCCGA 546  Qy 130 GlyValAsnThrAlaHisThrProSerProValAlaValCinSorCartagagagagagagagagagagagagagagagagagaga	AAGCACTCGGAAGAGATCTCGCAC	Db 445TTCGACTTCGACATCGATGGCATCTGGCCAAGCATGCGCATCTGCAC 495  Oy 90 LeuAsnTrDArgGluTleGluHieTleArgangcatatatatatatatatatatatatatatatatatatat	Db 400 GCCACGGCTCAGCGGCGAGGATCTGGTGTATTCTACGACGAGATG 444  Qy 70 ProAsnArgTyrGlnValLysGlnGlyAspThrValSerTysIleAlaciacher. 444	313 CAC	US-10-018-706-2 (1-322) x US-10-087-667-4 (1-1520)  Qy	H H	i

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 164
LENGTH: 7277
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CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US/09/173,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schlauder, George G. APPLICANT: Erker, James C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: US 60/061,199
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SOFTWARE: PastSEQ for Windows Version 3.0
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ORGANISM: Hepatitis E Virus
FEATURE:
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                                                              AGATACAATAGGTTCACCCÁĞCĞĞCATTCĞCTĞACAGGCGGACTATĞĞCTACATCCTGAG
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                                                                                                                                          CCYGGTGGCGCCCCTAGCGCCGCGCGGGGAGGTGGCSGCCTTCTGCAGTGCTCTTTAT 1994
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                                                                                                                                                                                                                                                                                                                                                                                                             ThrCysIleLeuAlaGlyCys-----AlaSerLysProThrTyrAsnSerThrSer
                                                                                                  ----LysIleAlaGlnArgTyrGlyLeuAsn---
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Conservative:
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APPLICANT: Abbott Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Erker, James C.
APPLICANT: Desai, Suresh M.
APPLICANT: Desai, Suresh M.
APPLICANT: Dawson, George J.
APPLICANT: Mushahwar, I. K.
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
FITHE OF INVENTION: HEPATITIS E VIRUS
FILE REFERENCE: 6232.US.P1
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER FILING DATE: 1999-10-15
EARLIER FILING DATE: 1998-10-15
EARLIER FILING DATE: 1997-10-15
FEARLIER FILING DATE: 1997-10-15
SEQ ID NO 165
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                                                                                                                  LeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSerPro 139
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                                                                                               GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HAROSHI
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HARTYORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2407
LENGTH: 774
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(774)
US-10-156-761-2407
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US-10-156-761-2407
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     Percent Similarity:
Best Local Similarity:
                                                                                          Alignment Scores:
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RESULT 21
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APPLICANT:
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                                                                                                  An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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                                                                                 Yu,
 Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
                                                  Page, Amy
                                                                     Rameaka, Joshua G.
                                                                                 Yang
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RESULT 22
US-09-468-147-141
; Sequence 141, Application US/09468147A
; Publication No. US20030049601A1
; Publication No. US20030049601A1
; GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Dessai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSIT
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Best Local Similarity:
Query Match:
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SEQ ID NO 354
LENGTH: 942
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APPLICANT: Hurban, Patrick
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR PILING DATE: 2000-01-27
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      OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
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Davis, Keith R.
Allen, Keith
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Kricker, Maja
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FITLE OF INVENTION: HEPATITIS E VIRUS
FILE REFERENCE: 6232.US.P1
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/173,141
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1998-10-15
EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FASTSEQ for Windows Version 3.0
ESEQ ID NO 141
ENOTH: 903
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CRGANISM: Hepatitis E Virus
FEATURE:
INFORMATION: us2-851
US-09-468-147-141
291 IleAlaSerMetLysAsnGlnPro---SerGlyAlaAlaLeuPheGluPheArgIleSer
                               661
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                                                                                                           251 AspHisAsnMetAspGlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSer 270
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                            TATCAACGTTTCCCAGAAGCGTTCTACTCGACTGAATTCATCATGCGCGAGGGCCTTGCA
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                                                   ŢyrIleHisIleLysAspAļaGlnValLysThrGlyAspThrValArgThrGlyGlnArg
                                                                                     ---CATCGCCCGGGGGTGGC-----CTCTGCCAT
                                                                                                                                                                 PheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAla
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US-10-018-706-2 (1-322) x US-10-063-547-99 (1-2436)
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US-10-063-547-99
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US-10-063-547-99
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CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEQ ID NO 99
LENGTH: 236
TYPES - NN 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 99, Application Publication No. US200201 GENERAL INFORMATION: APPLICANT: Eaton, Dan L. APPLICANT: Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Filvaroff, Fil
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                                                                                      1027 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGGCCAG 1086
                                                                                                                                                                                                                                                                    967 TGAGTCCAGAACGACCTCCAATGGGGCTGGCACAGCCAACTCTGAGTCCAGCACGAC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                            907 CACTGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGGGGCCAGCACCAGCCACCAACTC 966
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nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProVal-----G
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Grimaldi, Christopher. J.
Gurney, Austin L.
Watanabe, Colin K.
Wood, William I.
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Gerritsen, Mary E.
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Alignment Scores:  0.00289  Pred. No.:  122.50  Score:  Percent Similarity:  39.04%  Conservative:  Conservative:  Mismatches:  145	CURRENT FILING DATE: 2002-06-18  Prior application removed - See File Wrapper or Palm  NUMBER OF SEQ ID NOS: 612  SEQ ID NO 309  LENGTH: 2436  TYPE: DNA  ORGANISM: Homo Sapien  US-10-174-590-309	T: Gurney, Austin L. T: Pan, James T: Smith, Victoria T: Watanabe, Colin F T: Wood, William I. T: Chang, Zemin INVENTION: SECRETEI INVENTION: ACIDS I ERRNCE: P3430R1C42	H-309 Py, Application 1 No. US20030008 CMMATION: Baker, Kevin P. Chen, Jian Desnoyers, Luc Goddard, Audres Godowski, Paul		Qy 246 hrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHis 263	Qy       206 laThrAsnProValValArgArgPheGlyThrAlaThrValAlaGlySerThrValThrS       226	Db 1087 CACTGCCACCACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAG 1131  Qy 150 InGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThrP 170
302 1545	Db 1365 CCAACTCTGAGTCCAGCACGAGTGCCCAGTGGGCCAGCACCTGCCACCAACTCTGAGTCCA 1424  Qy 264ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrG 282  Qy 1425 GCACAACCTCCAGTGGGGTCAGCACAACTCTGAGTCCAGCACAACCTCCAGTG 1484  Qy 282 lyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaA 302  Qy 282 lyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSerGlyAlaA 302  1485 GGGTAGAGCACAGCCAACTCCAGGCACAACTCCAGGGGGGGG	Qy 206 laThrAsnProValValArgArgPneGlyThrAlaThrValAlThrS 226	Db 1132 CACAGCCACCAACTCTGAGTCCAGCACGACCTTCCAGTGGGGCTAGCACAGCCACCAACTC 1191  Qy 170 roThrProProValValGlnGlnProAlaProValAlaProProValT 186  Qy 170 roThrProProValValGlnGlnProAlaProValAlaProProValT 186	ь	Db 907 CACTGCCACCACTCTGAGTCCAGCACAACCTCCAGTGGGGCCAGCACAGCCACACTC 966  Qy 98IleAsnAsnLeu-AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLe 115	Db 788 GACTICCAGCACAACTGGAGTGGGGCTAGCAACCACCAACTCTGAGTCCAGCAACAACC 847  Qy 66 SerGlnGlyValProAsnArgTyrGlnVallysGlnGlyAsp 79	Query Match: 7.34% Indels: 60 DB: 9 Gaps: 12  US-10-018-706-2 (1-322) x US-10-174-590-309 (1-2436)  Qy 6 AlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeuIlePheGlyValIle 25 [

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RESULT 25
US-10-176-758-309
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Best Local Similarity:
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SEQ ID NO 309
LENGTH: 2436
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
CURRENT FILING DATE: 2002-06-21
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
APPLICANT: Godowski, Paul
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150 lnGlnHisProAlaValGlnLysProThrProProValValValLysLysProThrP 170
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                                                                                    CACTGCCACCAACTCTGAGTCCA
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Goddard, Audrey
Godowski, Paul
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b. US20030008353A1
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Publication No. US20030013855A1

GENERAL INFORMATION.

APPLICANT: Eaton, Dan L.

APPLICANT: Eaton, Dan L.

APPLICANT: Gerriteen, Mary E.

APPLICANT: Goddard, Andrey

APPLICANT: Goddard, Andrey

APPLICANT: Goddard, Christopher J.

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APPLICANT: Goddard, Christopher J.

APPLICANT: Gorimadd, Christopher J.

APPLICANT: Gorimadd, Christopher J.

APPLICANT: Wood, William I.

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US-10-063-616-99
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Best Local Similarity:
                                                                                 US-10-018-706-2 (1-322) x US-10-063-616-99 (1-2436)
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Pred. No.:
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; ORGANISM: Homo Sapien
US-10-063-616-99
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RESULT: 27
US-10-175-737-309
Sequence 309, Application US/10175737
Publication No. US20030013153A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343B1C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
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                                          TGACTCCA-----GCACAACCTCCAGTGGGGCCGGCACAGCCAACTCTGAGTCCAG 1245
                                                                           roThrProProValValGlnGlnPro---AlaProValAlaProProVal------ 186.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
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RESULT 28
US-10-063-502-99
Sequence 99, Application US/10063502
Publication No. US20030023042A1
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-502-99
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CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrap;
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 99
LENGTH: 2436
TYPE: DNA
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APPLICANT: Filvaroff, El
APPLICANT: Gerritsen, Me
APPLICANT: Goddard, Audt
APPLICANT: Goddowski, Pau
APPLICANT: Godowski, Pau
APPLICANT: Gurney, Austi
APPLICANT: Gurney, Austi
APPLICANT: Watanabe, Col
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Godowski, Paul J.
Grinaldi, Christopher J
Gurney, Austin L.
Watanabe, Colin K.
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GlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIleThrAsp 65
                                     TCTAGCACACTCTCCAGTGGGGCC----
                                                                         ThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySer 45
                                                                                                                 GCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGCACTGCCACCAACTCTGAG 745
                                                                                                                                                AlaIleAsnSerGlnAsnGlnLysProlleLysArgLeuGlyLeuIlePheGlyValIle
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                                                Sequence 309, Application US
Publication No. US200302229
SENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Godowski, Paul (
APPLICANT: Godowski, Paul (
APPLICANT: Gurney, Austin I
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                                                       Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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    Smith, Victoria
Watanabe, Colin
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TYPE: DNA
CORGANIZM: Homo Sapien
US-10-173-706-309
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CURRENT FILING DATE: 2002-06-17
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                                                                         CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCC-AGTG
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US-10-175-738-309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C45 CURRENT APPLICATION NUMBER: US/10/175,738 CURRENT FILING DATE: 2002-06-19 Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 309, Application US/10175738 Publication No. US20030022294A1 GENERAL INFORMATION:
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ORGANISM: Homo
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                                                      788 GACTCCAGCACAACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACC 847
                                                                                                                             746 TCTAGCACACTCTCCAGTGGGGCC---
                                                                                                                                                                                                 686 GCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCCAACTCTGAG 745
66 SerGlnGlyValProAsnArgTyrGln---
                                                                                      46 GlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIleThrAsp 65
                                                                                                                                                             26 ThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsnSerThrSerGlySer 45
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                                                                                                                                                                                                                                     AlaIleAsnSerGlnAsnGlnLysProIleLysArgLeuGlyLeuIlePheGlyValIle 25
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Godowski, Paul
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                  ---ValLysGlnGlyAsp
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RESULT 31
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                                                       APPLICANT:
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lication No. US20030022295A1
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                                                                                                                                                                                                                                                              INFORMATION
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T: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
INVENTION: ACIDS ENCODING THE SAME
ERENCE: P3430R1C60
                                                                    Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                           Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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CURRENT FILTM DATE: 2002-06-19
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
TYPE: DNA
ORGANIZM: Homo Sapien
US-10-175-752-309
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US-10-176-482-309
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CURRENT FILING DATE: 2002-06-20
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Watanabe, Colin K.
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 309, Application US/10176757 Publication No. US20030022297A1
                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                     APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93430R1C86
CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrG 282
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                                                                                                                                                                    Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                   Pan, James
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Godowski, Paul J.
Gurney, Austin L.
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Percent Similarity:
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; TYPE: DNA
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US-10-176-757-309
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                                                                                hrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHis-----
                                                                                                                                                   erAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsnAlaGlyT
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                                                     CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCAACCTCTGAGTCCA 142
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US-10-176-913-309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/176,913
CURRENT FILING DATE: 2002-06-20
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TYPE: DNA
ORGANISM: Homo Sapien
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                       TGAGTCCAGAACGACCTCCAATGGGGCTGGCACAACTCAACTCTGAGTCCAGCACGAC 1020
                                                                                                                  ThrValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHis-----
                                                                                                                                                                                     SerGlnGlyValProAsnArgTyrGln------
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                                                     -----IleAsnAsnLeu-AsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLe 115
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o. US20030022298A1
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612; SEQ ID NO 309; LENGTH: 2436; TYPE: DNA ORGANISM: Homo Sapien
US-10-180-552-309
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US-10-180-552-309
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                                                                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 19430R1C153
CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
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APPLICANT:
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Gurney, Austin L.
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; ORGANISM: Homo Sapien
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APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

APPLICANT: Wood, William I.

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FILE REFERENCE: PA$30RIC147

CURRENT APPLICATION NUMBER: US/10/180,557

CURRENT FILING DATE: 2002-06-25

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 309

LENGTH: 2436
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Goddard, Audrey
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Watanabe, Colin K.
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RESULT 37
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
TYPE: DNA
ORGANISM: Homo Sapien
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Publication No. US20030027262A1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
CURRENT APPLICATION NUMBER: US/10/173,700
CURRENT FILING DATE: 202-06-17
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CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper |
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
TYPE: DNA
ORGANISM: Homo Sapien
US-10-174-572-309
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APPLICANT: Baker, Kevin P.
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lnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThrP 170
                                                                                                                               CTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAG 1086
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                                                         CACTGCCACCAACTCTGAGTCCA-----
                                                                                          nThrAla-HisThrProSerProValAlaValGlnSerSerArgProProVal-----G
                                                                                                                                                              uTrpSerGlyAspLeuLysValArg------GluArgSerIleSerSerGlyValAs 132
                                                                                                                                                                                                      TGAGTCCAGAACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGAC 1026
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Goddard, Audrey
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RESULT 39
US-10-174-579-309
; Sequence 309, A
                               US-10-018-706-2 (1-322)
                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Homo Sapien
US-10-174-579-309
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FILE REFERENCE: 93430R1C31
CURRENT FILIKO SOUTHON NUMBER: US/10/174,579
CURRENT FILIKO BATE: 2002-06-18
PRIOR APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 309
LENGTH: 2436
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APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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o. US20030027264A1
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RESULT 40
US-10-174-582-309
J. Sequence 309, Application US/10174582
Publication No. US20030027265A1
GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-582-309
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NUMBER OF SEQ ID NOS: 612
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                               roThrProProValValGlnGlnPro---AlaProValAlaProProVal------- 186
                                                                                                     lnGlnHisProAlaValGlnLysProThrProProValValValValLysLysProThrP 170
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Gurney, Austin L.
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CCAACTCTGAGTCTAGCACAGTGTCCAGTGGGATC 1579
                                   laLeuPheGluPheArgIleSerArgAsnGlyVal 313
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Search completed: July 4, 2003, 00:39:18 Job time : 8989 secs THIS PAGE BLANK (USPTO)

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-ggn2 1/USPTO_spool/US10018706/runat_30062003_091105_23805/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE_LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10018706_@CGN 1 1 1456 @runat_30062003 091105_23805 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEU TIMEOUT=120 -WARN INMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## SUMMARIES

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## ALIGNMENTS

RESULT 1 BF866446/c LOCUS SOURCE ORGANISM KEYWORDS VERSION ACCESSION DEFINITION BF866446 963069All.xl C. r , Lambda Zap BF866446 BF866446.1 GI:12256590 784 bp mRNA linear EST 19-JAN-2001 reinhardtii CC-1690, Stress condition I, normalized Chlamydomonas reinhardtii cDNA, mRNA sequence.

BST. Chlamydomonas reinhardtii. Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 784)

REFERENCE

AUTHORS

Grossman, A., Lefebvre, P., Davies, J., Federspiel, N., Hamader, J., Shrager, J., Harris, E., Hauser, C., ., Silflow, C. and Stern, D.

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JOURNAL COMMENT
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Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                    ArgGluArgSer------IleSerSerGlyValAsnThrAlaHisThrProSerPro 139
                                                                                                                                                                                                           valAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGlnLysProThr 159
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                                                                                                                                                          TCGTGTACGAGGGCGGTGCGCCGGCGGTG------CCCCCCAAGAAGTCGGGCGGCG 248
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/clone lib="CC reinhardtii CC-1690 condition I,
/nore="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-P (30 min, 1hr, 4hr) to NH4 (30 min, 1hr
/hr) AHr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30 min, 1hr
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                                                 903 TACACMATCGA-GGTGGGCAGCAGCTGAAGGTT---AGCGGC
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Ş Q	US-10-0:	Alignmer Pred. No Score: Percent Best Loo Query Mo DB:	FEATURES SOU BASE COU ORIGIN	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	ACCESSION VERSION KEYWORDS SOURCE ORGANIS	RESULT 2 CNS01JER/c LOCUS DEFINITION	Db Qy	g dy	B &	Db Qy	מם
105 TyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrp	10-018-706-2 (1-322) x CNS01JER (1-906)	Alignment Scores: 0.0329 Length: 906 Pred. No.: 136.00 Matches: 51 Score: 36.74% Conservative: 28 Percent Similarity: 23.72% Mismatches: 80 Best Local Similarity: 23.72% Mismatches: 87 Query Match: 8.14% Indels: 57 BB:	RES Location/Qualifiers 1: .906 /organism="Anopheles gambiae" /strain="PEST" /strain="PEST" /clone="13F15" /clone="13F15" /clone="1b="NotreDame1" /clone="1b="NotreDame1" /note="end: T7" /note="end: T7" /note="248 g 214 t 2 o	This clone is from an A. gambiae BAC libra Collins and sequenced by Genoscope in coll Laboratory of Biochem. and Biol. Molec. of Pasteur.	- Web: www.yenbecker	I (bases 1 to 906) I (bases 1 to 906) Genoscope. Direct Submission Submitted (16-FEB-2000) Genoscope - Centre Submitted (16-FEB-2000) Genoscope - Centre BP 191 91006 EVRY Cedex - FRANCE (E-mail :	AL146948.1 GI:7005094 AL146948.1 GI:7005094 GSS: African malaria mosquito. M Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse	CNSOIJER  Anopheles gambiae GSS T7 end of clone 13F15 of from strain PEST of Anopheles gambiae (African from strain PEST of Anopheles gambiae (African from strain PEST of Anopheles gambiae)	245 yThrVallleGlnAla 250	226 SerAsnGlyMet-TrpPheSerGlyArgAspGlyAspLeuileAsnAlaSerAsnAlaGl 	206 AlaThrAgnProValValArgArgPheGlyThrAlaThrValAlaGlyS	189 ProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGly	211 CCGGCGGCAAGGAAGGAAGGCAAGAAGTAAATGGCTGGCCCCACCGTTGCGTGC-GCG
SerGlyAspLeuLysValArgGlu 124       AGCGGCGGATCGTCCGCGGGCAAA 848			thers .	ry provided by F.H. aboration with the Insects, Institut		National de Sequencage : seqref@genoscope.cns.fr	octa, Pterygota; Culicoidea;	ar GSS 12-JUN-2001 NotreDame1 library malaria mosquito),	,	AlaSerAsnAlaGl 245 	aGlySerThrValThr 225       CGGCATGTAGCTCTTA 78	н 2	

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INRA
CRJ INRA, Domaine de Vilvert,
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
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Class: shotgun
High quality sequence start: 30
High quality sequence stop: 4784
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Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales;
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subsp. cremoris genomic, DNA sequence
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                                                                                          quality sequence start: 30 quality sequence stop: 478
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/organism="Lactococcus lactis subsp. cremoris"
/strain="MG153"
/db xrefe="taxon:1159"
/clone_lib="MG1363 Random Sequence Tag Library"
                                                                               Location/Qualifiers
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                                                             rAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnValLysThrGlyAspTh
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                                                                                                                           aGlyThrValIleGlnAlaAspHisAsnMetAspGlyAlaSerIleValIleGlnHisTh
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ACCESSION
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Contact: Lim, C.O.
Contact: Lim, C.O.
Plant Molecular Biology & Biotechnology Research Centre
gyeongsang National University
#900 Gazwa-dong, Jinju 660-701, Korea
Tel: 82 55 751 6255
Fax: 82 55 759 9363
Email: colimonogae.gsnu.ac.kr
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridisplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
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Chinese cabbage etiolated seedling library Brassica rapa subsp. pekinensis cDNA clone E3832, mRNA sequence.

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Ryu,S.H., Yang,K.A., Lee,S.Y., Kim,H.-I., Cho,M.J. and Lim,C.O.
Expressed Sequence Tags of Chinese Cabbage Etiolated Seedling CDNA
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/cultivar="Jangwon"
/db xref="raxon:51351"
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/clone="EB332"
/clone="E"Chinese cabbage etiolated seedling library"
/tissue_type="Etiolated seedling"
/lab host="XL-1 Blue"
/note="Vector: pspORT 1; Site_1: Sal I; Site_2: Not I"
/209 c 50 g 49 t
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155 alGlnLysProThrProProValValValValLysLysProThrPro 170	711 GGGGGACTGGGTCAACAGTCTGCTGAAAGGTACGGTAGGGGGTAGCTTTGTCGCCAGCGC 652	146 rgProPro	771 TGAAACGCGTACCTACGATCGCACTGCCAACGGTTTTAAAATGAGCAGTGAAATGCAGCA 712	130 yValAsnThrAlaHisThrProSer-ProValAlaValGinSerSerA 146	110 yGLNTTpLeuThrLeuTrpSerGLyAspLeuLysVaLArgGLuArgSerILeSerSerGL 130	ACTTGCCGCTTCTGATAAGGGACTGCGCAATCTGAAAATTTGGCCAACAGCTT 83	TyrThrGl	TATGAGCG	SerLysIleAlaGlnArgTyrGlyLeuAsnTrpArg 	999 TGAGCTGGACGATAAAACCGCAGGCGAAGTCGGCGTCCATGAATACGTCGTCTCCAC 943	61 nVallleThrAspSerGlnGlyValProAsnArgTyrGlnValLysGl 77		/vo-4 (1-322) A AFV34333 (1-1030)  42 ThrSerGlySerGlySerHisArgThrSerGlySerGly-GlyLeuAlaIleGlySerGl 61	-2 (1-202) w Amnologo (1-	gnment Scores:       0.0998       Length:       1096         i. No.:       132.00       Matches:       85         ce:       132.00       Matches:       85         cent Similarity:       34.06%       Conservative:       40         conservative:       40       Matches:       134         cy Match:       7.90%       Indeb:       108         cy Match:       17       Gaps:       14	239 a 323 c 272 g 262 t	! `````		Sidney Kimmel Cancer Center 3)099 Science Park Road, San Diego, CA 92121, USA Email: mcclelland@lifsci.sdsu.edu Class: shotgun.	Unpublished (1999) Contact: McClelland M	1 (bases 1 to 1096) 1 (bases 1 to 1096) Wong,R.M.Y. and McClelland,M. End Sequences of Salmonella typhimurium LT2 Lambda DASHII Clones,		AF094939 AF094939.1 GI:4322781 GSC	

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RESULT 6
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Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Bukasica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                       BG543924 596 bp mRNA linear EST 01-MAY E1673 Chinese cabbage etiolated seedling library Brassica rapa subsp. pekinensis cDNA clone E1673, mRNA sequence.
                                            Gyeongsang National University
#900 Gazwa-dong, Jinju 660-701, Korea
Tel: 82 55 751 6255
                                                                                Contact: Lim, C.O.
Plant Molecular Biology & Biotechnology
                                                                                                               Ryu, S.H., Kang, J.S., Kang, C.-h., Kim, C.Y., Bahk, J.D., Lee, S.Y., Cho, M.J. and Lim, C.O. Expressed Sequence Tags of Chinese Cabbage Unpublished (2001)
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primer: T7.
                            82 55 751 6255
82 55 759 9363
            colim@nongae.gsnu.ac.kr
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                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1306 bp
AGENCOURT 6626294 NIH MGC_115 Homo
5', mRNA sequence.
                                                                                                                           found through the I.M.A.G.E. Consonttp://image.llnl.gov
Plate: LLAM12787 row: p column:
High quality sequence start: 90
High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5752955"
/clone_lib="NIH_MGC_115"
                                                                                                         Location/Qualifiers
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/tissue_type="Btiolated seedling"
/lab_host="XL-1 Blue"
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cultivar="Jangwon"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

0.158 131.00 39.60% 26.73% 7.84%

US-10-018-706-2 (1-322)

147

42

BASE COUNT ORIGIN

No.:

δ B δ В 5

207

61

267

90

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BO791640 398 bp mRNA linear EST 30 EBO791640 in the company Brassica E3323 Chinese cabbage etiolated seedling library Brassica subsp. pekinensis cDNA clone E3323, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCACATCAGCATTCTCAAGACTGGAGAAGTTAGGCCTCAGACATCCCAAGCCTTCTCC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATGGCCCCATGGTGACGGTGGCCCTGTCAGTGGCTCTCTTGGCCCTCCTGAAATGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTCATTGGAAACTTGACATTTTTCCGCCAGGGTTTTTGGGAAAGCCAAATGGAGCTCAG 386
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                                                                                                                                                                                                                                                                                                                                                                           oValAlaProProValThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPh
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                                                                                                                                                                                                                                                                                   eArgTyrProVal-----GlyAlaThrAsnProValValArgArgPheGlyThrAlaTh 218
                                                                                                                                                                                                                                                                                                                                oProValValValLysLysProThrProThrProProValValGlnGlnProAlaPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCCÁGACATGATCAAGCAGGTGTCGGCTGACAACTTCAGCCACTTTACCCACCATAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ValArgGluArgSerIleSer-SerGlyValAsnThrAlaHisThrProSerProVa 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLys-----
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//note="Crgan: pooled brain, lung, testis; Vector:
/note="Crgan: pooled brain, lung, testis; Vector:
pCWV-SPORT6; Site 1: Notl; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library.

a 24 c 344 g 213 t 2 others
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                             ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                RESULT 9
CNS03DYV/c
LOCUS
DEFINITION
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AUTHORS
TITLE
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Pred. No.:
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ORIGIN
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COMMENT
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Best Local Similari
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Tetraodon
019021 of
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BQ791640.1
EST.
ALC39728.1 GI:7898863
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Lim, C.O.
Plant Molecular Biology & Biotechnology
Gyeongsang National University
#900 Gazwa-dong, Jinju 660-701, Korea
Tel: 82 55 751 6255
Tel: 82 55 759 9363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica rapa subsp. pekinensis.
Brassica rapa subsp. pekinensis.
Brassica rapa subsp. pekinensis
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 398)
Ryu.S.H., Yang, K.A., Lee, S.Y., Kim, H.-I., Cho, M.J. and Lim, C.O.
Expressed Sequence Tags of Chinese Cabbage Etiolated Seedling of Chinese Cabbage Etiolated Seedling of Chinese Cabbage (Ed. Marchalletter)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValLysLysProThrProThrProProValValGlnGlnProAlaPro-----ValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGCCACCGACA------CCAACTCCTCCTGTCGTAACACCACCAACACCACCGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Brassica rapa subsp. pekinens
/cultivar="Jangwon"
/db_xref="taxon:51351"
/clone="E3323"
/clone="E3323"
/clone="E5101ated seedling"
/tissue_type="Etiolated seedling"
/lab_host="XL-1 Blue"
/lab_host="XL-1 Blue"
/lab_host="XL-1 Site_1: Sal I;
/note="Vector: psport 1; Site_1: Sal I;
a 165 c 67 g 61 t
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                                                                                                                                                                                        890 bp DNA linear GSS 15-MAY-:
nigroviridis genome survey sequence T7 end of clone
library G from Tetraodon nigroviridis, genomic survey
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129.50
48.57%
47.14%
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Matches:
Conservative:
Mismatches:
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Gaps:
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RESULT 8
BQ791640
LOCUS
DEFINITION

5 g

> 218 999 200 909 180

rVal

219 729

726

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447 122

160 507

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Best Local Similarity:
Query Match:
DB:
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AUTHORS
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                         498
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                                                  139
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                                                                                                                                                                                                                                                                                                                                          765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bernot, A., Fizames, C., Wincker, P., Brottier Saurin, W. and Weissenbach, J.
Human gene number estimate provided by deno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the circshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis DNA sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                  TACGCGAACGCGCGCGCGTMACAGTTGTTTTTGGAATTAAAACCCTGAGTCACCCCGTTT
                                                                                                                                                                                                                                                                                                                                     TIGACCTCTGCAGCGTCTCCGGCTGCAGGCGGAAGCTGGCAGCATCTGAGGCAGCGTCC 706
                                                                                                                                                      AsnAsnLeuAsnSerSerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGly
                                                                                                                                                                                                                                                         IleThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThr-----
                                                                                                                                                                                                                                                                                     GAGTCTTTTGGAGMAAAGGCCACCGTTGGAAGC-----ATG
                                                                                                                                                                                                                                                                                                             Ser-----GlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnVal 62
                                                                                                   AspLeuLysValArgGluArgSerIleSerSerGlyValAsnThrAlaHisThrProSer
                                                                                                                                                                                CACCCTACGGAGAAAAACCAGGACGATGGGGTTCAAAC----
                        CCGTGGGGCTGTCAGTCCCCAGTCCCCAGTCCCCAGTCCCCAGTCCTCCCCAGT
                                                ProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVal---
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                                                                                                                                                                                                       ---ValSerLysIleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="019021"
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/note="Genoscope sequence
/note="Genoscope sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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127.00
36.73%
26.55%
7.60%
                                                                                                                              AGCCTGACCTGTTTGACAACGCTAACCCTAACATGCTGG-----
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                                                                                                                                                                                                                                                                                                                                                                                            (1-890)
GlnLysProThrProProValValValValLysLys 167
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Matches:
Conservative:
Mismatches:
Indels:
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9 others
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Bn01_AAFC_ECORC_transgenic Brassica napus overexpressing_BNCBF17_
nstitutively_frost_tolerant Brassica napus cDNA clone Bn01_03006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Singh, J., Allard, G., Tinker, N., Robert, L., Lacrois Chagnon, J., Farah, S., Couroux, P. and Hattori, J. Expressed Sequence Tags from constitutively frost
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(613) 759-1701
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                                                                                                                                                                                                     /tissue_type="fourth leaf"
/dev_stage="3 weeks seedling grown at room temperature"
/ndev_stage="3 weeks seedling grown at room temperature"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI,
Site 2: XhoI; Germinated in soil flats and seedlings grx
for 3 weeks in a Conviron E-15 cabinet set at 200C /16 l
fight (250 Em-2sec-1) and 16 oC / 8 h
collected at 9 am and immediately frozen."
203 c 124 g 168 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                          /clone="Bn01_03006"
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/clone_lib="Bn0BF17_constitutively_frost_tolerant"
//xyressing_BNCBF17_constitutively_frost_tolerant
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eudicots;
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Thale cress.

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Spermatophyta; Magnoliophyta; eudicotyledons; cc
Rosidae; eurosids II; Brassicales; Brassicaceae;
E 1 (bases 1 to 628)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis th
of 12,028 non-redundant expressed sequence tags
size-selected cDNA libraries
L DNA Res. 7, 175-180 (2000)
E 20363093
C COntact: Erika Asamizu
The First Laboratory for plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazurce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GlnHisProAlaValGlnLysProThrProProValVal----
131 ValAsnThrAlaHisThrProSerProValAlaValGlnSer(
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AV520024 Arabidopsis thaliana aboveground org
old Arabidopsis thaliana cDNA clone APZ04g09F
AV520024 GI:8679551
EST:
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                                                                                                                                                                                                                                                                            157
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/clone="Ib="Arabidopsis thaliana above
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/clone "Apzound organs"
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/tissue_type="aboveground organs"
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Xhol"
                                                                                                                        0.174
125.50
46.25%
38.75%
7.51%
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Matches:
Conservative:
Mismatches:
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Oy 41 SerThrSerGlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySer 60	rSerArgProProValGln 150        ACACCGCCAACGCCA 559
US-10-018-706-2 (1-322) x BM911051 (1-1279)	
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Length:	
(Stratagene) and Superscript II RT (Life Technologies).  Note: this is a NIH MGC Library."  BASE COUNT 332 a 531 c 231 g 184 t 1 others  ORIGIN	Site_1: EcoRI; Site_2:
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EccRI/KhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit	boveground organs two to
/db_xref="taxon:9606"  /clone=_lib="NIH_MGC_98"  /clone_lib="NIH_xocytoma grade IV, cell line"  /tissue_type="astrocytoma grade IV, cell line"  /lab_host="DH10B (phage-resistant)"	.kazusa.or.jp/en/plant/.
source 11279 /organism="Homo sapiens"	<b>.</b>
High quality sequence stop: 259. FEATURES Location/Qualifiers	<b>b</b>
http://lmage.ilni.gov Plate: LICM1951 row: c column: 03 High quality segmence start: 6	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:	is thaliana: Generation tags from normalized and
cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	ceae; Arabidopsis.
	ryophyta; Tracheophyta;
AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JURNAL Unpublished (1999)	
Eukaryota; Metazoa; Choroata; Craniata; vercebrata; Butereoscomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1279)	rgans two to six-week 9F 3', mRNA sequence.
	linear EST 06-SEP-2000
N BM9	
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Db 441 CCAACTCCTCCTACG	ACCACMAACACCACCGGTC 145 DAlaProValAla 182
Qy 191 AlaThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProVal 210	
Qy 171 ThrProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPhe 190	ACCAACACCACCGGTCGTA 94
ACTCCACCGTCATTACACCACCAACACCAACTCCACCGTCATTACACCAACACCAACACCA	
Ov 151 GlnHisProAlaValGlnLvsProThrProProValValValValLysLysProThrPro 170	

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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                      Generations of ESTs from sprouting potato eyes Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics,
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 666)
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EST492606 cSTS
                                                                                                                                                                                                                                                                                                                                                             van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
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                                                                                                                                                                                                                                         primer: M13F-R
                                                                  /clone="cSTS5N16"
/clone lib="cSTS"
/tissue_type="sprouting e
/dev stage="12-14 weeks p
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoR1; Site 2: Xho1; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in tl dark for 2-3 weeks prior to sprouting. The eyes were
                                                                                                                                                     /organism="Solanum tuberoвum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
                                                                                                                                                                                                                         Location/Qualifiers
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                   JOURNAL COMMENT
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EST612957 Generation of a set analyses mixed potato tissues
Unpublished (2002 On Jun 10, 2002 t Other_ESTs: EST61
                                                Buell, C.R., Hart, A., Baker, B., Restrepo, S., Griffiths, H., van Karamycheva, S.A.
Generation of a set of potato c
                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 767)
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Conservative:
Mismatches:
Indels:
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                                                 cDNA clones for microarray analyses
                 version
                                                                                   Tanksley, S., F der Hoeven, R.,
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                 gi:21364411
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s for microarray
NA clone STMGE76
                                                                                     Smart,C.
J. and
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The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850,
Email: potato@tigro.org
This clone is available through the Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: potato@rigr.org
This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuTrpSerGlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn-----
                                            TCTGGGTGCTCCGTC---
                                                                                 AspGlyAlaSerIleValIleGlnHisThrAsnGlyPheValSerSerTyrIle
                                                                                                                                                                                                                                                                                                                                                                                    GCTACTCCTCCAGTGAGTGCTCCTCCACCTGTGAGTACTCCACC-TCCACCGGCAGC
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                                                                                                                                                                     AspGlyAspLeuIleAsnAlaSerAsnAlaGlyThrValIleGlnAlaAspHisAsnMet
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                                                                                                                           AAAGGTAGCTACATCTCCGGCACCTTCGCCGGTGGGATTGTTGAGTCCTCCAGCACCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte
/db xref="taxon:4113"
/clone="STMGE76"
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AUTHORS
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Query Match:
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No.:
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Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8179
Fax: 919 613 8179
Email: Chauser@duke.edu.
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963001CIO.y3 C. reinhard
, Lambda Zap II Chlamydd
BF859163
BF859163.1 GI:12249254
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1 (bases 1 to 839)
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                                       SerTyrThrIleTyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArg
                                                                                                                                                                                                                                                                                              GlySerGlySerHisArgThrSerGlySerGlyGlyLeuAlaIleGlySerGlnValIle
                                                                                                                        {\tt IleAlaGlnArgTyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSer}
                                                                                                                                                                                                               ThrAspSerGlnGlyValProAsnArgTyrGlnValLysGlnGlyAspThrValSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Chlamydomonas reinhardtii"
/organism="CC-1690 wild type mt+ 21gr"
/db_xref="raxon:3055"
/clone_lib="CC-1690 wild type mt+ 21gr"
/clone_lib="CC-reinhardtii CC-1690, Stress condition I,
/clone_lib="CC-reinhardtii CC-1690, Stress condition I,
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, lhr, 4hr), TAP-S (30 min,
lhr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30 min,
lhr, 4hr) and NH4 to NO3 (30 min, lhr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoRI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                            ----CAGGAATTCGGCACGAGGCACCATTAATGACAACCTAGC---
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C. reinhardtii CC-1690, Stress condition I, normalized
II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                  (1-839)
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Matches:
Conservative:
Mismatches:
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BH705150/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 285)
Town, C.D., Van Aken,S., Utterbac
Whole genome shotgun sequencing
Unpublished (2001)
Other_GSSs: BOMKT37TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cdtown@tigr.org
DNA is from a doubled haploid
Seg primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica oleracea
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BOMKT37TF BO_2_3_KB
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Class: sheared ends.
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BH705150.1 GI:18787488
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                    GlnLysProThr-----ProProValValValValLysLysProThrProThrProPro
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                                                         ACACCAATCCCACCTGTTGTAACGCCACCAACACCAACACCAACACCCAACTCCACCAGTCGTT
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ACGCCACCAACACCAGCCCCACCTGTTGTAACGCCAACACCAACACCAACACCACCG
                                                                                      ThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301-838-0208
                                                                                                                                                                                                                                                                                   /clone_lib="BO_2_3_KB"
//note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
26 c 143 g 89 t
                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3712"
/clone="BOMKT37"
                                                                                                                                                                                                                                                                                                                                                                           organism="Brassica oleracea"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Brassica
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Matches:
Conservative:
Mismatches:
Indels:
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BOMKT37,
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735 bp DNA linear GSS 30-AUG-2000 SP 1009 A2 D09 SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1009 Col=18 Row=G, DNA sequence.

735 bp DNA linear GSS 30-AUG-2000 SP 1009 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-2000 AUG-20
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Location/Qualifiers
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Class: BAC ends
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California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,B.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ187441.1 GI:8370620 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: acameron@caltech.edu
Plate: 1009 row: G column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20402566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad.
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--- CCCCTCCGTCTGCGACCTATAACAACTAGCCCACCCACCTCTCACCCCCACACCCC
                                                       GlyAspLeuLysValArgGluArgSerIleSerSerGlyValAsn-ThrAlaHisThrPr
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                                                                                                                                                                                                                                                 ThrValSerLysIleAlaGlnArgTyrGlyLeuAsn-----TrpArgGluIleGlyHis
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/db xref="taxon:7668"
/clone="plate=1009 Col=18 Row=G"
/clone= lib="Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC CDH10B"
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Best Local Similarity:
Query Match:
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ORGANISM
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                                US-10-018-706-2 (1-322) \times BM913728
                                                                                                                                                                                                BASE COUNT
ORIGIN
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 21
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1252)
11 (hases 1 to 1252)
12 (hational Institutes of Health, Mammalian Gene Collection (MGC)
13 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EM913728 1252 bp
AGENCOURT 6612844 NIH MGC_98 Homo
5', mRNA Sequence.
EM913728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM913728.1 GI:19364107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
ftp://image.llnl.gov
Plate: LLCM1995 row: g column: 24
High quality sequence stop: 398.
   11ePheGlyValIleThrThrCysIleLeuAlaGlyCysAlaSerLysProThrTyrAsn
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                                                                                                                                                                                                                   218
                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                0.644
124.00
32.77%
23.53%
7.43%
                                    (1-1252)
                                                               Conservative:
Mismatches:
Indels:
Gaps:
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sapiens
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IMAGE:5477423
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AUTHORS
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BE240905
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                                                                                                                                Suaeda maritima subsp. salsa.

Suaeda maritima subsp. salsa.

Suaeda maritima subsp. salsa

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Chenopodiaceae; Suaeda.

1 (bases 1 to 538)

1 (bases 1 to 538)

2hang,L., Ma,C.L., Wang,P.P., Sun,Y.F., Zhao,Y.X. and Zhang,H.

Expressed sequence tags from a halophyte Suaeda salsa cDNA library

Unpublished (2000)

Contact: Hui Zhang

Contact: Hui Zhang
                                                                                                                                                                                                                                                                                                                                                BE240905
SsS0423 Suaeda salsa
CDNA, mRNA sequence.
                                                   Key Laboratory of Plant Stress Research
The Biology Department of Shandong Normal University
No.88, Wenhua East Road, Jinan, Shandong Province, 2:
Tel: (86)531-2960864
Fax: (86)531-2966954
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       zhangh@sdnu.edu.cn.
Location/Qualifiers
1. .538
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RESULT 20
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170H14 of
                                                                      2 (bases 1 to 1002)
Roest-Crollius, H., Jaille
Bouneau, L., Billault, A.,
                                                                                                                                                   Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome
Tetrapdon nigroviridis DNA sequence
                                                                                                                                                                                                           1 (bases 1 to 1002)
Roest-Crollius,H., Jaillon,O., Dass
Bernot,A., Fizames,C., Wincker,P.,
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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              Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
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                                                       Weissenbach, J
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/db xref="taxon:126914"
/clone lib="Suaeda salsa ZAP cDNA library"
/dev_stage="seedling"
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123.50
45.68%
40.74%
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                                                                                             Jaillon, O.,
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                                                                      on,O., Dasilva,C., Fizar
Quetier,F., Saurin,W.,
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3 6 4 8 8 8 8 8
                                                                                             Fizames, C.,
                                                                                                                                                                                                                                   Bouneau, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                            Bernot, A.
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                                                                                             Fisher, C.,
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Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                        GlnAlaAspHisAsn----
                                                                                                                                                                                                 SerGlyArgAspGlyAspLeuIleAsnAla-----SerAsnAlaGlyThrValIle
                                                                                                                                                                                                                             AAATWAGGCCACAGCCTCACCCTTGCCGGCAGC-----GGTGGGGGGCATTGGGAGC 395
                                                                                                                                                                                                                                                        ArgPheGly---ThrAlaThrValAlaGlySerThrValThrSerAsnGlyMetTrpPhe
                                                                                                                                                                                                                                                                                                                                                                       GlnGlnProAlaProValAlaProProValThrGluAla---ProPheAla-----Thr 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGAGGAGAGACTTCAAAGTGGCGACCAAAGCGCTGCAACTCGACCTTACCCAGAG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GluArgSerIleSerSerGlyValAsnThrAlaHisThr---ProSerProVal 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTACACCACATACGAGGATCAT-----ACGGTGTGGGATTTGGACTACTTTGAGAGA
 TCC--
                         LysThrGlyAspThrValArgThrGlyGlnArgIleAlaSerMetLysAsnGlnProSer 299
                                                                                IleGlnHis---ThrAsnGlyPheValSerSerTyrIleHisIleLysAspAlaGlnVal
                                                                                                              ATTGGGAGAAGTGCAACTCTTGGTCGTACTACGTTCAACAGCAGCMAGGGCCAGAMCAGT
                                                                                                                                                                                                                                                                                    TCATCTTCCGGCAGTWATCGTTCCAAGTATGCMAACGGTACCTCTGGATCCCTGCCCCGC
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/note="Genoscope sequence
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                   108
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BJ220947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 81-559-51-0000
Email: tshinl@genes.nig.ac.jp.
Location/Qualifiers
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Ogihara, Y. and Murai, K.
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TCGCAACAGCTGTTTGAGTTTGAGAGGGAGCTTGACGGCTTTGAGCGGGGATCCC 656
TyrThrGlyGlnTrpLeuThrLeuTrpSerGlyAspLeuLysValArgGluArgSerIle ::::::
                                                         ATGGGGCTC-
                                                                                          TyrGlyLeuAsnTrpArgGluIleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIle 107
                                                                                                                                                                   GlyValProAsnArgTyrGlnValLysGlnGlyAspThrValSerLysIleAlaGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                                            /clone ib="V Ogihara unpublished cDNA library, Wh"
/clone lib="V Ogihara unpublished cDNA library, Wh"
/tissue type="spike at meiosis"
/dev stage="peekes' scale 9"
/dev stage="peekes' scale 9"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/site_1: EcoRI; Site_2: XhoI; Plants were grown under
/hydroponic conditions at UC Davis, salt stressed for 12
/hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
/tissue, equal quantities of RNA were pooled RNA, a cDNA
/sibrary was made, and the cDNA clones were in vivo
/excised to give paluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
/lose, Fenton, Kianian, Otto, Simons, Zhang).
/lose, Fenton, Kianian, Otto, Simons, Zhang).
/plasmid DNA preparations and DNA sequencing were
/performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum.

Dictyostelium discoideum

Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.

1 (bases 1 to 500)

Trushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H.,

Takeuchi, I., Kohara, Y. and Tanaka, Y.

Population analysis of cDNAs from unicellular and multice stages of Dictyostelium discoideum

Unpublished (2002)

Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU268480 VS Dictyostelium discoideum cDNA clone VSI307 5', mRNA
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AU268480
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1-1-1 Tennoudai, Tsukuba, Ibaraki
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                                                                                                                                                                                                                                                                                                             Tel: 81-298-53-4664 Fax: 81-298-53-6614
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                                                                                                   212
                                                                                                                                                                                                                                                                                           hideko@biol.tsukuba.ac.jp
                                                                                                                                                                        /organism="Dictyostelium
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSI307"
                                                                                                 /sex="mat A"
/sex="mat A"
/dev_stage="vegetative"
151 c 50 g
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                                                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 722)
Rujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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AG130154.1 GI:16659319
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
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                                                                                                                                                                              Sequencing: M13Rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACCAGCCCCAGTTGTAGCAGCCCCAGTTGTAGCAACCCCAACTCCAGCCCCAGTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---ProvalAlaProProvalThrGluAlaProPhe-----AlaThrGlySerSer 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAACCCCAACCCCAACTCCAACCCCAACTCCAGTTACACCCAAATCCAACTGTTAGAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             troglodytes male lymphoblast DNA, Library clone:PTB-141N09.R.
                                                                                                                          R.Site 1
R.Site 2
                                                                                                                                                                                                                                tracking errors.
                                                                                                        Location/Qualifiers
                                   /db_xref="taxon:9598"
/clone="PTB-141N09.R"
cell_type="lymphoblast"
                                                                        organism="Pan troglodytes"
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36.61%
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PTB-141N09.R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357
                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:hhttp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                    Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                          BAC end sequences of Library PTB Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes male lymphoblast DNA, BAC Library clone:PTB-040D10.F.
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GSS.
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                                                                                                                                                                            clone tracking errors.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                        R.Site 1
R.Site 2
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Y., Watanabe,H. and Sakaki,Y.
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397 c 89 g 65 t 5 others
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                                                    Location/Qualifiers
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linear GSS 02-NOV-200 genomic survey sequence.

02-NOV-2001

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 LeuAlaIleGlySerGlnValIleThrAspSerGlnGlyValPro---AsnArgTyrGln 74
                                                                                                                                                   AlaGlyThrValIleGlnAla--------AspHisAsnMetAspGly 256
                                                                                                                                                                                                                                                                                                                                                                                                         GCTCCG------CCCCGAGTTCCCGTGCCGGTTCCCACCGCTATCCTTGTTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleGlyHisIleAsnAsnLeuAsnSerSerTyrThrIleTyrThrGly-----GlnTrp 112
             TGTACACATCCTGACGGATCGCAGGGGGGTTGCCTCCGCCATCACGAATCCGCAGCGTAAA 102
                                                                                                                         ValThrSerAsnGlyMetTrpPheSerGlyArgAspGlyAspLeuIleAsnAlaSerAsn 243
                                                                                                                                                                                                                                                                                                                                                   TTCCCCTATTACCCGCGCCCGGTTACTATGCACCCACCCCAACCACCCCGAACATC
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                                                                                                                                                                                                                                    GCCTCCGGTCATCCACCGTTATGTCGCCAATACGGTGCGGCTACCTGCGGAGGGACGCGT 826
                                                                                                                                                                                                                                                         AlaThrAsn-----ProValValArgArgPheGlyThrAlaThrValAlaGlySerThr 223
                                                                                                                                                                                                                                                                                                                       ThrGluAlaProPheAlaThrGlySerSerGlyValMetGlnPheArgTyrProValGly 205
                                                                                                                                                                                                                                                                                                                                                                              LysPro---ThrProThrProProValValGlnGlnProAlaProValAlaProProVal 185
                                                                                                                                                                                                                                                                                                                                                                                                                                     ProProValGlnGlnHisProAlaValGlnLysProThrProProValValValValLys
                                       -----HisThrAsnGly-----PheValSerSerTyrIle------
                                                                   GCGTCGACTGCTTTGCGCTTGTCTTTAGCCGTCCAAACTCGGGCGCGATGTTTCCACTGT 967
                                                                                               AlaSerIleValIleGln-----
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/Becx="lymploblast"
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122.50
34.38%
21.56%
7.34%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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265 CCACCTATTGTCACCTCCAATCATTCCAACCACCTATTGTTTCTCCACCTTTTGTC 324
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B &			Db 1	US-10-018-7	Alignment Spred. No.: Score: Score: Percent Sin Best Local Query Match DB:	BASE COUNT			FEATURES source		TITLE JOURNAL COMMENT	AUTHORS	~	ACCESSION VERSION KEYWORDS	RESULT 25 BM109778 LOCUS DEFINITION	Db 10	Qy :	Ο _γ .
1/2 PROPEOVALVALGINGINETOPLAREFOVALALGE OF TOWN OF THE CONTROL	05 CCATCACCAACACCACCTATTGTTTCACCCCCTATTGTTTATCCACCAATCACACCAACA 2	56 GlnLysProThrProProValValValValLysLysProThrProThr 1	136 ThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaVal 155       :::    160 ACTCCAACACCACCTATTGTCCATCCACCAATCACTCCAAAACCA 204	706-2 (1-322) x BM109778 (1-450)	nment Scores: 0.225 Length: 450 No.: 122.00 Matches: 31 e: 122.00 Matches: 31 coral Similarity: 48.19% Conservative: 9 Local Similarity: 37.35% Mismatches: 31 Local Similarity: 7,31% Indels: 12 y Match: 13 Gaps: 5	125 a	issue_type="roots"  y stage="in vitro gr	/cultivar="Kennebec" /db xref="taxon:4113" /db xref="taxon:4113" /clone="cptato roots"	,	Email: cdna@resgen.com  Email: cdna@resgen.com  For clone info: please contact Research Genetics, Libraries  For clone tel 1-800-711-6195, email cdna@resgen.com  Seq primer: T3.	Generation of ESTs from potato roots Unpublished (2001) Contact: Research Genetics, Libraries Division Tel: 1-800-711-6195	1 (Dases 1 C0 450) van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S., Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.	potato.  Solanum tuberosum  Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  Asteridae; euasterids I; Solanales; Solanaceae; Solanum.	BM109778 1 GI:17070945 EST.		079 TGTGGNGCCGANTATAATCCGACGGGCGTGCGGCTCGTGTGGTTGCGGTACGGTA	291 IleAlaSerMetLysAsnGlnProSerGlyAlaAlaLeuPheGluPheArgIleSerArg 310	273HisIleLysAspAlaGlnValLysThrGlyAspThrValArgThrGlyGlnArg 290 ::::::      :::

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end was generated during the R&D process and may have higher chance
of clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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/clone_lib="RPCI-43 Chimpanzee
347 c 476 g 282 t
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/db_xref="taxon:9598"
/clone="RP43-025C14.TJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 philippe_vaglio@dfci.harvard.edu
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans (
cloning project : Contact jerome_reboul@dfci.harvard.edu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dana Farber Cancer Institute
44 Binney Street, Boston, MA
Tel: 617 632 5180
Fax: 617 632 2425
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/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly/
RNA isolated from both hermaphrodite and male N2 worms
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
a 148 c 104 g 115 t
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                                       TITLE
N AL252396.1 GI:7973408
AL252396.1 GI:7973408
S GSS; genome survey sequence.
Tetracdon nigroviridis.

ISM Tetracdon nigroviridis.
Chordata; Craniata; Vertebrata; Eureleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes; CE (bases 1 to 969)
RS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
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REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 29 AL377972 LOCUS DEFINITION		Qy 2	Db 4		0у 1	Db 5	Qy 1	Db 6	92	US-10-018-7	Alignment Sco Pred. No.: Score: Percent Simil Best Local Si Query Match: DB:	BASE COUNT ORIGIN		source	FEATURES	JOURNAL	AUTHORS	JOURNAL REFERENCE	TITLE	AULHORS	REFERENCE
1 (bases 1 to 365) Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson	sequence. AL377972 AL377972.1 GI:9677724 AL377972.1 GI:9677724 EST. barrel medic. barrel medic, barrel medicado truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rogidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae; Modicaro	AL377972 365 bp mRNA linear EST 03-AUG-2000 MtBB35B07F1 MtBB Medicago truncatula cDNA clone MtBB35B07 T3, mRNA	05 CCTGCACCTGTA 3	07 ThrAsnProVal 210	26 GTAGCTCCACCTGTAGCTCCA 406	CCACCTGCACCTGTAGCTCCACCTGTAGCTCCACCTGCACCTGTAGCTCCACCTGTAGCT 42		46 CACGTGCCTGCGCTGTTTGCACCAGTGGATGCACCTGCACCCCGGCTGCACCTGTAGCT 487	55	06 CA	135 HisThrProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAla 154	06-2 (1-322) x CNS03NQR (1-969)	COOPES: 0.926 Length: 969 120.50 Matches: 30 121.50 Matches: 30 121.50 Matches: 3 17.22* Conservative: 3 17.22* Indels: 21 17 Gaps: 2	/note="Genoscope sequence ID : CDBG04CB1LFF1~end : T7" 215 a 198 c 398 g 151 t 7 others	99883"	1969	<pre>genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. Location/Oualifiers</pre>	PR-2000) s a single read and was gen sequencing project of the	enoscope.	69)	Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis	Roese-Ciolius, n., daliidi, O., Dasiiva, C., Fizames, C., Fishet, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Waissenbach. T	Dacilys C Rivamoc C Richer

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AW586923
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                                                            EST318546 MHAM Medicago truncatula/Glomus versiforme library cDNA clone pMHAM-56C5, mRNA sequence. AW586923 AW586923.1 GI:7266437
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Contact: Pascal Gamas and Etienne-Pascal Journet, Laborato
Biologie Moleculaire des Relations Plantes Microorganismes
                Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed
  Eukaryota; mixed EST libraries.
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http://sequence.toulouse.inra.fr/Mtruncatula.html).
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Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mass-excised from phage stocks using ExAssit helper phage not propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Eyry, France)."
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/tissue_type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoc
Sinorhizobium meliloti"
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BQ147993 650 bp mRNA 1
NF049E09FL1F1070 Developing flower Medicago
NF049E09FL 5', mRNA sequence.
BQ147993
BQ147993.1 GI:20285052
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Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Noble EST name:N253964e
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More information is available at.
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                                                                                                                                                                                                                                                                 CCTCCTTTGGTGAAAACACCACCTTATCAATCACCACCTATAGTGAAGGCACCA 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhOI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 dypost-inoculation with Glomus versiforme. The library with made from a mixture of RNA from each of these stages." /lab_host="E. coli_strain_XLOLR"
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/clone="pMHAM~56C5"
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truncatula cDNA clone
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Pred. No.:
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula flower library
Unpublished (2001)
Contact: May GD
BI271940 THE BI271940 PARNA Linear EST 18-UTL-2001 NF016F08FL1F1074 Developing flower Medicago truncatula cDNA clone NF016F08FL 5', mRNA sequence.
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Plant Biology Division
Plant Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Noberts Noble Foundation
The Samuel Noberts Noble Foundation
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Insert Length: 650 Std Error: 0.00
Plate: 049 row: E column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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/db_xref="taxon:3880"
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Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580 221 7381
Fax: 580 221 7381
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 710 Std Error: 0.00
Plate: 016 row: F column: 08
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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BI271940.1 GI:14880858
                                                                                                                      GCACCTTCTCCCCCCTCTAGTGAAACCAACTCCACCTATTGTGAAATCACCT---CCTTCT
                                                                                                                                                                                  LysProThrProProValVal-------ValValLysLysProThrProThr 171
                                                                                                                                                                                                                                                 CCTTCTCCACCATTGGTAAAATCA-----CCACCTTATCAATCACCACCTATTGTTAAG
                                                                                                                                                                                                                                                                                              ProSerProValAlaValGlnSerSerArgProProValGlnGlnHisProAlaValGln 156
CCTCCTTTGGTGAAAACACCACCTTATCAATCACCACCTATAGTGAAGGCACCA
                                                    ProProValValGlnGlnProAlaProValAlaProProValThrGluAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Medicago truncatula"
/ob xref="taxon:3880".
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/clone="NR016F08FL"
/clone="NR016F08FL"
/clone="NR016F08FL"
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/dev_stage="Developing, fully-opened flowers and flowers
in early transition into pods."
/note="Vector: Lambda Zap; cDNA was prepared from polyA-
enriched, pooled samples of equivalent amounts of total
enriched, pooled samples of equivalent amounts of total
flowers transitioning into pods. The cDNA was
firectionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-Zap XR vector
using ExAssist helper phage and the E. coli strain
xL1-Blue MRF' (Stratagene). Excised plasmids were plated
using SOLR cells."

119 a 205 c 94 g 187 t 5 others
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Plate: LLAM12346 row: m column: 21
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BM457264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                 GlualaProPheAlaThrGlySerSerGlyValMet-----
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GlnPheArgTyrProValGlyAlaThrAsnProValValArgArgPheGlyThrAla 217
                                                                                                                                                               LysProThrProThrProProValValGlnGlnProAlaProValAlaProProValThr 186
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/clone="IMAGE:5583548"
/clone=lib="NIH MGC 92"
/tissue_type="embryonal carcinoma, cell line"
/lab host="UH108 (phage-resistant)"
/lab host="UH108 (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1;
Site_1: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
33 a 669 c 208 g 350 t
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  36
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Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
US Department of Regional Research Center
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence with phred score Seq primer: Stratagene SK primer.
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Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsi,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L., Stamova,B. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Early reproductive apex cDNA library from Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; ; Triticeae; Triticum.
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library Triticum m
TCCCCGCCGGCGTACAAGCCTGCCCCCAAGTCTCACCTCCGACGTACAAGCCATCCCCCA
                                   SerLysProThrTyrAsnSerThrSerGlySerGlySerHisArgThrSerGly-SerGl
                                                                               (1-322)
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                                                                                                                                                                                                                                                                                                                       /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoR1; Site 2: Xhol; The tissue, total RNA, and poly(A) RNA were prepared from apex at double-ridge stage to terminal-spikelet stage during transition from vegetative state to flower state, a cDNA library was made, and the cDNA clones were in vivo excised at the University of California, Davis (V. Echenique, B. Stamova, J. Dubcovsky). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Early reproductive apex"
/dev_stage="Seven week-old plants"
/lab_host="E. coli XLOLR"
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/clone_lib="Triticum monococcum early reproductive
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Bukaryota; Metazoa; Chordata; Craniata; Uertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

CB 1 (bases 1 to 909)

NH-MGC http://mgc.nci.nih.gov/.

RS NIH-MGC http://mgc.nci.nih.gov/.

RN NIH-MGC (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CGAP (Stanford)

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2512 row: c column: 15

High quality sequence stop: 589.
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                                         /tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: liver; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: liver; Vector: poTB7; Site_1: XhoI; Site_2:
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                                                                                                                                                                            AI484465
AI484465 tomato ovary, TAMU Lycopersicon esculentum cDN CLED1H16 similar to proline rich protein, mRNA sequence.
  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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AI484465.1 GI:4379836
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Generation of ESTs from tomato carpel tissue Unpublished (1999)
Other ESTs: EST242465
                                                                                    esculentum
BE460175
                                                                                                BE460175

443 bp mRNA linear EST 18-MAY
EST415467 tomato developing/immature green fruit Lycopersicon
esculentum cDNA clone cLEM9019, mRNA sequence.
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., H., Liang,F., Upton,J., Romning,C.M., Craven,M.B., Fujii,C.Y., C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., T
Lycopersicon
Eukaryota; Vi
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days post-anthesis to 5 days post-anthesis"
/dev_stage="5 days lue MRP'"
/lab_host="XLI-Blue MRP'"
/note="Yector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; CLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
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Streptophyta; Embryophyta; Tracheophyta;
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Email: http://www.genome.clemson.edu/orders/index.html
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
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ACCCATAGTT 402
                                                                 CCCCAATCCTCCCGTGGTAATACCACCACCCTACGTGCCAAGTCCTCCGGTTGTTACTCC
                                                                                                  aThrGlySerSerGlyValMetGlnPheArgTyr----ProValGlyAlaThrAs 208
                                                                                                                                     ACCACCTGTTGTGTCACCTCCAATCATTCCAACACCACCTATTGTCTCTCCACCTTTTGT
                                                                                                                                                                                                                                                                                                             ProValAlaValGlnSerSerArg-ProProValGlnGlnHisProAlaValGlnLys--
                                                                                                                                                                                                                                                                                                                                                prime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were tagged at 5 dpa (0.5 cm) and harvested at 7 day intervals through 35 dpa. Equal masses of tissue from each stage were combined (including seeds and locules) prior to mRNA isolation."
                                                                                                                                                                                                                                       ProThrProProValVal------ValValLysLysPro---ThrProTh
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/lab_host="SOLR"
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clone="cLEM9019"
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.

Genes galore: a sunmary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                         189
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MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DDE-PRL, Michigan State Univer
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: 517-353-9168
il: 22313tcn@ibm.cl.meu.edu
primer: T7 dye primer.
ProPheAlaThrGlySerSerGlyVal-MetGlnPheArgTyrProValGlyAlaThrAs
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/clone libe "Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_2: Not;
/note="Vector: lambda Zip-Lox; The cDNA siliques." The vector is BRL's lambda Zip-Lox. The cDNA sinserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

a 154 c 123 g 182 t 24 others
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/strain="var columbia"
/db_xref="taxon:3702"
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s thaliana cDNA clone 196014T7, mRNA
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Kaul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utt.
Feldblyum, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T6J16
Unpublished (2001)
Contact: Chris Town
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Faax: 301-838-0208
Email: cdtown@tigr.org
From Wash. U contig 1144. Ca
some non-Arabidopsis source
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                            ThrGlySerSerGlyValMetGlnPheArgTyrProValGlyAlaThrAsnProValVal 211
                                                                                ProProValValGlnGlnProAlaProValAlaProProValThrGluAlaProPheAla 191
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/strain="Columbia"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kyeong Tae Pih
Department of Plant Molecular Biology
Gyeongsang National Univ., Plant Molecular Biology and
Biotechnology Research Center
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Pih,K.T., Park,J.M., Jang,H.J., Kang,S.G., Piao,H.L. and Hwang,I.
EST of salt inducible mRNA in Arabidopsis thaliana
Unpublished (1997)
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ATU74096 NaCl-treated Arabidopsis subtraction library Arabidopsis
thaliana cDNA clone OSO01, mRNA sequence.
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Location/Qualifiers
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Tel: 82-591-751-5193
Fax: 82-591-759-9363
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